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OM protein - nucleic search, using frame_plus_p2n model

Run on: May 1, 2003, 05:43:36 ; Search time 829 Seconds
(without alignments)
111.178 Million cell updates/sec

Title: US-09-092-296-15
Perfect score: 399
Sequence: 1 MSGGLPLVLLTLTGSSHGT.....SGTSTVLHAKSQHHVVCNT 78

Scoring table: BLOSUM62

Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 746064 seqs, 590810554 residues

Total number of hits satisfying chosen parameters: 1492128

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

-Q /cgn2_1/USPTO.spool/US09092296/runat_30042003_133104_14466/app_query.fasta_1.263
-DB PublishedApplications.NA -OFMT=fastap -SUFFIX=p2n.rnpb -MINMATCH=0.1
-LOOPCL=0 -LOOPEXT=0 -UNITS=bits -SWAP=1 -END=1 -MATRIX=blosum62
-TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100
-THR_MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=ptc -HEAPSIZE=500 -MINLEN=0
-MAXLEN=2000000000 -USER=US09092296.ccg_1.1.88.atrunat_30042003_133104_14466
-ICPU=6 -ICPU3 -NO_XLPHY -NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT
-DSPBLOCK=100 -LONGLOG -DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10
-XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Published Applications.NA.*

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3:	/cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq.*
4:	/cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq.*
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6:	/cgn2_6/ptodata/2/pubpna/PCTUS_PUBCOMB.seq.*
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12:	/cgn2_6/ptodata/2/pubpna/US10_PUBCOMB.seq.*
13:	/cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq.*
14:	/cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	399	100.0	413	9	US-09-092-296-6
2	399	100.0	422	9	US-09-992-598-362
3	399	100.0	422	9	US-09-989-293A-362
4	399	100.0	422	9	US-10-063-547-65

5	399	100.0	422	9	US-09-989-735-362	Sequence 362, App
6	399	100.0	422	9	US-09-990-444-362	Sequence 362, App
7	399	100.0	422	9	US-09-989-730-362	Sequence 362, App
8	399	100.0	422	9	US-09-990-436-362	Sequence 362, App
9	399	100.0	422	9	US-09-991-181-362	Sequence 362, App
10	399	100.0	422	9	US-09-993-687-362	Sequence 362, App
11	399	100.0	422	9	US-09-989-734-362	Sequence 362, App
12	399	100.0	422	9	US-09-997-653-362	Sequence 362, App
13	399	100.0	422	9	US-10-174-590-241	Sequence 241, App
14	399	100.0	422	9	US-10-176-758-241	Sequence 241, App
15	399	100.0	422	9	US-10-063-616-65	Sequence 65, Appl
16	399	100.0	422	9	US-10-175-737-241	Sequence 241, App
17	399	100.0	422	9	US-09-993-667-362	Sequence 362, App
18	399	100.0	422	9	US-10-063-502-65	Sequence 65, Appl
19	399	100.0	422	9	US-10-173-706-241	Sequence 241, App
20	399	100.0	422	9	US-10-175-738-241	Sequence 241, App
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22	399	100.0	422	9	US-10-176-482-241	Sequence 241, App
23	399	100.0	422	9	US-10-176-757-241	Sequence 241, App
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25	399	100.0	422	9	US-10-180-552-241	Sequence 241, App
26	399	100.0	422	9	US-10-180-557-241	Sequence 241, App
27	399	100.0	422	9	US-09-990-438-362	Sequence 362, App
28	399	100.0	422	9	US-09-990-562-362	Sequence 362, App
29	399	100.0	422	9	US-09-997-428-362	Sequence 362, App
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32	399	100.0	422	9	US-10-174-572-241	Sequence 241, App
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34	399	100.0	422	9	US-10-174-582-241	Sequence 241, App
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36	399	100.0	422	9	US-10-175-739-241	Sequence 241, App
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38	399	100.0	422	9	US-10-175-743-241	Sequence 241, App
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42	399	100.0	422	9	US-10-176-750-241	Sequence 241, App
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44	399	100.0	422	9	US-10-176-987-241	Sequence 241, App
45	399	100.0	422	9	US-10-176-991-241	Sequence 241, App

ALIGNMENTS

RESULT 1
US-09-092-296-6
; Sequence 6, Application US/09092296
; Publication NO. US20020188114A1
GENERAL INFORMATION:
APPLICANT: BILLING-MEDEL, PATRICIA
APPLICANT: COHEN, MAURICE
APPLICANT: COLPITTS, TRACEY L.
APPLICANT: FRIEDMAN, PAULA N.
APPLICANT: KLASS, MICHAEL R.
APPLICANT: RUSSELL, JOHN C.
APPLICANT: STROUPE, STEPHEN D.
TITLE OF INVENTION: REAGENTS AND METHODS USEFUL FOR DETECTING DISEASES OF THE LUNG
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
ADDRESSEE: Abbott Laboratories
STREET: 100 Abbott Park Road
CITY: Abbott Park
STATE: IL
COUNTRY: USA
ZIP: 60064-3500
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:

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; APPLICATION NUMBER: US/09/092,296
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/048,810
; FILING DATE: 05-JUN-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Becker, Cheryl L.
; REGISTRATION NUMBER: 35,441
; REFERENCE/DOCKET NUMBER: 6104.US.01
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 847/935-1729
; TELEFAX: 847/938-2623
; TELEX:
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 413 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-09-092-296-6
Alignment Scores:
Pred. No.: Length: 413
Score: 399.00 Matches: 78
Percent Similarity: 100.00% Conservatives: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 9 Gaps: 0
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Oy 21 GlyProGlyMetThrLeuGlnLeuLysLeuLysGluSerPheLeuThrAsnSerSerTyr 40
Db 107 GGGCCGGGTATGACTTGTCACTGAAGCTGAAGAGTCTTTCGTGACAAATTCCTCCAT 166
Oy 41 GluSerSerPheLeuGlnLeuGluLysLeuCysLeuLeuHisLeuProSerGly 60
Db 167 GAGTCACAGCTTCTCGAAGTGTGTTGAAAGCTCTGCCCTCCCTCCATCTCCCTCAGGG 226
Oy 61 ThrSerValThrLeuHisHisAlaArgSerGlnHisHisValValCysAsnThr 78
Db 227 ACCAGCGTCACCTCCACCATGCAAGATCTCAACACCATGTGTGTGCAACACA 280
RESULT 2
US-09-992-598-362
; Sequence 362, Application US/09992598
; Patent No. US20020160384A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnovers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Kijavins, Ivar J.
; APPLICANT: Nepier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tamas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2730P1C20
; CURRENT APPLICATION NUMBER: US/09/992,598
; PRIOR FILING DATE: 2001-11-14
; PRIOR APPLICATION NUMBER: 60/049787
; PRIOR FILING DATE: 1997-06-16
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
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; PRIOR FILING DATE: 1998-06-10
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APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Kljavin, Ivar J.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paonli, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2730PIC66
CURRENT APPLICATION NUMBER: US/09/989,293A
CURRENT FILING DATE: 2001-11-20
PRIOR APPLICATION NUMBER: 60/049787
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; PRIOR APPLICATION NUMBER: 60/091633
; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/091978
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/091982
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/092182
; PRIOR FILING DATE: 1998-07-09

Alignment Scores:
Pred. No.: 4.15e-49 Length: 422
Score: 399.00 Matches: 78
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 9 Gaps: 0

US-09-092-296-15 (1-78) x US-09-989-293A-362 (1-422)

QY 1 MetGlySerGlyLeuProLeuValLeuLeuThrLeuLeuGlySerHisGlyThr 20
Db 58 ATGGGGCTGGGCTGCCCTTGCTCTTGACCTCTTGACCTCAATGGAACA 117
QY 21 GlyProGlyMetThrLeuGlnLeuLysLeuLysGluSerPheLeuThrAsnSerTyr 40
Db 118 GGGCCGGGTAIGACTTTCACACTGAAGCTGAAGAGTCTTTCTGACAAATTCCTCTAT 177
QY 41 GluSerSerPheLeuGluLeuLysLeuCysLeuLeuHisLeuProSerGly 60
Db 178 GAGTCCAGCTTCTGGAATTCCTTGAAAGCTCTGCCCTCTCCATCTCCCTTCAGGG 237
QY 61 ThrSerValThrLeuHisAlaArgSerGlnHisValValCysAsnThr 78
Db 238 ACCAGCGTCACCTCCACCATGCAAGATCTCAACACCATGTTGTCTGCAACACA 291

RESULT 4

US-10-063-547-65
; Sequence 65, Application US/10063547
; Publication No. US2002018263A1
; GENERAL INFORMATION:

; APPLICANT: Eaton, Dan L.
; APPLICANT: Flivaroff, Ellen
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Watanabe, Collin K.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE OF INVENTION: ACIDS ENCODING THE SAME
; CURRENT APPLICATION NUMBER: US/10/063,547
; CURRENT FILING DATE: 2002-05-02
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 170
; SEQ ID NO 65
; LENGTH: 422
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-063-547-65

Alignment Scores:

Pred. No.: 4.15e-49 Length: 422
Score: 399.00 Matches: 78
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 9 Gaps: 0

US-09-092-296-15 (1-78) x US-10-063-547-65 (1-422)

QY 1 MetGlySerGlyLeuProLeuValLeuLeuThrLeuLeuGlySerHisGlyThr 20
Db 58 ATGGGGCTGGGCTGCCCTTGCTCTTGACCTCTTGACCTCAATGGAACA 117
QY 21 GlyProGlyMetThrLeuGlnLeuLysLeuLysGluSerPheLeuThrAsnSerTyr 40
Db 118 GGGCCGGGTAIGACTTTCACACTGAAGCTGAAGAGTCTTTCTGACAAATTCCTCTAT 177
QY 41 GluSerSerPheLeuGluLeuLysLeuCysLeuLeuHisLeuProSerGly 60
Db 178 GAGTCCAGCTTCTGGAATTCCTTGAAAGCTCTGCCCTCTCCATCTCCCTTCAGGG 237
QY 61 ThrSerValThrLeuHisAlaArgSerGlnHisValValCysAsnThr 78
Db 238 ACCAGCGTCACCTCCACCATGCAAGATCTCAACACCATGTTGTCTGCAACACA 291

RESULT 5

US-09-989-735-362
; Sequence 362, Application US/09989735
; Publication No. US20020193299A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel

; APPLICANT: Watanabe, Collin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2730PIC61
; CURRENT FILING DATE: 2001-11-19
; PRIOR APPLICATION NUMBER: US/09/989,735
; PRIOR FILING DATE: 1997-06-16
; PRIOR APPLICATION NUMBER: 60/049787
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;; PRIOR APPLICATION NUMBER: 60/091982
;; PRIOR FILING DATE: 1998-07-07
;; PRIOR APPLICATION NUMBER: 60/092182
;; PRIOR FILING DATE: 1998-07-09

Alignment Scores:

Pred. No.:	4.15e-49	Length:	422
Score:	399.00	Matches:	78
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	9	Gaps:	0

US-09-092-296-15 (1-78) x US-09-990-444-362 (1-422)

Cy 1 MetGlySerGlyLeuProLeuValLeuLeuThrLeuLeuGlySerSerHisGlyThr 20
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Db 58 ATGGGCTCGGGTGGCCCTTGTCTCTCTGACCTCTTGACCTCTTGCGCAGCTCACATGGAACA 117
|||
Cy 21 GlyProGlyMetThrLeuGlnLeuLeuLeuGlySerPheLeuThrAsnSerSerTyr 40
|||||
Db 118 GGCGCGGTATGACTTTGCAACTGAAGCTGAAGAGTCTTTCTGACAAATTCCTCTAT 177
|||
Cy 41 GluSerSerPheLeuGluLeuLeuGluLeuLeuGluLeuLeuLeuHisLeuProSerGly 60
|||||
Db 178 GAGTCAGCTTCCTGGAATTTGCTTGAAAAGCTCTGCGCTCTCTCTCTCTCTCTCTCAGG 237
|||
Cy 61 ThrSerValThrLeuHisHisAlaArgSerGlnHisHisValValCysAsnThr 78
|||||
Db 238 ACAGCGTCACCCCTCCACCATCTCAACACCATGTTGTCTGCAACACA 291
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RESULT 7

US-09-989-730-362
; Sequence 362, Application US/09989730
; Publication No. US20020197674A1
; GENERAL INFORMATION:

APPLICANT: Ashkenazi, Avi J.	PRIOR APPLICATION NUMBER: 60/088161
APPLICANT: Baker, Kevin P.	PRIOR FILING DATE: 1998-06-05
APPLICANT: Botstein, David	PRIOR APPLICATION NUMBER: 60/088202
APPLICANT: Desnoyers, Luc	PRIOR FILING DATE: 1998-06-05
APPLICANT: Eaton, Dan L.	PRIOR APPLICATION NUMBER: 60/088212
APPLICANT: Ferrara, Napoleone	PRIOR FILING DATE: 1998-06-05
APPLICANT: Fong, Sherman	PRIOR APPLICATION NUMBER: 60/088217
APPLICANT: Gerber, Hanspeter	PRIOR FILING DATE: 1998-06-05
APPLICANT: Gerritsen, Mary E.	PRIOR APPLICATION NUMBER: 60/088655
APPLICANT: Goddard, Audrey	PRIOR FILING DATE: 1998-06-09
APPLICANT: Godowski, Paul J.	PRIOR APPLICATION NUMBER: 60/088734
APPLICANT: Grimaldi, J. Christopher	PRIOR FILING DATE: 1998-06-10
APPLICANT: Gurney, Austin L.	PRIOR APPLICATION NUMBER: 60/088738
APPLICANT: Kijaviri, Iwar J.	PRIOR FILING DATE: 1998-06-10
APPLICANT: Napier, Mary A.	PRIOR APPLICATION NUMBER: 60/088742
APPLICANT: Pan, James	PRIOR FILING DATE: 1998-06-10
APPLICANT: Peoni, Nicholas F.	PRIOR APPLICATION NUMBER: 60/088810
APPLICANT: Roy, Margaret Ann	PRIOR FILING DATE: 1998-06-10
APPLICANT: Stewart, Timothy A.	PRIOR APPLICATION NUMBER: 60/088822
APPLICANT: Tumas, Daniel	PRIOR FILING DATE: 1998-06-10
APPLICANT: Watanabe, Colin K.	PRIOR APPLICATION NUMBER: 60/088826
APPLICANT: Williams, P. Mickey	PRIOR FILING DATE: 1998-06-10
APPLICANT: Wood, William I.	PRIOR APPLICATION NUMBER: 60/088858
APPLICANT: Zhang, Zemin	PRIOR FILING DATE: 1998-06-11
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic	PRIOR APPLICATION NUMBER: 60/088861
TITLE OF INVENTION: Acids Encoding the Same	PRIOR FILING DATE: 1998-06-11
FILE REFERENCE: P2730PIC69	PRIOR APPLICATION NUMBER: 60/088876
CURRENT APPLICATION NUMBER: US/09/989,730	PRIOR FILING DATE: 1998-06-11
CURRENT FILING DATE: 2001-11-20	PRIOR APPLICATION NUMBER: 60/089105
PRIOR APPLICATION NUMBER: 60/049787	PRIOR FILING DATE: 1998-06-12
PRIOR FILING DATE: 1997-06-16	PRIOR APPLICATION NUMBER: 60/089440
PRIOR APPLICATION NUMBER: 60/062250	PRIOR FILING DATE: 1998-06-16
PRIOR FILING DATE: 1997-10-17	PRIOR APPLICATION NUMBER: 60/089512
PRIOR APPLICATION NUMBER: 60/065186	PRIOR FILING DATE: 1998-06-16
PRIOR FILING DATE: 1997-11-12	PRIOR APPLICATION NUMBER: 60/089514
PRIOR APPLICATION NUMBER: 60/065311	PRIOR FILING DATE: 1998-06-16
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;; PRIOR FILING DATE: 1998-07-09

Alignment Scores:
Pred. No.: 4.15e-49 Length: 422
Score: 399.00 Matches: 78
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 9 Gaps: 0

US-09-092-296-15 (1-78) x US-09-989-730-362 (1-422)

QY 1 MetGlySerGlyLeuProLeuValLeuLeuThrLeuGlySerHisGlyThr 20
DB 58 ATGGGGCTGGGCTGCCCTTGCTCTCTTGACCCCTCTTGGCAGCTCATGGACA 117
QY 21 GlyProGlyMetThrLeuGlnLeuLysLeuLysGluSerPheLeuThrAsnSerSerTyr 40
DB 118 GGCCCGGATGACTTTGCAACTGGAAGCTGAAGGAGCTTTTCTGACAAATTCCTCTAT 177
QY 41 GluSerSerPheLeuGluLeuLeuGluLysLeuCysLeuLeuLeuHisLeuProSerGly 60
DB 178 GAGTCCAGCTCTCGAATGCTTGAAGGCTCTGCCCTCTCTCTCTCTCTCTCAGG 237

OY 61 ThrSerValThrLeuHisHisAaArgSerGlnHisHisValValValCysAsnThr 78
DB 238 ACCAGCTCACCTCCACATGCAAGATCTCAACACCATGTTGTGTGCACACA 291
RESULT 8
US-09-990-436-362
; Sequence 362, Application US/09990436
; Publication No. US20020198148A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
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; APPLICANT: Gurney, Austin L.
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; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
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; CURRENT APPLICATION NUMBER: US/09/990.436
; CURRENT FILING DATE: 2001-11-14
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; PRIOR APPLICATION NUMBER: 60/091982
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/092182
; PRIOR FILING DATE: 1998-07-09

Alignment Scores:

Pred. No.:	4.15e-49	Length:	422
Score:	399.00	Matches:	78
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	9	Gaps:	0

US-09-092-296-15 (1-78) x US-09-990-436-362 (1-422)

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Db 118 GGGCGGGTATGACTTGCAGCTGAAGTCTTTCTGACAAATTCCTCCAT 177
Qy 41 GluSerSerPheLeuGlnLeuGluLysLeuLysCysLeuLeuLeuHisLeuProSerGly 60
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Db 178 GAGTCCAGCTCTCTGAAATGCTTGAAGAAGCTCTGCCTCCCTCCATCTCCCTTCAGGG 237
Qy 61 ThrSerValThrLeuHisHisAlaArgSerGlnHisHisValValCysAsnThr 78
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Db 238 ACCAGCTCACCTCCACATGCAAGATCTCACACCATGTTGTCTGCAACACA 291

RESULT 9
US-09-991-181-362
; Sequence 362, Application US/09991181
; Publication No. US20020197613A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Kijavlin, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2730PIC53
; CURRENT APPLICATION NUMBER: US/09/991,181
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; PRIOR APPLICATION NUMBER: 60/091982
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/092182
; PRIOR FILING DATE: 1998-07-09
; PRIOR FILING DATE: 1998-07-09

Alignment Scores:

Pred. No.: 4,15e-49 Length: 422
Score: 399.00 Matches: 78
Percent Similarity: 100.00% Conservatives: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 9 Gaps: 0
US-09-092-296-15 (1-78) x US-09-991-181-362 (1-422)
Qy 1 MetGlySerGlyLeuProLeuValLeuLeuThrLeuLeuGlySerSerHisGlyThr 20
Db 58 ATGGGCTCGGGCTGCCCTTGCTCTGACCTCTTGAGCTCTGGAGCTCATGGAACA 117
Qy 21 GlyProGlyMetThrLeuGlnLeuLysLeuLysGluSerPheLeuThrAsnSerSerTyr 40
Db 118 GGCGCGGTATGACTTTGCAACTGAAGCTGAAGGAGTCTTTCTGACAAATTCCTCTAT 177
Qy 41 GluSerSerPheLeuGlnLeuLeuGluLysLeuLysLeuCysLeuLeuHisLeuProSerGly 60
Db 178 GAGTCAGCTTCTGGAAATGCTTGAAAAGCTCTGCTCTCTCCATCTCCTTCAGGG 237
Qy 61 ThrSerValThrLeuHisHisAlaArgSerGlnHisHisValValCysAsnThr 78
Db 238 ACCAGCGTCACCTCCACCATGCAAGATCTCAACACCATGTTGTCTGCAACACA 291
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US-09-993-687-362
; Sequence 362, Application US/09993687
; Publication No. US20020198149A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
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; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2730P1C11
; CURRENT APPLICATION NUMBER: US/09/993,687
; CURRENT FILING DATE: 2002-11-14
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; PRIOR APPLICATION NUMBER: 60/091982
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/092182
; PRIOR FILING DATE: 1998-07-09

Alignment Scores:
Pred. No.: 4.15e-49 Length: 422
Score: 399.00 Matches: 78
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
Db: Gaps: 0

US-09-092-296-15 (1-78) x US-09-993-687-362 (1-422)

Qy 1 MetGlySerGlyLeuProLeuValLeuLeuLeuThrLeuLeuGlySerHisGlyThr 20
Db 58 ATGGGGTCTGGGCTGCCCTTGTCTCTTGGACCTCTTGGCAGCTCACATGGAACA 117

Qy 21 GlyProGlyMetThrLeuGlnLeuLysLeuGluSerPheLeuThrAsnSerSerTyr 40
Db 118 GGGCCGGGTGACTTGGCACTGAAGCTGAAGGAGCTTTTCTGACAAATTCCTCTAT 177

Qy 41 GluSerSerPheLeuLeuLeuLysLeuCysLeuLeuHisLeuProSerGly 60
Db 178 GAGTCAGCTCTCGAATGCTTGAAGCTCTGCTCTCTCTCATCTCCCTTCAGGG 237

Qy 61 ThrSerValThrLeuHisHisAlaArgSerGlnHisHisValValCysAsnThr 78
Db 238 ACCAGGTCACCTCCACCATGCAAGATCTCAACACCACTGTGTGTGCAACACA 291

RESULT 11
US-09-989-734-362
; Sequence 362, Application US/0989734
; Publication No. US20030003531A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
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; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Kijavio, Ivar J.
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; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P273091C64
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; PRIOR APPLICATION NUMBER: 60/088212
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/088217
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/088655
; PRIOR FILING DATE: 1998-06-09
; PRIOR APPLICATION NUMBER: 60/088734
; PRIOR FILING DATE: 1998-06-10
; PRIOR APPLICATION NUMBER: 60/088738
; PRIOR FILING DATE: 1998-06-10
; PRIOR APPLICATION NUMBER: 60/088742
; PRIOR FILING DATE: 1998-06-10
; PRIOR APPLICATION NUMBER: 60/088810
; PRIOR FILING DATE: 1998-06-10
; PRIOR APPLICATION NUMBER: 60/088824
; PRIOR FILING DATE: 1998-06-10
; PRIOR APPLICATION NUMBER: 60/088826
; PRIOR FILING DATE: 1998-06-10
; PRIOR APPLICATION NUMBER: 60/088858
; PRIOR FILING DATE: 1998-06-11
; PRIOR APPLICATION NUMBER: 60/088861
; PRIOR FILING DATE: 1998-06-11
; PRIOR APPLICATION NUMBER: 60/088876
; PRIOR FILING DATE: 1998-06-11
; PRIOR APPLICATION NUMBER: 60/089105
; PRIOR FILING DATE: 1998-06-12
; PRIOR APPLICATION NUMBER: 60/089440
; PRIOR FILING DATE: 1998-06-16
; PRIOR APPLICATION NUMBER: 60/089512

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;
; PRIOR FILING DATE: 1998-06-16
; PRIOR APPLICATION NUMBER: 60/089514
; PRIOR FILING DATE: 1998-06-16
; PRIOR APPLICATION NUMBER: 60/089532
; PRIOR FILING DATE: 1998-06-17
; PRIOR APPLICATION NUMBER: 60/089538
; PRIOR FILING DATE: 1998-06-17
; PRIOR APPLICATION NUMBER: 60/089598
; PRIOR FILING DATE: 1998-06-17
; PRIOR APPLICATION NUMBER: 60/089599
; PRIOR FILING DATE: 1998-06-17
; PRIOR APPLICATION NUMBER: 60/089600
; PRIOR FILING DATE: 1998-06-17
; PRIOR APPLICATION NUMBER: 60/089653
; PRIOR FILING DATE: 1998-06-17
; PRIOR APPLICATION NUMBER: 60/089801
; PRIOR FILING DATE: 1998-06-18
; PRIOR APPLICATION NUMBER: 60/089907
; PRIOR FILING DATE: 1998-06-18
; PRIOR APPLICATION NUMBER: 60/089908
; PRIOR FILING DATE: 1998-06-18
; PRIOR APPLICATION NUMBER: 60/089947
; PRIOR FILING DATE: 1998-06-19
; PRIOR APPLICATION NUMBER: 60/089948
; PRIOR FILING DATE: 1998-06-19
; PRIOR APPLICATION NUMBER: 60/089952
; PRIOR FILING DATE: 1998-06-19
; PRIOR APPLICATION NUMBER: 60/090246
; PRIOR FILING DATE: 1998-06-22
; PRIOR APPLICATION NUMBER: 60/090252
; PRIOR FILING DATE: 1998-06-22
; PRIOR APPLICATION NUMBER: 60/090254
; PRIOR FILING DATE: 1998-06-22
; PRIOR APPLICATION NUMBER: 60/090349
; PRIOR FILING DATE: 1998-06-23
; PRIOR APPLICATION NUMBER: 60/090355
; PRIOR FILING DATE: 1998-06-23
; PRIOR APPLICATION NUMBER: 60/090429
; PRIOR FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: 60/090431
; PRIOR FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: 60/090435
; PRIOR FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: 60/090444
; PRIOR FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: 60/090445
; PRIOR FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: 60/090472
; PRIOR FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: 60/090535
; PRIOR FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: 60/090540
; PRIOR FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: 60/090542
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; PRIOR FILING DATE: 1998-06-25
; PRIOR APPLICATION NUMBER: 60/090678
; PRIOR FILING DATE: 1998-06-25
; PRIOR APPLICATION NUMBER: 60/090690
; PRIOR FILING DATE: 1998-06-25
; PRIOR APPLICATION NUMBER: 60/090694
; PRIOR FILING DATE: 1998-06-25
; PRIOR APPLICATION NUMBER: 60/090695
; PRIOR FILING DATE: 1998-06-25
; PRIOR APPLICATION NUMBER: 60/090696
; PRIOR FILING DATE: 1998-06-25
; PRIOR APPLICATION NUMBER: 60/090862
; PRIOR FILING DATE: 1998-06-26
; PRIOR APPLICATION NUMBER: 60/090863
; PRIOR FILING DATE: 1998-06-26

;
; PRIOR APPLICATION NUMBER: 60/091360
; PRIOR FILING DATE: 1998-07-01
; PRIOR APPLICATION NUMBER: 60/091478
; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/091544
; PRIOR FILING DATE: 1998-07-01
; PRIOR APPLICATION NUMBER: 60/091519
; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/091626
; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/091633
; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/091978
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/091982
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/092182
; PRIOR FILING DATE: 1998-07-09

Alignment Scores:
Pred. No.: 4,15e-49 Length: 422
Score: 399.00 Matches: 78
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 9 Gaps: 0

US-09-092-296-15 (1-78) x US-09-989-734-362 (1-422)

QY 1 MetGlySerGlyLeuProLeuValLeuLeuLeuThrLeuLeuGlySerSerHisGlyThr 20
|||||
Db 58 ATGGGGTCTGGGCTGCCCTTGTCTCTTGACCTCTTGGCAGCTCAGTGAACA 117
|||||
QY 21 GlyProGlyMetThrLeuGlnLeuLysLeuLysGluSerPheLeuThrAsnSerSerTyr 40
|||||
Db 118 GGGCGGGTATGACTTTGCAACTGAAGCTGAAGAGTCTTTCTGACAAATTCCTCTAT 177
|||||
QY 41 GluSerSerPheLeuGlnLeuLeuGluLysLeuCysLeuLeuHisLeuProSerGly 60
|||||
Db 178 GAGTCCAGCTTCTCGGAATTGCTTGAAAAGCTCTGCTCTCTCCATCTCCCTTCAGGG 237
|||||
QY 61 ThrSerValThrLeuHisHisIalaargSerGlnHisHisValValCysAsnThr 78
|||||
Db 238 ACCAGCGTCACTCCCTCCACCATGCAAGATCTCAACACCATGTTGTCTGCAACACA 291
|||||

RESULT 12
US-09-997-653-362
; Sequence 362, Application US/09997653
; Publication No. US20030008297A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Kijavlin, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Pacini, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tamas, Daniel
; APPLICANT: Watanabe, Collin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.

APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2730PIC38
CURRENT APPLICATION NUMBER: US/09/997,653
CURRENT FILING DATE: 2001-11-15
PRIOR APPLICATION NUMBER: 60/049787
PRIOR FILING DATE: 1997-06-16
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/065186
PRIOR FILING DATE: 1997-11-12
PRIOR APPLICATION NUMBER: 60/065311
PRIOR FILING DATE: 1997-11-13
PRIOR APPLICATION NUMBER: 60/066770
PRIOR FILING DATE: 1997-11-24
PRIOR APPLICATION NUMBER: 60/075945
PRIOR FILING DATE: 1998-02-25
PRIOR APPLICATION NUMBER: 60/078910
PRIOR FILING DATE: 1998-03-20
PRIOR APPLICATION NUMBER: 60/083322
PRIOR FILING DATE: 1998-04-28
PRIOR APPLICATION NUMBER: 60/084600
PRIOR FILING DATE: 1998-05-07
PRIOR APPLICATION NUMBER: 60/087106
PRIOR FILING DATE: 1998-05-28
PRIOR APPLICATION NUMBER: 60/087607
PRIOR FILING DATE: 1998-06-02
PRIOR APPLICATION NUMBER: 60/087609
PRIOR FILING DATE: 1998-06-02
PRIOR APPLICATION NUMBER: 60/087759
PRIOR FILING DATE: 1998-06-02
PRIOR APPLICATION NUMBER: 60/087827
PRIOR FILING DATE: 1998-06-03
PRIOR APPLICATION NUMBER: 60/088021
PRIOR FILING DATE: 1998-06-04
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PRIOR FILING DATE: 1998-06-04
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PRIOR FILING DATE: 1998-06-04
PRIOR APPLICATION NUMBER: 60/088030
PRIOR FILING DATE: 1998-06-04
PRIOR APPLICATION NUMBER: 60/088033
PRIOR FILING DATE: 1998-06-04
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PRIOR FILING DATE: 1998-06-05
PRIOR APPLICATION NUMBER: 60/088202
PRIOR FILING DATE: 1998-06-05
PRIOR APPLICATION NUMBER: 60/088212
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PRIOR APPLICATION NUMBER: 60/088217
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PRIOR APPLICATION NUMBER: 60/088655
PRIOR FILING DATE: 1998-06-09
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PRIOR APPLICATION NUMBER: 60/088861
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PRIOR APPLICATION NUMBER: 60/088876
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PRIOR APPLICATION NUMBER: 60/089105
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PRIOR APPLICATION NUMBER: 60/089440
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PRIOR FILING DATE: 1998-06-17
PRIOR APPLICATION NUMBER: 60/089600
PRIOR FILING DATE: 1998-06-17
PRIOR APPLICATION NUMBER: 60/089653
PRIOR FILING DATE: 1998-06-17
PRIOR APPLICATION NUMBER: 60/089801
PRIOR FILING DATE: 1998-06-18
PRIOR APPLICATION NUMBER: 60/089907
PRIOR FILING DATE: 1998-06-18
PRIOR APPLICATION NUMBER: 60/089908
PRIOR FILING DATE: 1998-06-18
PRIOR APPLICATION NUMBER: 60/089947
PRIOR FILING DATE: 1998-06-19
PRIOR APPLICATION NUMBER: 60/089948
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PRIOR APPLICATION NUMBER: 60/090254
PRIOR FILING DATE: 1998-06-22
PRIOR APPLICATION NUMBER: 60/090349
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PRIOR APPLICATION NUMBER: 60/090355
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PRIOR APPLICATION NUMBER: 60/090431
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090435
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PRIOR FILING DATE: 1998-06-24
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PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090535
PRIOR FILING DATE: 1998-06-24
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PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090542
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090557
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090676
PRIOR FILING DATE: 1998-06-25
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PRIOR FILING DATE: 1998-06-25
PRIOR APPLICATION NUMBER: 60/090690
PRIOR FILING DATE: 1998-06-25

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; FILE REFERENCE: P3430RIC42
; CURRENT APPLICATION NUMBER: US/10/174,590
; PRED FILING DATE: 2002-06-18
; PRIOR APPLICATION REMOVED - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 241
; LENGTH: 422
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-174-590-241
```

Alignment Scores:

```
Pred. No.: 4,15e-49 Length: 422
Score: 399.00 Matches: 78
Percent Similarity: 100.00% Conservatives: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 9 Gaps: 0
```

US-09-092-296-15 (1-78) x US-09-997-653-362 (1-422)

```
QY 1 MetGlySerGlyLeuProLeuValLeuLeuThrLeuGlySerSerHisGlyThr 20
Db 58 ATGGGGTCTGGGCTGCCCTTGTCTTGTGACCTCTTGGCAGCTCAGATGGACA 117
QY 21 GlyProGlyMetThrLeuGlnLeuLysLeuLysGluSerPheLeuThrAsnSerTyr 40
Db 118 GGGCGGGTATGACTTGGCAACTGAGCTGAGGAGTCTTTCTGACAAATCTCTCTAT 177
QY 41 GluSerSerPheLeuGluLeuLysLeuLysLeuCysLeuLeuHisLeuProSerGly 60
Db 178 GAGTCAGCTTCTGGAATGCTTGAAGAGCTTGCCTCTCTCCATCTCCCTTCAGGG 237
QY 61 ThrSerValThrLeuHisHisAlaArgSerGlnHisHisValValCysAsnThr 78
Db 238 ACCAGCGTCCACCTCCACCATGCAAGATCTCAACACCATGTTGTCTGCAACACA 291
```

RESULT 13

```
US-10-174-590-241
; Sequence 241, Application US/10174590
; Publication No. US2003008352A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Chen, Jian
; APPLICANT: Desnoyers, Luc
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Smith, Victoria
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
```

```
; FILE REFERENCE: P3430RIC42
; CURRENT APPLICATION NUMBER: US/10/174,590
; PRED FILING DATE: 2002-06-18
; PRIOR APPLICATION REMOVED - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 241
; LENGTH: 422
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-174-590-241
```

Alignment Scores:

```
Pred. No.: 4,15e-49 Length: 422
Score: 399.00 Matches: 78
Percent Similarity: 100.00% Conservatives: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 9 Gaps: 0
```

US-09-092-296-15 (1-78) x US-10-174-590-241 (1-422)

```
QY 1 MetGlySerGlyLeuProLeuValLeuLeuThrLeuGlySerSerHisGlyThr 20
Db 58 ATGGGGTCTGGGCTGCCCTTGTCTTGTGACCTCTTGGCAGCTCAGATGGACA 117
QY 21 GlyProGlyMetThrLeuGlnLeuLysLeuLysGluSerPheLeuThrAsnSerTyr 40
Db 118 GGGCGGGTATGACTTGGCAACTGAGCTGAGGAGTCTTTCTGACAAATCTCTCTAT 177
QY 41 GluSerSerPheLeuGluLeuLysLeuLysLeuCysLeuLeuHisLeuProSerGly 60
Db 178 GAGTCAGCTTCTGGAATGCTTGAAGAGCTTGCCTCTCTCCATCTCCCTTCAGGG 237
QY 61 ThrSerValThrLeuHisHisAlaArgSerGlnHisHisValValCysAsnThr 78
Db 238 ACCAGCGTCCACCTCCACCATGCAAGATCTCAACACCATGTTGTCTGCAACACA 291
```

RESULT 14

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US-10-176-758-241
; Sequence 241, Application US/10176758
; Publication No. US2003008353A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Chen, Jian
; APPLICANT: Desnoyers, Luc
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Smith, Victoria
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3430RIC104
; CURRENT APPLICATION NUMBER: US/10/176,758
; PRED FILING DATE: 2002-06-21
; PRIOR APPLICATION REMOVED - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 241
; LENGTH: 422
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-176-758-241
```

Alignment Scores:

```
Pred. No.: 4,15e-49 Length: 422
Score: 399.00 Matches: 78
Percent Similarity: 100.00% Conservatives: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 9 Gaps: 0
```

Search completed: May 1, 2003, 06:19:31
Job time : 831 secs

US-09-092-296-15 (1-78) x US-10-176-758-241 (1-422)

QY	1	MetGlySerGlyLeuProLeuValLeuLeuThrLeuLeuGlySerSerHisGlyThr	20
DB	58	ATGGGGTCTGGGCTGGCCCTTCTCTCTTGACCCCTTGGCAGCTCACATGAACA	117
QY	21	GlyProGlyMetThrLeuGlnLeuLysLeuLysGluSerPheLeuThrAsnSerSerTyr	40
DB	118	GGCGCGGTATGACTTTGCAACTGAAGCTGAAGGAGCTTTTCTGACAAATTCCTCCTAT	177
QY	41	GluSerSerPheLeuGluLeuLeuGluLysLeuCysLeuLeuHisLeuProSerGly	60
DB	178	GAGTCCAGCTTCCTGGAATTGCTTGAAAGCTCTGCCCTCCTCCATCTCCCTTCAGGG	237
QY	61	ThrSerValThrLeuHisHisAlaArgSerGlnHisHisValValCysAsnThr	78
DB	238	ACCAGCGTCACCCCTCCACCATGCAAGATCTCAACACCATGTTGTTCTGCAACACA	291

RESULT 15
US-10-063-616-65
; Sequence 65, Application US/10063616
; Publication No. US20030013855A1
; GENERAL INFORMATION:
; APPLICANT: Eaton, Dan L.
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3230R1C1
; CURRENT APPLICATION NUMBER: US/10/063, 616
; CURRENT FILING DATE: 2002-05-03
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 170
; SEQ ID NO 65
; LENGTH: 422
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-063-616-65

Alignment Scores:
Pred. No.: 4,15e-49 Length: 422
Score: 399.00 Matches: 78
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 9 Gaps: 0

US-09-092-296-15 (1-78) x US-10-063-616-65 (1-422)

QY	1	MetGlySerGlyLeuProLeuValLeuLeuThrLeuLeuGlySerSerHisGlyThr	20
DB	58	ATGGGGTCTGGGCTGGCCCTTCTCTCTTGACCCCTTGGCAGCTCACATGAACA	117
QY	21	GlyProGlyMetThrLeuGlnLeuLysLeuLysGluSerPheLeuThrAsnSerSerTyr	40
DB	118	GGCGCGGTATGACTTTGCAACTGAAGCTGAAGGAGCTTTTCTGACAAATTCCTCCTAT	177
QY	41	GluSerSerPheLeuGluLeuLeuGluLysLeuCysLeuLeuHisLeuProSerGly	60
DB	178	GAGTCCAGCTTCCTGGAATTGCTTGAAAGCTCTGCCCTCCTCCATCTCCCTTCAGGG	237
QY	61	ThrSerValThrLeuHisHisAlaArgSerGlnHisHisValValCysAsnThr	78
DB	238	ACCAGCGTCACCCCTCCACCATGCAAGATCTCAACACCATGTTGTTCTGCAACACA	291

GenCore version 5.1.5
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OM protein - nucleic search, using frame_plus_p2n model

Run on: May 1, 2003, 05:21:26 ; Search time 62 Seconds
(without alignments)
385.819 Million cell updates/sec

Title: US-09-092-296-15

Perfect score: 399

Sequence: 1 MGSGLPVLVLLTLGSSHGT.....SGTSTVLHARSQHVVVNCVT 78

Scoring table:

BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 441362 seqs, 153338381 residues

Total number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

-MODEL=frame+ p2n.model -DEV=xlp
-Q=/cgn2_1/USPTO.spool/US09092296/runat_30042003_133103_14436/app_query.fasta_1.263
-DB=Issued_Patents.NA -QMT=fastap -SUFFIX=p2n.rni -MINMATCH=0.1 -LOPCL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15
-MODE=LOCAL -OUTPM=pt -NORM=ext -HEADSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US09092296.@cgn_1_36@runat_30042003_133103_14436 -NCPU=6 -ICPU=3
-NO_XLPXY -NO_MAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIME=30 -THREADS=1 -XGAPOP=10 -XGAPOP=0.5 -FGAPOP=6
-FGAPOP=7 -YGAPOP=10 -YGAPOP=0.5 -DELOP=6 -DELEXT=7

Database :

Issued_Patents.NA.*
1: /cgn2_6/ptodata/2/ina/5A_COMB.seq.*
2: /cgn2_6/ptodata/2/ina/5B_COMB.seq.*
3: /cgn2_6/ptodata/2/ina/6A_COMB.seq.*
4: /cgn2_6/ptodata/2/ina/6B_COMB.seq.*
5: /cgn2_6/ptodata/2/ina/PCTUS_COMB.seq.*
6: /cgn2_6/ptodata/2/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
C 1	69	17.3	2520	1	US-08-405-254-9
C 2	69	17.3	4000	4	US-09-780-049-18
C 3	68.5	17.2	9751	2	US-09-238-303-7
C 4	68	17.0	3195	2	US-08-951-648-5
C 5	68	17.0	3195	3	US-09-174-437-5
C 6	68	17.0	111282	4	US-09-754-250-3
C 7	67.5	16.9	2835	4	US-09-134-001C-1515
C 8	67.5	16.9	3561	4	US-09-134-001C-1685
C 9	67.5	16.9	5892	3	US-09-134-001C-1626
C 10	67	16.8	5892	3	US-08-755-587-27
C 11	67	16.8	7240	3	US-08-755-587-15
C 12	67	16.8	11283	2	US-08-603-753D-3

C 13	67	16.8	11283	3	US-09-099-753-3
C 14	67	16.8	11283	4	US-08-986-106-3
C 15	67	16.8	11385	2	US-08-639-501-1
C 16	67	16.8	11385	3	US-09-044-946-1
C 17	67	16.8	11385	3	US-09-044-908-1
C 18	66.5	16.7	1867	1	US-07-772-087-1
C 19	66	16.5	1910	2	US-09-009-438-1
C 20	66	16.5	1910	3	US-09-207-493-1
C 21	65	16.3	4389	2	US-08-951-648-3
C 22	65	16.3	4389	3	US-09-174-437-3
C 23	64.5	16.2	2680	1	US-08-588-821-1
C 24	64.5	16.2	2680	1	US-08-915-214-1
C 25	64.5	16.2	2680	2	US-09-005-532-1
C 26	64.5	16.2	2680	3	US-09-255-888-1
C 27	64.5	16.2	2680	4	US-09-312-748-3
C 28	64	16.0	1687	4	US-08-630-915A-191
C 29	64	16.0	4002	2	US-08-231-193A-53
C 30	64	16.0	4002	2	US-08-486-273A-53
C 31	64	16.0	4002	3	US-08-480-474-53
C 32	64	16.0	4002	3	US-08-940-086A-53
C 33	64	16.0	4002	4	US-08-940-035A-53
C 34	64	16.0	4002	4	US-08-935-105A-53
C 35	64	16.0	4002	4	US-09-648-797-53
C 36	64	16.0	4017	2	US-08-231-193A-49
C 37	64	16.0	4017	2	US-08-486-273A-49
C 38	64	16.0	4017	3	US-08-480-474-49
C 39	64	16.0	4017	3	US-08-940-086A-49
C 40	64	16.0	4017	4	US-08-940-035A-49
C 41	64	16.0	4017	4	US-08-935-105A-49
C 42	64	16.0	4017	4	US-09-648-797-49
C 43	64	16.0	4053	2	US-08-231-193A-47
C 44	64	16.0	4053	2	US-08-486-273A-47
C 45	64	16.0	4053	3	US-08-480-474-47

ALIGNMENTS

RESULT 1

US-08-405-254-9/c
; Sequence 9, Application US/08405254
; Patent No. 5773288
; GENERAL INFORMATION:
; APPLICANT: BRIGGS, STEVEN P.
; TITLE OF INVENTION: PLANT GENES AFFECTING GIBBERELLIC ACID
; TITLE OF INVENTION: BIOSYNTHESIS
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FOLEY & LARDNER
; STREET: 3000 K STREET, NW, SUITE 500
; CITY: WASHINGTON
; STATE: DC
; COUNTRY: USA
; ZIP: 20007
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/405,254
; FILING DATE: 16-MAR-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/261,465
; FILING DATE: 17-JUN-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: BENT, STEPHEN A.
; REGISTRATION NUMBER: 29,768
; REFERENCE/DOCKET NUMBER: 33229/299/PIHI
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)672-5300
; TELEFAX: (202)672-5399

```
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2520 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-405-254-9

Alignment Scores:
Pred. No.: 16 Length: 2520
Score: 69.00 Matches: 26
Percent Similarity: 37.76% Conservativeness: 11
Best Local Similarity: 26.53% Mismatches: 29
Query Match: 17.29% Indels: 32
DB: 1 Gaps: 3

US-09-092-296-15 (1-78) x US-08-405-254-9 (1-2520)
QY 7 LeuValLeuLeuThrLeuLeuGlySerSerHisGlyThrGlyProGlyMet----- 24
Db 2128 CTCCTCCCTGCTGCTGCTTTGGCCACGGATACGGATCGGATCGGACCTG 2059
QY 25 -----ThrLeuGlnLeuLysLeuLysSerPheLeuThrLeuThrLeuSerSerTyGluSer 42
Db 2068 ATTGACGAGCTGCAGCTGCAGCGCAAGTCAAGACGAGAAAGCAAGACGCGGTGAGGAAC 2009
QY 43 SerPheLeuGluLeuLeuLys----- 50
Db 2008 TCGACCATCAGGACACACAAAGAGCTAGCCTAGCAGCAGCGCGCTGACTG 1949
QY 51 -----LeuCysLeuLeuHisLeuPro 58
Db 1948 CTGCGCTCCCTCTCCATCTGCTATGTTTCTTTGCTGATGCGCCATCGCCT 1889
QY 59 SerGlyThrSerValThrLeuHisHisAlaArgSerGlnHisHisValCys 76
Db 1888 -----GTGTGTGCTGCTACCTAAGACGACGACGACGCTGCTTCT 1847

RESULT 2
US-09-780-049-18
; Sequence 18, Application US/09780049
; Patent No. 6465250
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Jacqueline Wyatt
; TITLE OF INVENTION: ANTISENSE MODULATION OF PROTEIN PHOSPHATASE 2 CATALYTIC SUBUNIT
; FILE REFERENCE: RTS-0134
; CURRENT APPLICATION NUMBER: US/09780,049
; CURRENT FILING DATE: 2001-02-09
; NUMBER OF SEQ ID NOS: 96
; SEQ ID NO 18
; LENGTH: 40000
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
US-09-780-049-18
Alignment Scores:
Pred. No.: 772 Length: 40000
Score: 69.00 Matches: 22
Percent Similarity: 40.00% Conservativeness: 12
Best Local Similarity: 25.88% Mismatches: 15
Query Match: 17.29% Indels: 36
DB: 4 Gaps: 3

US-09-092-296-15 (1-78) x US-09-780-049-18 (1-40000)
QY 5 LeuProLeuValLeuLeuLeuGlySerSerHisGlyThrGlyPro----- 22
Db 20067 ATTCCAGTCTCCAAATCTGTGATTTATTAGGGGAAGGAATGGCATTTGTTTGT 20126

QY 23 -----GlyMetThrLeuGlnLeuLysLeuLysGluSerPheLeu 35
Db 20127 TTTGTTTGGACAGAGTCTTGTCTCTCACCAGCGTGGAGTGCAGTGCATCTTG 20186
QY 36 ThrAsnSerSerTyGluSerPheLeuGluLeuGluLysLeuCysLeuLeuLeu 55
Db 20187 GCTCAGCGCAAC-----CTC 20201
QY 56 HisLeuProSer-----GlyThrSerVal 63
Db 20202 CACCTCCCAAGTTTAAGCAATTCCTCTGCCTCAGCTCCCAAGTAGCTGTACAGTC 20261
QY 64 ThrLeuHisHisAla 68
Db 20262 ATGACACCCATGCC 20276

RESULT 3
US-09-238-303-7
; Sequence 7, Application US/09238303B
; Patent No. 6284253
; GENERAL INFORMATION:
; APPLICANT: Barr, Margaret C.
; TITLE OF INVENTION: NO.6284253el Feline Immunodeficiency Virus Nucleotide Sequence
; FILE REFERENCE: 18617.0059
; CURRENT APPLICATION NUMBER: US/09/238,303B
; EARLIER FILING DATE: 1999-01-28
; EARLIER FILING DATE: 1998-01-29
; NUMBER OF SEQ ID NOS: 17
; SEQ ID NO 7
; LENGTH: 9751
; TYPE: DNA
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: recombinant viral clone constructed from the genomic DNA of
; OTHER INFORMATION: a Pallas's cat feline immunodeficiency virus
US-09-238-303-7
Alignment Scores:
Pred. No.: 125 Length: 9751
Score: 68.50 Matches: 24
Percent Similarity: 47.30% Conservativeness: 11
Best Local Similarity: 32.43% Mismatches: 34
Query Match: 17.17% Indels: 5
DB: 4 Gaps: 2

US-09-092-296-15 (1-78) x US-09-238-303-7 (1-9751)
QY 2 GlySerGlyLeuProLeuValLeuLeuThr-----LeuLeuGlySerSer 17
Db 8384 GGATTAGGATTAAGTCTAGCTCTGTTTACTGCTACAACTGCAGGGTTTAATAGGAACA 8443
QY 18 HisGlyThrGlyProGlyMetThrLeuGlnLeuLysLeuLysGluSerPheLeuThrAsn 37
Db 8444 ACGGGGACATCT---GCATGCGCAGTGTCTATTAAATTAAGAAGTGTATTACACAA 8500
QY 38 SerSerTyGluSerSerPheLeuGluLeuLysLeuCysLeuLeuHisLeu 57
Db 8501 TCACAAATAAATGAAGCAACATTTGGGAATGTTAAATCTTACAAAGAGACTAAACAG 8560
QY 58 ProSerGlyThrSerValThrLeuHisHisAlaArgSerGln 71
Db 8561 GCAGAAAGAGTGAATTTAAACGTTTACATCAGAGAGTATCTAGG 8602

RESULT 4
US-08-951-648-5/c
; Sequence 5, Application US/08951648
; Patent No. 5932465
; GENERAL INFORMATION:
; APPLICANT: Loughney, Kate
; TITLE OF INVENTION: Phosphodiesterase 8
; NUMBER OF SEQUENCES: 38
; CORRESPONDENCE ADDRESS:
```

ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 233 South Wacker, Sears Tower Suite 6300
CITY: Chicago
STATE: Illinois
COUNTRY: US
ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/951,648
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Williams Jr., Joseph A.
REGISTRATION NUMBER: 38,659
REFERENCE/DOCKET NUMBER: 27866/34038
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-474-6300
TELEFAX: 312-474-0446
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 3195 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 67..2403
US-08-951-648-5

Alignment Scores:
Pred. No.: 30.4 Length: 3195
Score: 68.00 Matches: 26
Percent Similarity: 42.53% Conservative: 11
Best Local Similarity: 29.89% Mismatches: 21
Query Match: 17.04% Indels: 21
DB: 2 Gaps: 3

US-09-092-296-15 (1-78) x US-08-951-648-5 (1-3195)

QY 3 SerGlyLeuProLeuValLeuLeuThrLeuLeuGlySerSerHisGlyThrGlyPro 22
Db 1090 TCAGGACTCCCTGCTCTCTACTT-----GCCAG 1058
QY 23 GlyMetThrLeuGlnLeuLysLeuLysGluSerPhe-LeuThrAsnSerSerTyrGluSe 42
Db 1057 CAATTCCTTTCTCAATTGAAATCTTATCTCTTGTGCTCTTGAAGACAGGTTTCTT 998
QY 42 rSerPheLeuGluLeuLeuLys-----LeuCysLeuLeuHisLe 57
Db 997 CTTTCTCTCCATATCAAAAGGCTGAATATACTCTTGTCTTATGTCACCT 938
QY 57 uProSerGlyThrSerValThrLeuHisHisAlaArgSerGlnHisHisValVal 75
Db 937 GGAAGAGTCACACAGCATCGGCATTCACCAGGTTTTTGGCATATATCATATGTTGTTCAA 878
QY 76 -----CysAsn 77
Db 877 GTAGAGAACTATTGCAAC 859

RESULT 5

US-09-174-437-5/C
; Sequence 5, Application US/09174437A
; Patent No. 6133007
; GENERAL INFORMATION:
; APPLICANT: Loughney, Kate
; TITLE OF INVENTION: Phosphodiesterase 8A
; FILE REFERENCE: 27866/35047
; CURRENT APPLICATION NUMBER: US/09/174,437A

; CURRENT FILING DATE: 1998-10-16
; EARLIER APPLICATION NUMBER: 08/951,648
; EARLIER FILING DATE: 1997-10-16
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5
; LENGTH: 3195
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (67)..(2403)
US-09-174-437-5

Alignment Scores:
Pred. No.: 30.4 Length: 3195
Score: 68.00 Matches: 26
Percent Similarity: 42.53% Conservative: 11
Best Local Similarity: 29.89% Mismatches: 21
Query Match: 17.04% Indels: 21
DB: 3 Gaps: 3

US-09-092-296-15 (1-78) x US-09-174-437-5 (1-3195)

QY 3 SerGlyLeuProLeuValLeuLeuThrLeuLeuGlySerSerHisGlyThrGlyPro 22
Db 1090 TCAGGACTCCCTGCTCTCTACTT-----GCCAG 1058
QY 23 GlyMetThrLeuGlnLeuLysLeuLysGluSerPhe-LeuThrAsnSerSerTyrGluSe 42
Db 1057 CAATTCCTTTCTCAATTGAAATCTTATCTCTTGTGCTCTTGAAGACAGGTTTCTT 998
QY 42 rSerPheLeuGluLeuLeuLys-----LeuCysLeuLeuHisLe 57
Db 997 CTTTCTCTCCATATCAAAAGGCTGAATATACTCTTGTCTTATGTCACCT 938
QY 57 uProSerGlyThrSerValThrLeuHisHisAlaArgSerGlnHisHisValVal 75
Db 937 GGAAGAGTCACACAGCATCGGCATTCACCAGGTTTTTGGCATATATCATATGTTGTTCAA 878
QY 76 -----CysAsn 77
Db 877 GTAGAGAACTATTGCAAC 859

RESULT 6

US-09-754-250-3/c
; Sequence 3, Application US/09754250
; Patent No. 6376225
; GENERAL INFORMATION:
; APPLICANT: Wei, Ming-Hui et al
; TITLE OF INVENTION: ISOLATED HUMAN PHOSPHODIESTERASE
; TITLE OF INVENTION: PROTEINS, NUCLEIC ACID MOLECULES ENCODING HUMAN
; TITLE OF INVENTION: PHOSPHODIESTERASE PROTEINS, AND USES THEREOF
; FILE REFERENCE: CL001063
; CURRENT APPLICATION NUMBER: US/09/754,250
; CURRENT FILING DATE: 2001-01-05
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 111282
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(111282)
; OTHER INFORMATION: n = A,T,C or G
US-09-754-250-3

Alignment Scores:
Pred. No.: 4.42e+03 Length: 111282
Score: 68.00 Matches: 19
Percent Similarity: 56.82% Conservative: 6
Best Local Similarity: 43.18% Mismatches: 19


```
Query Match: 16.79% Indels: 0
DB: 3 Gaps: 0
US-09-092-296-15 (1-78) x US-08-755-587-15 (1-7240)
QY 27 GlnLeuLysLeuLysGluSerPheLeuThrAsnSerSerTyrGluSerSerPheLeuGlu 46
Db 4015 AAATATCATCTTAAGAGCTTAAAGTGGCCACACAGTCTCAATAGAACAGGTTTTTATCA 3956
QY 47 LeuLeuGluLysLeuLysLeuLeuLeuHisLeuProSerGlyThrSerValThrLeuHis 66
Db 3955 TTATGAGAGAATTCGTCATCTTACACTTTGGGCAGCTGTGATCTCAATGGTCTCA 3896
QY 67 HisAlaArgSerGln 71
Db 3895 CATGCTAATTCGAAG 3881
RESULT 12
US-08-603-753D-3/c
: Sequence 3, Application US/08603753D
: Patent No. 5891857
: GENERAL INFORMATION:
: APPLICANT: HOLT, JEFFREY T.
: APPLICANT: JENSEN, ROY A.
: APPLICANT: PAGE, DAVID L.
: APPLICANT: KING, MARY-CLAIRE
: APPLICANT: SZABO, CSILLA I.
: APPLICANT: JETTON, THOMAS L.
: APPLICANT: ROBINSON-BENTON, CHERYL L.
: APPLICANT: THOMPSON, MARILYN E.
: TITLE OF INVENTION: CHARACTERIZED BRCA1 AND BRCA2
: TITLE OF INVENTION: PROTEINS AND SCREENING AND THERAPEUTIC METHODS BASED ON
: TITLE OF INVENTION: CHARACTERIZED BRCA1 AND BRCA2 PROTEINS.
: NUMBER OF SEQUENCES: 29
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: ARLES A. TAYLOR, JR.
: STREET: SUITE 1401, UNIVERSITY TOWER, 3100 TOWER
: CITY: DURHAM
: STATE: NORTH CAROLINA
: COUNTRY: USA
: ZIP: 27707
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Diskette, 3.50 inch, 800 kB storage
: COMPUTER: IBM PC/XT/AT compatible
: OPERATING SYSTEM: Windows 3.1
: SOFTWARE: WORD PERFECT 6.1 and ASCII
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/603,753D
: FILING DATE: 20 FEB 1996
: CLASSIFICATION: 514
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: U.S. 08/373,799
: FILING DATE: 17 JAN 1995
: ATTORNEY/AGENT INFORMATION:
: NAME: ARLES A. TAYLOR, JR.
: REGISTRATION NUMBER: 39,395
: REFERENCE/DOCKET NUMBER: 1242/2
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (919) 493-8000
: TELEFAX: (919) 419-0383
: TELEX:
: INFORMATION FOR SEQ ID NO: 3:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 11283
: TYPE: nucleic acid
: STRANDEDNESS: double
: TOPOLOGY: linear
: MOLECULE TYPE: cDNA to mRNA
: HYPOTHETICAL: no
: ANTI-SENSE: no
: ORIGINAL SOURCE:
: ORGANISM: Homo sapiens sapiens
```

```
INDIVIDUAL ISOLATE:
DEVELOPMENTAL STAGE: adult
TISSUE TYPE: female breast
CELL TYPE: normal and cancerous breast cells
CELL LINE: MCF-7
ORGANELLE: no
IMMEDIATE SOURCE:
LIBRARY: cDNA library derived from human
CLONE: obtained using published sequence
POSITION IN GENOME:
CHROMOSOME/SEGMENT: unknown
MAP POSITION: unknown
UNITS: unknown
FEATURE:
NAME/KEY: BRCA2
LOCATION:
IDENTIFICATION METHOD:
OTHER INFORMATION: gene encoding BRCA2 protein
PUBLICATION INFORMATION:
AUTHORS: Wooster, R. et al.
TITLE: Identification of the breast cancer
TITLE: susceptibility gene BRCA2
JOURNAL: Nature
VOLUME: 379
PAGES: 789-792
DATE: 1995
RELEVANT RESIDUES IN SEQ ID NO: 3
US-08-603-753D-3
Alignment Scores:
Pred. No.: 243 Length: 11283
Score: 67.00 Matches: 16
Percent Similarity: 51.11% Conservative: 7
Best Local Similarity: 35.56% Mismatches: 22
Query Match: 16.79% Indels: 0
DB: 2 Gaps: 0
US-09-092-296-15 (1-78) x US-08-603-753D-3 (1-11283)
QY 27 GlnLeuLysLeuLysGluSerPheLeuThrAsnSerSerTyrGluSerSerPheLeuGlu 46
Db 5055 AAATATCATCTTAAGAGCTTAAAGTGGCCACACAGTCTCAATAGAACAGGTTTTTATCA 4996
QY 47 LeuLeuGluLysLeuLysLeuLeuLeuHisLeuProSerGlyThrSerValThrLeuHis 66
Db 4995 TTATGAGAGAATTCGTCATCTTACACTTTGGGCAGCTGTGATCTCAATGGTCTCA 4936
QY 67 HisAlaArgSerGln 71
Db 4935 CATGCTAATTCGAAG 4921
RESULT 13
US-09-099-753-3/c
: Sequence 3, Application US/09099753
: Patent No. 6149903
: GENERAL INFORMATION:
: APPLICANT: HOLT, JEFFREY T.
: APPLICANT: JENSEN, ROY A.
: APPLICANT: PAGE, DAVID L.
: APPLICANT: KING, MARY-CLAIRE
: APPLICANT: SZABO, CSILLA I.
: APPLICANT: JETTON, THOMAS L.
: APPLICANT: ROBINSON-BENTON, CHERYL L.
: APPLICANT: THOMPSON, MARILYN E.
: TITLE OF INVENTION: CHARACTERIZED BRCA1 AND BRCA2
: TITLE OF INVENTION: PROTEINS AND SCREENING AND THERAPEUTIC METHODS BASED ON
: TITLE OF INVENTION: CHARACTERIZED BRCA1 AND BRCA2 PROTEINS.
: NUMBER OF SEQUENCES: 29
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: ARLES A. TAYLOR, JR.
: STREET: SUITE 1401, UNIVERSITY TOWER, 3100 TOWER
: CITY: DURHAM
```

STATE: NORTH CAROLINA
COUNTRY: USA
ZIP: 27707
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 800 KB storage
COMPUTER: IBM PC/XT/AT compatible
OPERATING SYSTEM: Windows 3.1
SOFTWARE: WORD PERFECT 6.1 and ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/099,753
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/603,753
FILING DATE: 20 FEB 1996
APPLICATION NUMBER: U.S. 08/373,799
FILING DATE: 17 JAN 1995
ATTORNEY/AGENT INFORMATION:
NAME: ARLES A. TAYLOR, JR.
REGISTRATION NUMBER: 39,395
REFERENCE/DOCKET NUMBER: 1242/2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (919) 493-8000
TELEFAX: (919) 419-0383
TELEX:
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 11283
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA to mRNA
HYPOTHETICAL: no
ANTI-SENSE: no
ORIGINAL SOURCE:
ORGANISM: Homo sapiens sapiens
INDIVIDUAL ISOLATE:
DEVELOPMENTAL STAGE: adult
TISSUE TYPE: female breast
CELL TYPE: normal and cancerous breast cells
CELL LINE: MCF-7
ORGANELLE: no
IMMEDIATE SOURCE:
LIBRARY: cDNA library derived from human
CLONE: obtained using published sequence
POSITION IN GENOME:
CHROMOSOME/SEGMENT: unknown
MAP POSITION: unknown
UNITS: unknown
FEATURE:
NAME/KEY: BRCA2
LOCATION:
IDENTIFICATION METHOD:
OTHER INFORMATION: gene encoding BRCA2 protein
PUBLICATION INFORMATION:
AUTHORS: Wooster, R. et al.
TITLE: Identification of the breast cancer
TITLE: susceptibility gene BRCA2
JOURNAL: Nature
VOLUME: 379
PAGES: 789-792
DATE: 1995
RELEVANT RESIDUES IN SEQ ID NO: 3
US-09-099-753-3
Alignment Scores:
Pred. No.: 243
Score: 67.00
Length: 11283
Matches: 16
Percent Similarity: 51.11%
Conservative: 7
Best Local Similarity: 35.56%
Mismatch: 16.79%
Query Match: 3
Indels: 0
Gaps: 0
DB:

US-092-296-15 (1-78) x US-09-099-753-3 (1-11283)
QY 27 GlnLeuLysLeuLysGluSerPheLeuThrAsnSerSerTyGluSerSerPheLeuGlu 46
Db 5055 AATATATACATTAAGAGCTTAGTGGCCACACAGTCTCAATAGAAACAAGGTTTATCA 4996
QY 47 LeuLeuGluLysLeuLysLeuLeuLysLeuProSerGlyThrSerValThrLeuHis 66
Db 4995 TTATTGAGAGAATTCGCAATTCCTTTACACATTTGGGCGACGCTGATCTCAATGGTCTCA 4936
QY 67 HisAlaArgSerGln 71
Db 4935 CATGTAATTCAGG 4921
RESULT 14
US-08-986-106-3/c
Sequence 3, Application US/08986106
Patent No. 6177410
GENERAL INFORMATION:
APPLICANT: HOLT, JEFFREY T.
APPLICANT: JENSEN, ROY A.
APPLICANT: KING, MARY-CLAIRE
APPLICANT: STEINER, MITCHELL S.
APPLICANT: ROBINSON-BENTON, CHERYL L.
APPLICANT: THOMPSON, MARILYN E.
TITLE OF INVENTION: THERAPEUTIC METHODS FOR
TITLE OF INVENTION: PROSTATE CANCER
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: ARLES A. TAYLOR, JR.
STREET: SUITE 1401, UNIVERSITY TOWER, 3100 TOWER
STREET: BOULEVARD
CITY: DURHAM
STATE: NORTH CAROLINA
COUNTRY: USA
ZIP: 27707
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.44MB storage
COMPUTER: IBM PC/XT/AT compatible
OPERATING SYSTEM: Windows 3.1
SOFTWARE: WORD PERFECT 6.1 and ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/986,106
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/603,753
FILING DATE: 20 FEB 1996
ATTORNEY/AGENT INFORMATION:
NAME: ARLES A. TAYLOR, JR.
REGISTRATION NUMBER: 39,395
REFERENCE/DOCKET NUMBER: 1242/3
TELECOMMUNICATION INFORMATION:
TELEPHONE: (919) 493-8000
TELEFAX: (919) 419-0383
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 11283
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
FEATURE:
NAME/KEY: BRCA2
PUBLICATION INFORMATION:
AUTHORS: Wooster, R. et al.
TITLE: Identification of the breast cancer
TITLE: susceptibility gene BRCA2
JOURNAL: Nature
VOLUME: 379
PAGES: 789-792
DATE: 1995
US-08-986-106-3

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Alignment Scores:
Pred. No.: 243 Length: 11283
Score: 67.00 Matches: 16
Percent Similarity: 51.11% Conservatives: 7
Best Local Similarity: 35.56% Mismatches: 22
Query Match: 16.79% Indels: 0
DB: 4 Gaps: 0

US-09-092-296-15 (1-78) x US-08-986-106-3 (1-11283)
QY 27 GlnLeuLysLeuLysGluSerPheLeuThrAsnSerSeryrGluSerSerPheLeuGlu 46
Db 5055 AAATATCATTTAGAGCTTAGTGGCACCACAGCTCAATAGAACAAAGGTTTTATCA 4996

QY 47 LeuLeuGluLysLeuLysGluSerPheLeuThrAsnSerSeryrGluSerSerPheLeuHis 66
Db 4995 TTATTGAGAGAAATCTGCATTTCTTACACTTTGGGGCAGCTGTGATCTCAATGGTCTCA 4936

QY 67 HisAlaArgSerGln 71
Db 4935 CATGCTAATTCAGG 4921

RESULT 15
US-08-639-501-1/c
; Sequence 1, Application US/08639501
; Patent No. 5837492
; GENERAL INFORMATION:
; APPLICANT: Tavtligian, Sean V.
; APPLICANT: Kamb, Alexander
; APPLICANT: Sinard, Jacques
; APPLICANT: Couch, Fergus
; APPLICANT: Roumens, Johanna
; APPLICANT: Weber, Barbara
; TITLE OF INVENTION: Chromosome 13-Linked Breast Cancer
; TITLE OF INVENTION: Susceptibility Gene
; NUMBER OF SEQUENCES: 124
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Venable, Baetjer, Howard & Civiletti
; STREET: 1201 New York Avenue N.W., Suite 1001
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 22204
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/639,501
; FILING DATE: 29-APR-1996
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/585,391
; FILING DATE: 11-JAN-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/576,559
; FILING DATE: 21-DEC-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/575,359
; FILING DATE: 20-DEC-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/573,779
; FILING DATE: 18-DEC-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Ihnen, Jeffrey L.
; REGISTRATION NUMBER: 28,957
; REFERENCE/DOCKET NUMBER: 24884-116802-04
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-962-4810
; TELEFAX: 202-962-8300
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11385 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 229..10482
; US-08-639-501-1

Alignment Scores:
Pred. No.: 246 Length: 11385
Score: 67.00 Matches: 16
Percent Similarity: 51.11% Conservatives: 7
Best Local Similarity: 35.56% Mismatches: 22
Query Match: 16.79% Indels: 0
DB: 2 Gaps: 0

US-09-092-296-15 (1-78) x US-08-639-501-1 (1-11385)
QY 27 GlnLeuLysLeuLysGluSerPheLeuThrAsnSerSeryrGluSerSerPheLeuGlu 46
Db 5087 AAATATCATTTAGAGCTTAGTGGCACCACAGCTCAATAGAACAAAGGTTTTATCA 5028

QY 47 LeuLeuGluLysLeuLysGluSerPheLeuThrAsnSerSeryrGluSerSerPheLeuHis 66
Db 5027 TTATTGAGAGAAATCTGCATTTCTTACACTTTGGGGCAGCTGTGATCTCAATGGTCTCA 4968

QY 67 HisAlaArgSerGln 71
Db 4967 CATGCTAATTCAGG 4953

Search completed: May 1, 2003, 06:05:50
Job time : 85 secs
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GenCore version 5.1.5
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OM protein - nucleic search, using frame_plus_p2n model

Run on: May 1, 2003, 05:17:21 ; Search time 1415 Seconds
(without alignments)
892.755 Million cell updates/sec

Title: US-09-092-296-15

Perfect score: 399

Sequence: 1 MGSGLPVLLTLTGSSHGT.....SGTSVTLHARSQHVVNCVT 78

Scoring table:

BLOSUM62
Xgapop 10.0, Xgapext 0.5
Ygapop 10.0, Ygapext 0.5
Fgapop 6.0, Fgapext 7.0
Delop 6.0, Delext 7.0

Searched: 16154066 seqs, 8097743376 residues

Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

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-DB=EST -QFMT=fastap -SUFFIX=p2n.rst -MINMATCH=0.1 -LOOPEXT=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS-human40.cdl -LIST=45
-DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US09092296 -CGEN_1.1.1525 -runat_30042003_133103_14414 -NCPU=6 -ICPU=3
-NO_XLPXY -NO_MAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

EST:*
1: em_estba:*
2: em_esthum:*
3: em_estin:*
4: em_estnu:*
5: em_estov:*
6: em_estpl:*
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8: em_hic:*
9: gb_est1:*
10: gb_est2:*
11: gb_hic:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_estfun:*
16: em_estim:*
17: gb_gss:*
18: em_gss_hum:*
19: em_gss_inv:*
20: em_gss_pln:*
21: em_gss_vrt:*
22: em_gss_fun:*
23: em_gss_mam:*
24: em_gss_mus:*
25: em_gss_other:*
26: em_gss_pro:*
27: em_gss_rod:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	399	100.0	456	12	BG506690
2	399	100.0	830	13	BI759796
3	394	98.7	449	10	AM293443
4	381	95.5	422	12	BF002050
5	334	83.7	895	13	BI820029
6	307	76.9	865	13	BI820110
7	304	76.2	404	9	AI857998
8	208	52.1	552	17	AQ718761
9	195.5	49.0	521	10	BB533837
10	195.5	49.0	522	10	BB664284
11	178	44.6	361	12	BF521842
12	156.5	39.2	328	9	AI136523
13	143	35.8	244	12	BF511043
14	115	28.8	506	17	AZ241329
15	115	28.8	633	17	AZ079350
16	90	22.6	557	14	BQ552414
17	85.5	21.4	338	13	BQ041163
18	85.5	21.4	374	13	BQ041184
19	85.5	21.4	397	13	BQ033159
20	85.5	21.4	402	13	BQ055543
21	85.5	21.4	644	13	BQ032429
22	85.5	21.4	685	13	BQ080213
23	82.5	20.7	260	13	BQ055523
24	82.5	20.7	613	10	BE533619
25	81.5	20.4	504	10	BE191954
26	81.5	20.4	608	13	BQ061093
27	80.5	20.2	329	13	BI312652
28	79.5	19.9	484	17	AZ367243
29	79.5	19.9	623	9	AA543778
30	78	19.5	525	17	AQ360660
31	78	19.5	896	17	CNS0454L
32	78	19.5	1175	17	AQ122004
33	77	19.3	713	17	AQ349213
34	77	19.3	909	14	BQ957881
35	77	19.3	1129	12	BF101152
36	76.5	19.2	360	14	C62342
37	76.5	19.2	711	12	BG701480
38	76.5	19.2	729	13	BI551383
39	76.5	19.2	783	13	BI553452
40	76.5	19.2	816	13	BI753758
41	76.5	19.2	1001	17	CNS03FE9
42	76.5	19.2	1054	13	BW547579
43	76	19.0	439	9	A3776143
44	76	19.0	576	13	BI359989
45	76	19.0	682	13	BJ140448

ALIGNMENTS

RESULT 1
BG506690
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE

BG506690
601861290F1 NIH_MGC_77 Homo sapiens cdna clone IMAGE:4070759 5',
mRNA sequence.
BG506690
BG506690.1 GI:13468207
EST.
human.
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 456)
NIH-MGC <http://mgc.nci.nih.gov/>.
National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL COMMENT	Unpublished (1999) Contact: Robert Strausberg, Ph.D. Email: c9apbs-r@mail.nih.gov Tissue Procurement: CLONTECH Laboratories, Inc. cDNA Library Preparation: CLONTECH Laboratories, Inc. cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Plate: LLC915 row: d column: 24 High quality sequence stop: 401. Location/Qualifiers 1. 456 /organism="Homo sapiens" /db_xref="taxon:9606" /clone="IMAGE:4070759" /clone_lib="NIH_MGC_77" /lab_host="DH10B (T1 phage-resistant)" /note="Organ: lung; Vector: pDNR-LIB (clontech); Site: 1: sfii (ggcgctggcc); Site: 2: sfii (ggccattatggcc); 5' and 3' adaptors were used in cloning as follows: 5' adaptor sequence: 5'-CACGCCATTATGGCC-3' and 3' adaptor sequence: 5'-ATTCTAGCGCGAGCGCGCATG-dt(30)BN-3' (where B = A, C, or G and N = A, C, G, or T). Average insert size 1.9 kb (range 0.5-4.0 kb). 12/15 colonies contained inserts by PCR. This library was enriched for full-length clones and was constructed by Clontech Laboratories (Palo Alto, CA). Note: this is a NIH_MGC Library."
FEATURES source	BASE COUNT 109 a 137 c 106 g 103 t 1 others ORIGIN
Alignment Scores:	Pred. No.: 1 59e-37 Length: 456 Score: 399.00 Matches: 78 Percent Similarity: 100.00% Conservat: 0 Best Local Similarity: 100.00% Mismatches: 0 Query Match: 100.00% Indels: 0 DB: 12 Gaps: 0
US-09-092-296-15 (1-78) x B6506690 (1-456)	
Qy 1 MetGlySerGlyLeuProLeuValLeuLeuThrLeuLeuGlySerHisGlyThr 20	
Db 45 ATGGGGTCTGGGCTGGCCCTTGCTCTCTTGACCCCTCTTGGCAGCTCACATGGAACA 104	
Qy 21 GlyProGlyMetThrLeuGlnLeuLysLeuLysGluSerPheLeuThrAsnSerTyr 40	
Db 105 GGGCCGGGTATGACTTGGAACTGAAGCTGAAGGAGTCTTTTCGACAAATTCCTCTAT 164	
Qy 41 GluSerPheLeuGluLeuLeuGluLysLeuCysLeuLeuHisLeuProSerGly 60	
Db 165 GAGTCCAGCTTCTGGAAATGCTTGAAGAGCTCGCTCCCTCCATCTCCCTTCAGGG 224	
Qy 61 ThrSerValThrLeuHisAlaArgSerGlnHisHisValValCysAsnThr 78	
Db 225 ACCAGCGTACCCCTCCACATGCAAGATCTCAACACCATGTTGTCGACACACA 278	
RESULT 2	
Bi759796	Bi759796 830 bp mRNA linear EST 25-SEP-2001
LOCUS	603045679F1 NIH_MGC_116 Homo sapiens cDNA clone IMAGE:5186107 5', mRNA sequence.
DEFINITION	
ACCESSION	Bi759796
VERSION	Bi759796.1 GI:15751374
KEYWORDS	EST.
SOURCE	human.
ORGANISM	Homo sapiens
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
AUTHORS	NIH-MGC http://mgi.nci.nih.gov/
TITLE	National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL COMMENT	Unpublished (1999) Contact: Robert Strausberg, Ph.D. Email: c9apbs-r@mail.nih.gov Tissue Procurement: Life Technologies, Inc. cDNA Library Preparation: Life Technologies, Inc. cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Plate: LLAM1464 row: m column: 20 High quality sequence stop: 432. Location/Qualifiers 1. 830 /organism="Homo sapiens" /db_xref="taxon:9606" /clone="IMAGE:5186107" /clone_lib="NIH_MGC_116" /lab_host="DH10B" /note="Organ: pooled colon, kidney, stomach; Vector: pCMV-SPORT6; Site: 1: NotI; Site: 2: EcoRV (destroyed); RNA source anonymous pool of 3 colons, age 26 yo male, 49 yo female, 71 yo male colon; 46 yo male kidney, and pool of 2 stomachs, 62 yo male and 70 yo female. Library is oligo-dT primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.4 kb, insert size range 1-3 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 023. Note: this is a NIH_MGC Library."
FEATURES source	BASE COUNT 175 a 276 c 210 g 168 t 1 others ORIGIN
Alignment Scores:	Pred. No.: 3 59e-37 Length: 830 Score: 399.00 Matches: 78 Percent Similarity: 100.00% Conservat: 0 Best Local Similarity: 100.00% Mismatches: 0 Query Match: 100.00% Indels: 0 DB: 13 Gaps: 0
US-09-092-296-15 (1-78) x Bi759796 (1-830)	
Qy 1 MetGlySerGlyLeuProLeuValLeuLeuThrLeuLeuGlySerHisGlyThr 20	
Db 81 ATGGGGTCTGGGCTGGCCCTTGCTCTCTTGACCCCTCTTGGCAGCTCACATGGAACA 140	
Qy 21 GlyProGlyMetThrLeuGlnLeuLysLeuLysGluSerPheLeuThrAsnSerTyr 40	
Db 141 GGACGGGTATGACTTGCACACTGAAGCTGAAGGAGTCTTTTCGACAAATTCCTCTAT 200	
Qy 41 GluSerPheLeuGluLeuLeuGluLysLeuCysLeuLeuHisLeuProSerGly 60	
Db 201 GAGTCCAGCTTCTGGAAATGCTTGAAGAGCTCTGCTCCCTCCATCTCCCTTCAGGG 260	
Qy 61 ThrSerValThrLeuHisAlaArgSerGlnHisHisValValCysAsnThr 78	
Db 261 ACCAGCGTACCCCTCCACATGCAAGATCTCAACACCATGTTGTCGACACACA 314	
RESULT 3	
AW293443/c	AW293443 449 bp mRNA linear EST 16-JAN-2000
LOCUS	UT-H-B12-ahm-c-08-0-UI.sl NCI_CGAP_Sub4 Homo sapiens cDNA clone IMAGE:272182 3', mRNA sequence.
DEFINITION	
ACCESSION	AW293443
VERSION	AW293443.1 GI:6700079
KEYWORDS	EST.
SOURCE	human.
ORGANISM	Homo sapiens
REFERENCE	Eukaryota; Metazoa; Chordata; Cranialata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
AUTHORS	1 (bases 1 to 449) NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.


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Db 377 ATGGGGTCTGGGGCTGCCCTTGTCTCTTGTGACCTCTCTGACGCTCACATGGACA 318
QY 21 GlyProGlyMetThrLeuGlnLeuLysLeuLysGluSerPheLeuThrAsnSerSerTyr 40
|||||
Db 317 GGGCCGGGTATGACTTTTGCACATGAAGCTGAAGGAGTCTTTTCTGACAAATTCCTCTAT 258
QY 41 GluSerSerPheLeuGluLeuLeuGlu-LysLeuCysLeuLeuLeuHisLeuProSerG1 60
|||||
Db 257 GAGTCCAGCTTCTCGAATGCTTGAAAAAGNTNGCTCCTCCTCCATCTCCCTCAGG 198
QY 60 YThrSerValThrLeuHisHisAlaArgSerGlnHisHisValValCysAsnThr 78
|||||
Db 197 GACCAGGTCACCTCCACCATGAAGATCTCAACACCATGTTGTCTGCAACACA 143

RESULT 5
B1820029 895 bp mRNA linear EST 04-OCT-2001
LOCUS 603037210F1 NIH_MGC_115 Homo sapiens cDNA clone IMAGE:5178171 5',
DEFINITION mRNA sequence.
ACCESSION B1820029
VERSION B1820029.1 GI:15931579
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 895)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone Distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM11444 row: c column: 04
High quality sequence start: 5
High quality sequence stop: 422.
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Location/Qualifiers
1..895
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/db_xref="taxon:9606"
/clone="IMAGE:5178171"
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/note="Organ: pooled brain, lung, testis; Vector:
pCMV-SPORT6; Site_1: NotI; Site_2: EcoRV (destroyed); RNA
source anonymous pool of 6 male brains, age range 23-27; 1
male lung, age 27; and 1 male testis, age 69. Library is
oligo-dT primed and directionally cloned (EcoRV site is
destroyed upon cloning). Average insert size 1.8 kb.
insert size range 1-3 kb. Library is normalized and
enriched for full-length clones and was constructed by C.
Gruber (Invitrogen). Research Genetics tracking code
021. Note: this is a NIH_MGC Library."
BASE COUNT 349 a 229 c 202 g 115 t
ORIGIN

Alignment Scores:
Pred. No.: 2,08e-29 Length: 895
Score: 334.00 Matches: 64
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 83.71% Indels: 0
DB: 13 Gaps: 0

US-09-092-296-15 (1-78) x B1820029 (1-895)

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QY 35 LeuThrAsnSerSerTyrGluSerSerPheLeuGluLeuLeuGluLysLeuCysLeuLeu 54
|||||
Db 73 CTGACAAATTCCTCTATGAGTCTGAGCTTCCTGGAATTCCTGAAAAGCTCTGCCTCCTC 132
QY 55 LeuHisLeuProSerGlyThrSerValThrLeuHisHisAlaArgSerGlnHisHisVal 74
|||||
Db 133 CTCATCTCTCCCTTCAGGACAGCGTCACTCCCTCCACCATCAAGATCTCAACACCATGTT 192
QY 75 ValCysAsnThr 78
|||||
Db 193 GTCTGCAACACA 204

RESULT 6
B1820110 865 bp mRNA linear EST 04-OCT-2001
LOCUS 603037110F1 NIH_MGC_115 Homo sapiens cDNA clone IMAGE:5178170 5',
DEFINITION mRNA sequence.
ACCESSION B1820110
VERSION B1820110.1 GI:15931660
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 865)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone Distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM11444 row: c column: 03
High quality sequence stop: 417.
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/db_xref="taxon:9606"
/clone="IMAGE:5178170"
/clone_lib="NIH_MGC_115"
/lab_host="DH10B"
/note="Organ: pooled brain, lung, testis; Vector:
pCMV-SPORT6; Site_1: NotI; Site_2: EcoRV (destroyed); RNA
source anonymous pool of 6 male brains, age range 23-27; 1
male lung, age 27; and 1 male testis, age 69. Library is
oligo-dT primed and directionally cloned (EcoRV site is
destroyed upon cloning). Average insert size 1.8 kb.
insert size range 1-3 kb. Library is normalized and
enriched for full-length clones and was constructed by C.
Gruber (Invitrogen). Research Genetics tracking code
021. Note: this is a NIH_MGC Library."
BASE COUNT 330 a 219 c 198 g 117 t 1 others
ORIGIN

Alignment Scores:
Pred. No.: 3.19e-26 Length: 865
Score: 307.00 Matches: 63
Percent Similarity: 98.44% Conservative: 0
Best Local Similarity: 98.44% Mismatches: 1
Query Match: 76.94% Indels: 1
DB: 13 Gaps: 0

US-09-092-296-15 (1-78) x B1820110 (1-865)

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QY 15 GlySerHisGlyThrGlyProGlyMetThrLeuGlnLeuLysLeuLysGluSerPhe 34
 DB 13 GGCAGCTCACAGGACGCGGTATGACTTTGCAACTGAGCTGAGGAGTCTTTT 72
 QY 35 LeuThrAsnSerSerTyrGluSerSerPheLeuGluLeuLeuGluLysLeuCysLeuLeu 54
 DB 73 CTGACAAATTCCTCTATGAGTCCAGCTTCCTGGAATG-CATTGAAAAGCTGCTGCTCTC 131
 QY 55 LeuHisLeuProSerGlyThrSerValThrLeuHisHisAlaArgSerGlnHisHisVal 74
 DB 132 CTCATCTCCCTTCAGGACCGTCACCTCCACCATCCAGATCTCAACACCAAGTT 191
 QY 75 ValCysAsnThr 78
 DB 192 GTCTGCAACACA 203
 RESULT 7
 LOCUS A1857998/c 404 bp mRNA linear EST 21-DEC-1999
 DEFINITION wj69b01.x1 NCI_CGAP_Lu19 Homo sapiens cDNA clone IMAGE:2408041 3',
 mRNA sequence.
 ACCESSION A1857998
 VERSION A1857998.1 GI:5511614
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 404)
 AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
 TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
 Tumor Gene Index
 JOURNAL Unpublished (1997)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgapb-remail.nih.gov
 Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
 Emmert-Buck, M.D., Ph.D.
 cDNA Library Preparation: M. Bento Soares, Ph.D.
 DNA Sequencing by: Washington University Genome Sequencing Center
 Clone distribution: NCI-CGAP clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
 www.bio.llnl.gov/obrp/image/image.html
 Insert length: 629 Std Error: 0.00
 Seq primer: -400P from Gbco
 High quality sequence stop: 395.
 Location/Qualifiers
 1..404
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="IMAGE:2408041"
 /clone_lib="NCI_CGAP_Lu19"
 /tissue_type="squamous cell carcinoma, poorly
 differentiated (4 pooled tumors, including primary and
 metastatic)"
 /dev_stage="adult"
 /lab_host="DH10B (phage-resistant)"
 /note="Organ: lung; Vector: pT73D-Pac (Pharmacia) with a
 modified polylinker; 1st strand cDNA was prepared from
 pooled lung tumor tissue, and was then primed with a Not I
 - oligo(dT) primer. Double-stranded cDNA was ligated to
 Eco RI adaptors (Pharmacia), digested with Not I and
 cloned into the Not I and Eco RI sites of the modified
 pT73 vector. Library went through one round of
 normalization. Library constructed by Bento Soares and M.
 Fatima Bonaldo."
 97 a 105 c 117 g 84 t 1 others
 BASE COUNT
 ORIGIN
 Alignment Scores:
 Pred. No.: 2.57e-26 Length: 404
 Score: 304.00 Matches: 59
 Percent Similarity: 95.24% Conservative: 1

Best Local Similarity: 93.65% Mismatches: 3
 Query Match: 76.19% Indels: 0
 DB: 9 Gaps: 0
 US-09-092-296-15 (1-78) x A1857998 (1-404)
 QY 16 SerSerHisGlyThrGlyProGlyMetThrLeuGlnLeuLysLeuLysGluSerPheLeu 35
 DB 324 ACTCTGGATCCGACGCGCGGTATGACTTTGCAACTGAGCTGAGGAGTCTTTCTG 265
 QY 36 ThrAsnSerSerTyrGluSerSerPheLeuGluLeuLeuGluLysLeuCysLeuLeu 55
 DB 264 ACAATTCCTCTATGAGTCCAGCTTCCTGGAATGCTTGAAGAAGCTGCTCCTCTC 205
 QY 56 HisLeuProSerGlyThrSerValThrLeuHisHisAlaArgSerGlnHisHisVal 75
 DB 204 CATCTCCCTTCAGGACCGTCACCTCCACCATCCAGATCTCAACACCAAGTTGTC 145
 QY 76 CysAsnThr 78
 DB 144 TGCAACACA 136
 RESULT 8
 LOCUS A0718761/c 552 bp DNA linear GSS 13-JUL-1999
 DEFINITION HS_5511_B2_F09_T7A RPCI-11 Human Male BAC library Homo sapiens
 genomic clone Plate=1087 Col=18 Row=L, DNA sequence.
 ACCESSION A0718761
 VERSION A0718761.1 GI:5468077
 KEYWORDS GSS.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 552)
 AUTHORS Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T.,
 Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D., and
 Hood,L.
 TITLE Sequence-tagged connectors: A sequence approach to mapping and
 scanning the human genome
 JOURNAL Proc. Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999)
 MEDLINE 99380589
 COMMENT Contact: Mahairas GG, Wallace JC, Hood L
 High Throughput Sequencing Center
 University of Washington
 401 Queen Anne Avenue North, Seattle, WA 98109, USA
 Tel: (206) 616-3618
 Fax: (206) 616-3887
 Email: jwallace@u.washington.edu
 Clones are derived from the human BAC library RPCI-11. For BAC
 library availability, please contact Pieter de Jong
 (pieter@dejong.med.buffalo.edu). Clones may be purchased from
 BACPAC Resources (http://bacpac.med.buffalo.edu/ordering.bac.htm)
 or from Research Genetics (info@resgen.com). BAC end Web Server:
 http://www.husc.washington.edu
 Plate: 1087 row: L column: 18
 Seq primer: T7
 Class: BAC ends
 High quality sequence stop: 552.
 Location/Qualifiers
 1..552
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="Plate=1087 Col=18 Row=L"
 /clone_lib="RPCI-11 Human Male BAC Library"
 /sex="male"
 /note="Vector: pBACE3.6; Site 1: EcoRI; Site 2: EcoRI;
 Male blood DNA was isolated from one randomly chosen donor
 and partially digested with a combination of EcoRI and
 EcoRI Methylase. Size selected DNA was cloned into the
 pBACE3.6 vector at EcoRI sites"
 141 a 153 c 124 g 117 t 17 others
 BASE COUNT
 ORIGIN


```
/clone="UI-R-C2p-nq-e-02-0-UI"  
/clone_lib="UI-R-C2p"  
/dev_stage="adult"
```

```
/lab_host="DH10B (Life Technologies)"  
/note="Vector: pT73D-Pac (Pharmacia) with a modified  
polylinker; Site 1: Not I; Site 2: Eco RI; The UI-R-C2p  
library is a subtracted library derived from the UI-R-C1  
library, which is a subtracted library derived from the  
UI-R-C0 library. The UI-R-C0 library consisted of a  
mixture of individually tagged normalized libraries  
constructed from rat placenta, adult lung, brain, liver,  
kidney, heart, spleen, ovary, muscle, 8, 12 and 18-day  
embryo. The tag is a string of 3-5 nucleotides present  
between the Not I site and the oligo-dT track which allows  
identification of the library of origin of a clone within  
the mixture. The subtracted library (UI-R-C2p) was  
constructed as follows: PCR amplified cDNA inserts from  
UI-R-C1 clones from which 3' ESTs had been derived was  
used as a driver in a hybridization with the UI-R-C1  
library in the form of single-stranded circles. The  
remaining single-stranded circles (subtracted library) was  
purified by hydroxyapatite column chromatography,  
converted to double-stranded circles and electroporated  
into DH10B bacteria (Life Technologies) to generate the  
UI-R-C2p library. This procedure has been previously  
described (Bonaldo, Lennon and Soares, Genome Research 6:  
791-806, 1996)"
```

```
BASE COUNT 79 a 121 c 91 g 70 t  
ORIGIN
```

Alignment Scores:

```
Pred. No.: 2,02e-11 Length: 361  
Score: 178.00 Matches: 38  
Percent Similarity: 65.79% Conservative: 12  
Best Local Similarity: 50.00% Mismatches: 26  
Query Match: 44.61% Indels: 0  
DB: 12 Gaps: 0
```

```
US-09-092-296-15 (1-78) x BF521842 (1-361)
```

```
Qy 1 MetGlySerGlyLeuProLeuValLeuLeuThrLeuLeuGlySerSerHisGlyThr 20  
Db 22 ATGGAGCCCTCGAGTGGCTCTCTCCCTGACCTCTCGAGCTCACTCGAAGGG 81  
Qy 21 GlyProGlyMetThrLeuGlnLeuLysLeuLysGluSerPheLeuThrAsnSerSerTyr 40  
Db 82 CCACCAAGAGTGACTTTGCAAGTAAAGTCAAGCGAGGCATCTCAGGCCAAGACCTCCCAA 141  
Qy 41 GluSerSerPheLeuGluLeuGluLysLeuCysLeuLeuLeuHisLeuProSerGly 60  
Db 142 GACTCGGCTTCTGGACATGCTCCAAAGATCTGCTCTCTCCACCTCTCACCAGGG 201  
Qy 61 ThrSerValThrLeuHisHisAlaArgSerGlnHisHisValValCys 76  
Db 202 ACCAATGTCAACCTTCATATAAAGGGCCACACACACACCTTACCTGC 249
```

RESULT 12

```
LOCUS A1136523 328 bp mRNA linear EST 11-FEB-1999  
DEFINITION UI-R-C2p-nq-e-02-0-UI.s1 UI-R-C2p Rattus norvegicus cDNA clone  
VERSION A1136523  
KEYWORDS EST.  
SOURCE Norway rat.  
ORGANISM Rattus norvegicus
```

```
ACCSSION A1136523  
VERSION A1136523.1 GI:3637300  
KEYWORDS EST.
```

```
REFERENCE 1 (bases 1 to 328)  
AUTHORS Bonaldo,M.F., Lennon,G. and Soares,M.B.  
TITLE Normalization and subtraction: two approaches to facilitate gene  
discovery
```

JOURNAL
MEDLINE
COMMENT

Genome Res. 6 (9), 791-806 (1996)
97044477

Contact: Soares, MB
Program for Rat Gene Discovery and Mapping
University of Iowa
451 Eckstein Medical Research Building Iowa City, IA 52242, USA
Tel: 319 335 8250
Fax: 319 335 9565

Email: mssoares@blue.weeg.uiowa.edu

The sequence tag present in the cDNA between the NotI site and the
oligo-dT track served to identify it as a clone from the normalized
adult lung library. cDNA library Preparation: M. Fatima Bonaldo,
Ph.D. Clone distribution: clones will be available through Research
Genetics

Seq primer: M13 Forward.

FEATURES
source

```
Location/Qualifiers  
1..328  
/organism="Rattus norvegicus"  
/strain="Sprague-Dawley"  
/db_xref="taxon:10116"  
/clone="UI-R-C2p-nq-e-02-0-UI"  
/clone_lib="UI-R-C2p"  
/dev_stage="adult"  
/lab_host="DH10B (Life Technologies)"  
/note="Vector: pT73D-Pac (Pharmacia) with a modified  
polylinker; Site 1: Not I; Site 2: Eco RI; The UI-R-C2p  
library is a subtracted library derived from the UI-R-C1  
library, which is a subtracted library derived from the  
UI-R-C0 library. The UI-R-C0 library consisted of a  
mixture of individually tagged normalized libraries  
constructed from rat placenta, adult lung, brain, liver,  
kidney, heart, spleen, ovary, muscle, 8, 12 and 18-day  
embryo. The tag is a string of 3-5 nucleotides present  
between the Not I site and the oligo-dT track which allows  
identification of the library of origin of a clone within  
the mixture. The subtracted library (UI-R-C2p) was  
constructed as follows: PCR amplified cDNA inserts from  
UI-R-C1 clones from which 3' ESTs had been derived was  
used as a driver in a hybridization with the UI-R-C1  
library in the form of single-stranded circles. The  
remaining single-stranded circles (subtracted library) was  
purified by hydroxyapatite column chromatography,  
converted to double-stranded circles and electroporated  
into DH10B bacteria (Life Technologies) to generate the  
UI-R-C2p library. This procedure has been previously  
described (Bonaldo, Lennon and Soares, Genome Research 6:  
791-806, 1996)"
```

BASE COUNT 62 a 77 c 98 g 91 t

ORIGIN

Alignment Scores:

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Pred. No.: 6,33e-09 Length: 328  
Score: 156.50 Matches: 30  
Percent Similarity: 71.93% Conservative: 11  
Best Local Similarity: 52.63% Mismatches: 15  
Query Match: 39.22% Indels: 1  
DB: 9 Gaps: 1
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US-09-092-296-15 (1-78) x A1136523 (1-328)

```
Qy 21 GlyPro--GlyMetThrLeuGlnLeuLysLeuLysGluSerPheLeuThrAsnSerSer 39  
Db 313 GGGCCCAACAAGGTGACTTTGCAAGTAAAGTCAAGCGAGGCATCTCAGGCCAAGACCTCC 254  
Qy 40 TyrGluSerSerPheLeuGluLeuLeuGluLysLeuLysCysLeuLeuHisLeuProSer 59  
Db 253 CAAGACTCCGGCTTTCTGGACATGCTCCAAAGATCTGCTCTCTCCACCTCTCCACCG 194  
Qy 60 GlyThrSerValThrLeuHisHisAlaArgSerGlnHisHisValValCys 76  
Db 193 GGGACCAATGTCAACCTTTCATATAAAGGGCCACACACCTTACCTGC 143
```

RESULT 13


```

BF511043/3
UI-H-B14-apl-f-12-0-UI.s1 NCI_CGAP_Sub8 Homo sapiens cDNA clone
IMAGE:3087887 3', mRNA sequence.
BF511043
BF511043.1 GI:11594341
EST.
human.
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 244)
NCI-CCGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: craps@remail.nih.gov
The sequence contained an oligo-dT track that was present in the
oligonucleotide that was used to prime the synthesis of first
strand cDNA and therefore this may represent a bonafide poly A
tail. cDNA library Preparation: M.B. Soares Lab Clone distribution:
NCI-CCGAP clone distribution information can be found through the
I.M.A.G.E. Consortium/LINL at:
www-bio.lnl.gov/bbrp/image/image.html
Seq primer: M13 Forward
POLYA=Yes.
Location/Qualifiers
1..244
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:3087887"
/clone_lib="NCI_CGAP_Sub8"
/lab_host="PH10B (Life Technologies)"
/notes="Vector: pT73D-Pac (Pharmacia) with a modified
polylinker; Site_1: Not I; Site_2: Eco RI; NCI_CGAP_Sub8
is a subcloned library derived from NCI_CGAP_Sub5. The
NCI_CGAP_Sub8 library had 2.5 million recombinants. A
single-stranded DNA preparation of NCI_CGAP_Sub5 was used
as a tracer in a subtractive hybridization with a driver
comprising: a pool of clones from NCI_CGAP_Sub5 (IMAGE
clone ids 2732833-2737415, 3068040-3069191; 25% of the
driver population), a pool of clones from NCI_CGAP_Sub4
(IMAGE clone ids 2723592-2729326; 25% of the driver
population), NCI_CGAP_Sub6 (pool A1F-A10, IMAGE ids
2728969-2733190; 25% of the driver population), and
NCI_CGAP_Sub7 (IMAGE ids 3069192-3072238, 3081864-3084550
; 25% of the driver population). Subtraction was
performed as previously described (Bonaldi, Lennon &
Soares (1996): Normalization and Subtraction: Two
Approaches to Facilitate Gene Discovery. Genome Research
6: 791-806.
TAG_LIB=NCI_CGAP_C04
TAG_TISSUE=COLON
TAG_SEQ=CTTCCG"
BASE COUNT 51 a 54 c 68 g 71 t
ORIGIN
Alignment Scores:
Pred. No.: 1,7e-07 Length: 244
Score: 143.00 Matches: 26
Percent Similarity: 93.33% Conservative: 2
Best Local Similarity: 86.67% Mismatches: 2
Query Match: 35.84% Indels: 0
DB: 12 Gaps: 0
US-09-092-296-15 (1-7B) x BF511043 (1-244)
QY 49 GlulysLeuLeuLeuHisLeuProSerGlyThrSerValThrLeuHisAla 68
||||| :|||:|||||:|||||:|||||:|||||:|||||:|||||
Db 243 GAAAGATGTACATCTCGTCCATCTCCCTCAGGACAAAGAGTCCCTCCACCATGCA 184
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 69 ArqSerGlnHisValValCysAsnThr 78
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

```

Db	341	ARCTCAGTCTCTCTGGACATCTCTCAARAAGGTAGTTTTT	AGGTAGCTAGCGGGATAGCAGTGGT	282
QY	50	-----	-----	50
Db	281	ACTGCACGCTTCTCTGGGTCCTGCAGGTCCTCTCTGCTGGGGCTGGCTGAGTGGAGCAGGG		222
QY	51	-----	-----	54
Db	221	AGTGGGTACCACTTACACCTCATCTCGGATCATTTATGTATACCCAGATCTGCTCCCT		162
QY	54	uLeuHisLeuProSerGlyThrSerValThrLeuHisHisAlaArgSerGlnHisIleVa		74
Db	161	CTTCCATCTGGCATCAGGACCAATGTCACCTCTCTTTCACAAAGGACCAACCACTACCT		102
QY	74	lValCys		76
Db	101	TACTGC		95
RESULT	15			
LOCUS	AZ079350/c			
DEFINITION	RPCI-23-438H19_TV RPCI-23 Mus musculus genomic clone RPCI-23-438H19			
ACCESSION	AZ079350	633 bp	DNA	linear
VERSION	AZ079350			
KEYWORDS	GSS.			
SOURCE	house mouse.			
ORGANISM	Mus musculus			
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.			
AUTHORS	Zhao,S., Nicrman,W., Feldblyum,T., Malek,J., Shatsman,S., Akinret ,B., Levins,M., McGann,S., Tsegaye,G., Geer,K., Krol,M., de Jong,P. and Fraser,C.M.			
TITLE	Mouse BAC End Sequences from Library RPCI-23			
JOURNAL	Unpublished (1999)			
COMMENT	Other_GSSs: RPCI-23-438H19_TV Contact: Shaying Zhao Department of Eukaryotic Genomics The Institute for Genomic Research 9712 Medical Center Dr., Rockville, MD 20850, USA Tel: 301 838 0200 Fax: 301 838 0208 Email: szhao@tigr.org Clones are derived from the mouse BAC library RPCI-23. For BAC library availability, please contact Pieter de Jong (pieter@jeng.med.buffalo.edu). Clones may be purchased from BACPAC Resources (http://bacpac.med.buffalo.edu/orderingframe.htm) or from Resea ch Genetics (info@resgen.com). BAC end page: http://www.tigr.org/tdb/bac_ends/mouse/bac_end_intro.html plate: 438 row: H column: 19 Seq primer: T7 Class: BAC ends.			
FEATURES	Location/Qualifiers			
source	1..633			
	/organism="Mus musculus"			
	/strain="C57BL/6J"			
	/db_xref="taxon:10090"			
	/clone="RPCI-23-438H19"			
	/clone.lib="RPCI-23"			
	/sex="Female"			
	/lab_host="DH10B"			
	/note="Organ: Kidney/Brain; Vector: pBACe3.6; Site_1: EcoRI; Site_2: EcoRI; Female C57BL/6J mouse kidney and/or brain genomic DNA was isolated and partially digested with a combination of EcoRI and EcoRI MethyIase. Size selected DNA was cloned into the pBACe3.6 vector at the EcoRI sites. The ligation products were transformed into DH10B electrocompetent cells (BRL Life Technologies)."			
BASE COUNT	138 a	191 c	161 g	143 t
ORIGIN				

GenCore version 5.1.5
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: May 1, 2003, 05:14:32 ; Search time 218 Seconds
(without alignments)
805.761 Million cell updates/sec

Title: US-09-092-296-15

Perfect score: 399

Sequence: 1 MGSGLPLVLLILLGSSHGT.....SGTSVTLHARSQHVVVNCVT 78

Scoring table:

BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 2185239 seqs, 1125999159 residues

Total number of hits satisfying chosen parameters: 4370478

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

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-DB=N_Geneseq_101002 -QFMT=p2n.rng -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS-human40.cdi
-LIST=45 -DOCALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFMT=ptc -NORM=ext -HEAPSIZ=500 -MINLEN=0 -MAXLEN=2000000000
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-NO_XLPAY -NO_MAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

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23: /SID52/gcgdata/geneseq/geneseq-emb1/NA2001B.DAT.*
24: /SID52/gcgdata/geneseq/geneseq-emb1/NA2002.DAT.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Length	DB	ID	Description
1	399	100.0	422	21	AAZ65087	Membrane-bound pro
2	399	100.0	422	21	AAZ65087	Human DNA encoding
3	399	100.0	422	22	AAF92090	Human PRO1098 CDNA
4	399	100.0	422	22	AAF42233	Human PRO1098 (ONQ
5	399	100.0	431	21	AAZ96124	Human signal pepti
6	399	100.0	439	20	AAV84366	Human stomach carc
7	349	87.5	624	24	ABK81818	DNA representing 1
8	161.5	40.5	729	23	AAZ65519	DNA encoding novel
9	75	18.8	715	22	AAH70861	Human cervical can
10	75	18.8	1248	23	ABL20661	Drosophila melanog
11	75	18.8	3323	23	ABL20660	Drosophila melanog
12	73	18.3	23580	22	AAZ85556	Genomic sequence #
13	73	18.3	23580	22	AAK87248	Human immune/haema
14	73	18.3	86080	24	ABQ88164	Human osteoblast d
15	73	18.3	86080	24	ABK83561	Human CDNA differe
16	72.5	18.2	785	21	AAA72675	plastidial phospho
17	72.5	18.2	1733	20	AAZ59149	Pea mutant plastid
18	72.5	18.2	1875	20	AAZ59146	Pea wild-type plas
19	72.5	18.2	2006	20	AAZ59147	Pea mutant plastid
20	72.5	18.2	2182	19	AAV00731	Human plastidial pho
21	71	17.8	1571	24	ABL90445	Human polynucleoti
22	71	17.8	1650	21	AAZ97083	Human secreted pro
23	71	17.8	1853	21	AAZ64286	Human membrane-ass
24	71	17.8	1949	22	AAH25763	Oesophagus cancer
25	71	17.8	1952	24	ABK49215	cDNA encoding huma
26	71	17.8	1970	21	AAZ76344	Human ORFX ORF1899
27	70.5	17.7	1668	23	ABL22127	Drosophila melanog
28	70.5	17.7	3905	23	ABL22126	Drosophila melanog
29	70	17.5	874	21	AAH76583	Human ORFX ORF2138
30	70	17.5	2545	22	AAH17805	Human CDNA sequenc
31	70	17.5	13485	22	AAZ31469	Human DNA for a no
32	70	17.5	13485	22	ABK44039	Genomic DNA encodi
33	70	17.5	13485	24	ABQ66793	Human polynucleoti
34	69	17.3	2094	23	AAZ78887	DNA encoding novel
35	69	17.3	3631	22	AAA09590	Human phosphodiester
36	69	17.3	3631	22	ABA03665	Human PDE10A CDNA
37	69	17.3	4576	21	AAA09589	Human phosphodiester
38	69	17.3	11809	22	AAZ21072	Human nervous syst
39	69	17.3	11809	22	AAZ21072	Human reproductive
40	68.5	17.2	9751	22	AAZ18386	Recombinant viral
41	68.5	17.2	9751	24	ABL60796	FIV-Oma3 recombin
42	68.5	17.2	23474	23	AAZ59511	Propionibacterium
43	68.5	17.2	26997	22	AAZ46748	Tumour suppressor
44	68	17.0	2554	21	AAZ36963	DNA encoding a hum
45	68	17.0	2798	21	AAZ36964	DNA encoding a hum

ALIGNMENTS

RESULT 1	
AAZ65087	
ID	AAZ65087 standard; cDNA; 422 bp.
XX	
AC	AAZ65087;
XX	
DT	05-APR-2000 (first entry)
XX	
DE	Membrane-bound protein PRO1098 encoding cDNA.
XX	
KW	Membrane-bound polypeptide; PRO polypeptide; LDL receptor; TIE ligand;
KW	pharmaceutical; receptor immunoadhesin; gene mapping; ss.
OS	Homo sapiens.
XX	
PN	W09963088-A2.
PD	09-DEC-1999.

XX 02-JUN-1999; 99WO-US12252.
PF 98US-0087607.
XX 02-JUN-1998;
PR 98US-0087609.
PR 02-JUN-1998;
PR 98US-0087759.
PR 03-JUN-1998;
PR 98US-0087827.
PR 04-JUN-1998;
PR 98US-0088021.
PR 04-JUN-1998;
PR 98US-0088025.
PR 04-JUN-1998;
PR 98US-0088028.
PR 04-JUN-1998;
PR 98US-0088029.
PR 04-JUN-1998;
PR 98US-0088030.
PR 04-JUN-1998;
PR 98US-0088033.
PR 04-JUN-1998;
PR 98US-0088326.
PR 05-JUN-1998;
PR 98US-0088167.
PR 05-JUN-1998;
PR 98US-0088202.
PR 05-JUN-1998;
PR 98US-0088212.
PR 05-JUN-1998;
PR 98US-0088217.
PR 09-JUN-1998;
PR 98US-0088655.
PR 10-JUN-1998;
PR 98US-0088722.
PR 10-JUN-1998;
PR 98US-0088730.
PR 10-JUN-1998;
PR 98US-0088734.
PR 10-JUN-1998;
PR 98US-0088738.
PR 10-JUN-1998;
PR 98US-0088740.
PR 10-JUN-1998;
PR 98US-0088741.
PR 10-JUN-1998;
PR 98US-0088742.
PR 10-JUN-1998;
PR 98US-0088810.
PR 10-JUN-1998;
PR 98US-0088811.
PR 10-JUN-1998;
PR 98US-0088824.
PR 10-JUN-1998;
PR 98US-0088825.
PR 10-JUN-1998;
PR 98US-0088826.
PR 11-JUN-1998;
PR 98US-0088858.
PR 11-JUN-1998;
PR 98US-0088861.
PR 11-JUN-1998;
PR 98US-0088863.
PR 11-JUN-1998;
PR 98US-0088876.
PR 12-JUN-1998;
PR 98US-0089090.
PR 12-JUN-1998;
PR 98US-0089105.
PR 16-JUN-1998;
PR 98US-0089440.
PR 16-JUN-1998;
PR 98US-0089512.
PR 16-JUN-1998;
PR 98US-0089514.
PR 17-JUN-1998;
PR 98US-0089532.
PR 17-JUN-1998;
PR 98US-0089538.
PR 17-JUN-1998;
PR 98US-0089598.
PR 17-JUN-1998;
PR 98US-0089599.
PR 17-JUN-1998;
PR 98US-0089600.
PR 17-JUN-1998;
PR 98US-0089653.
PR 18-JUN-1998;
PR 98US-0089801.
PR 18-JUN-1998;
PR 98US-0089907.
PR 18-JUN-1998;
PR 98US-0089908.
PR 19-JUN-1998;
PR 98US-0089947.
PR 19-JUN-1998;
PR 98US-0089948.
PR 19-JUN-1998;
PR 98US-0089952.
PR 22-JUN-1998;
PR 98US-0090246.
PR 22-JUN-1998;
PR 98US-0090252.
PR 22-JUN-1998;
PR 98US-0090254.
PR 23-JUN-1998;
PR 98US-0090349.
PR 23-JUN-1998;
PR 98US-0090355.
PR 24-JUN-1998;
PR 98US-0090429.
PR 24-JUN-1998;
PR 98US-0090431.
PR 24-JUN-1998;
PR 98US-0090435.
PR 24-JUN-1998;
PR 98US-0090444.
PR 24-JUN-1998;
PR 98US-0090445.
PR 24-JUN-1998;
PR 98US-0090451.
PR 24-JUN-1998;
PR 98US-0090472.
PR 24-JUN-1998;
PR 98US-0090535.
PR 24-JUN-1998;
PR 98US-0090538.
PR 24-JUN-1998;
PR 98US-0090540.
PR 24-JUN-1998;
PR 98US-0090557.
PR 25-JUN-1998;
PR 98US-0090676.
PR 25-JUN-1998;
PR 98US-0090678.
PR 25-JUN-1998;
PR 98US-0090688.
PR 25-JUN-1998;
PR 98US-0090690.
PR 25-JUN-1998;
PR 98US-0090691.

PR 25-JUN-1998;
PR 98US-0090694.
PR 25-JUN-1998;
PR 98US-0090695.
PR 25-JUN-1998;
PR 98US-0090696.
PR 26-JUN-1998;
PR 98US-0090862.
PR 26-JUN-1998;
PR 98US-0090863.
PR 01-JUL-1998;
PR 98US-0091358.
PR 01-JUL-1998;
PR 98US-0091360.
PR 01-JUL-1998;
PR 98US-0091544.
PR 02-JUL-1998;
PR 98US-0091478.
PR 02-JUL-1998;
PR 98US-0091486.
PR 02-JUL-1998;
PR 98US-0091519.
PR 02-JUL-1998;
PR 98US-0091626.
PR 02-JUL-1998;
PR 98US-0091628.
PR 02-JUL-1998;
PR 98US-0091633.
PR 02-JUL-1998;
PR 98US-0091646.
PR 02-JUL-1998;
PR 98US-0091673.
PR 02-JUL-1998;
PR 98US-0091678.
PR 07-JUL-1998;
PR 98US-0091978.
PR 07-JUL-1998;
PR 98US-0091982.
PR 09-JUL-1998;
PR 98US-0092182.
PR 10-JUL-1998;
PR 98US-0092472.
PR 20-JUL-1998;
PR 98US-0093339.
PR 30-JUL-1998;
PR 98US-0094651.
PR 04-AUG-1998;
PR 98US-0095282.
PR 04-AUG-1998;
PR 98US-0095285.
PR 04-AUG-1998;
PR 98US-0095301.
PR 04-AUG-1998;
PR 98US-0095302.
PR 04-AUG-1998;
PR 98US-0095318.
PR 04-AUG-1998;
PR 98US-0095321.
PR 04-AUG-1998;
PR 98US-0095325.
PR 10-AUG-1998;
PR 98US-0095916.
PR 10-AUG-1998;
PR 98US-0095929.
PR 10-AUG-1998;
PR 98US-0096012.
PR 11-AUG-1998;
PR 98US-0096143.
PR 11-AUG-1998;
PR 98US-0096146.
PR 12-AUG-1998;
PR 98US-0096329.
PR 17-AUG-1998;
PR 98US-0096757.
PR 17-AUG-1998;
PR 98US-0096766.
PR 17-AUG-1998;
PR 98US-0096768.
PR 17-AUG-1998;
PR 98US-0096773.
PR 17-AUG-1998;
PR 98US-0096791.
PR 17-AUG-1998;
PR 98US-0096867.
PR 17-AUG-1998;
PR 98US-0096891.
PR 17-AUG-1998;
PR 98US-0096894.
PR 17-AUG-1998;
PR 98US-0096895.
PR 17-AUG-1998;
PR 98US-0096897.
PR 18-AUG-1998;
PR 98US-0096949.
PR 18-AUG-1998;
PR 98US-0096950.
PR 18-AUG-1998;
PR 98US-0096959.
PR 18-AUG-1998;
PR 98US-0096960.
PR 18-AUG-1998;
PR 98US-0097022.
PR 19-AUG-1998;
PR 98US-0097141.
PR 20-AUG-1998;
PR 98US-0097218.
PR 24-AUG-1998;
PR 98US-0097661.
PR 26-AUG-1998;
PR 98US-0097951.
PR 26-AUG-1998;
PR 98US-0097952.
PR 26-AUG-1998;
PR 98US-0097954.
PR 26-AUG-1998;
PR 98US-0097955.
PR 26-AUG-1998;
PR 98US-0097971.
PR 26-AUG-1998;
PR 98US-0097974.
PR 26-AUG-1998;
PR 98US-0097978.
PR 26-AUG-1998;
PR 98US-0097979.
PR 26-AUG-1998;
PR 98US-0097986.
PR 26-AUG-1998;
PR 98US-0098014.
PR 31-AUG-1998;
PR 98US-0098525.
PR 16-SEP-1998;
PR 98US-0100634.
PR 12-JAN-1999;
PR 99US-0115565.

(GETH) GENENTECH INC.

XX Baker K, Chen J, Goddard A, Smith V, Watanabe CK;
PI Wood WI, Yuan J;
PI

XX WPT; 2000-072883/06.

DR

DR P-PSDB; AAY66741.
XX Membrane-bound proteins and related nucleotide sequences -
XX
XX
PS Claim 2; Fig 257; 822pp; English.
XX
CC The invention provides membrane-bound PRO polypeptides and
CC polynucleotides encoding them. The PRO sequences of the invention were
CC identified based on extracellular domain homology screening. The PRO
CC sequences have homology with proteins including LDL receptors, TIE
CC ligands and various enzymes. The membrane-bound proteins and receptor
CC molecules are useful as pharmaceutical and diagnostic agents. Receptor
CC immunoadhesins, for instance, can be used as therapeutic agents to block
CC receptor-ligand interactions. The membrane-bound proteins can also be
CC employed for screening of potential peptide or small molecule inhibitors
CC of the relevant receptor/ligand interaction. The PRO encoding sequences
CC are useful as hybridization probes, in chromosome and gene mapping and in
CC the generation of antisense RNA and DNA. PRO nucleic acid sequences
CC will also be useful for the preparation of PRO polypeptides, especially
CC by recombinant techniques.
XX
SQ Sequence 422 BP; 84 A; 134 C; 104 G; 100 T; 0 other;

Alignment Scores:
Pred. No.: 1-55e-43 Length: 422
Score: 399.00 Matches: 78
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
Dbs: 21 Gaps: 0

US-09-092-296-15 (1-78) x AAZ65087 (1-422)

QY 1 MetGlySerGlyLeuProLeuValLeuLeuThrLeuLeuGlySerHisGlyThr 20
|||||
Db 58 ATGGGGTCUGGGCTGCCCTTCCTCTCTGACCCCTCTTGCGGCGACTCACATGGAACA 117
QY 21 GlyProGlyMetThrLeuGlnLeuLeuGlySerPheLeuThrAsnSerSerTyr 40
|||||
Db 118 GGCCCGGGTATGACTTTGGCACTGAAGCTGAAGGAGTCTTTCTGACAAATTCCTCCTAT 177
QY 41 GluSerSerPheLeuGluLeuLeuGlyLeuGlyLeuLeuHisLeuProSerGly 60
|||||
Db 178 GAGTCCAGCTTCCTGGGAATTCCTGAAAAGCTCTGCCTCTCTCCATCTCCCTTCAGGG 237
QY 61 ThrSerValThrLeuHisHisAlaArgSerGlnHisHisValValCysAsnThr 78
|||||
Db 238 ACCAGCGTACCCCTCCACCATGCAAGATCTCAACACCATGTTGTCGCAACACA 291

RESULT 2
AAS46045
ID AAS46045 standard; cDNA; 422 BP.
XX
XX
AC AAS46045;
XX
XX
DT 18-DEC-2001 (first entry)
XX
DE Human DNA encoding PRO polypeptide sequence #121.
XX
KW PRO polypeptide; mammal; tumour; cancer; human; cattle; horse; sheep; ss;
KW dog; cat; pig; goat; rabbit; tumour necrosis factor alpha; TNF-alpha;
KW blood; chondrocyte cell; cell proliferation; cell differentiation; colon;
KW adrenal; lung; breast; prostate; rectum; cervix; liver; genetic disorder;
KW PCR primer.
XX
OS Homo sapiens.
XX
FN WO200168848-A2.
XX
PD 20-SEP-2001.
XX
PF 28-FEB-2001; 2001WO-US06520.

PR 01-MAR-2000; 2000WO-US05601.
PR 02-MAR-2000; 2000WO-US05641.
PR 03-MAR-2000; 2000US-187202P.
PR 06-MAR-2000; 2000US-186968P.
PR 14-MAR-2000; 2000US-189320P.
PR 14-MAR-2000; 2000US-189328P.
PR 15-MAR-2000; 2000WO-US06884.
PR 21-MAR-2000; 2000US-190828P.
PR 21-MAR-2000; 2000US-191007P.
PR 21-MAR-2000; 2000US-191048P.
PR 21-MAR-2000; 2000US-191314P.
PR 28-MAR-2000; 2000US-192655P.
PR 29-MAR-2000; 2000US-193032P.
PR 29-MAR-2000; 2000US-193053P.
PR 30-MAR-2000; 2000WO-US08439.
PR 04-APR-2000; 2000US-194449P.
PR 04-APR-2000; 2000US-194647P.
PR 11-APR-2000; 2000US-195975P.
PR 11-APR-2000; 2000US-196000P.
PR 11-APR-2000; 2000US-196187P.
PR 11-APR-2000; 2000US-196690P.
PR 11-APR-2000; 2000US-196820P.
PR 18-APR-2000; 2000US-198121P.
PR 18-APR-2000; 2000US-198585P.
PR 25-APR-2000; 2000US-199397P.
PR 25-APR-2000; 2000US-199550P.
PR 25-APR-2000; 2000US-199654P.
PR 03-MAY-2000; 2000US-201516P.
PR 17-MAY-2000; 2000WO-US13705.
PR 22-MAY-2000; 2000WO-US14042.
PR 30-MAY-2000; 2000WO-US14941.
PR 02-JUN-2000; 2000WO-US15264.
PR 05-JUN-2000; 2000US-209832P.
PR 28-JUL-2000; 2000WO-US20710.
PR 22-AUG-2000; 2000US-0644848.
PR 24-AUG-2000; 2000WO-US23328.
PR 08-NOV-2000; 2000WO-US30952.
PR 01-DEC-2000; 2000WO-US32678.
PR 20-DEC-2000; 2000WO-US34956.
XX
XX (GETH) GENENTECH INC.
XX
XX Baker KP, Chen J, Desnoyers L, Goddard A, Godowski PJ, Gurney AL;
PI Pan J, Smith V, Watanabe CK, Wood WI, Zhang Z;
XX
XX WPI; 2001-602746/68.
DR P-PSDB; AAU29144.
XX
XX Novel nucleic acids encoding PRO polypeptides, used to diagnose the
PT presence of tumours, such as prostate and breast tumours, in mammals and
PT to screen for modulators of the compounds -
XX
PS Claim 2; Fig 241; 774pp; English.
XX
CC Sequences AAS45925-AAS46231 represent DNA molecules encoding and PCR
CC primers for PRO polypeptides of the invention. The sequences of the
CC invention can be used to detect the presence of a tumour in a mammal by
CC comparing the level of expression of a PRO polypeptide in a test sample
CC of cells from the animal and a control sample of normal cells, whereby a
CC higher level of expression in the test sample indicates the presence of a
CC tumour in the mammal. Mammals include dogs, cats, cattle, horses, sheep,
CC pigs, goats and rabbits but are preferably human. The polypeptides can be
CC used to stimulate tumour necrosis factor (TNF) alpha release from human
CC blood, when contacted with it. A specific polypeptide can be used to
CC stimulate the proliferation or differentiation of chondrocyte cells. The
CC PRO proteins can be used to determine the presence of tumours and also
CC susceptibility to tumour development, particularly adrenal, lung, colon,
CC breast, prostate, rectal, cervical, or liver tumours, in mammalian
CC subjects. The oligonucleotide probes specific for the PRO nucleic acids
CC can be used for genetic analysis of individuals with genetic disorders.
XX
SQ Sequence 422 BP; 84 A; 134 C; 104 G; 100 T; 0 other;


```
SQ Sequence 431 BP; 93 A; 135 C; 101 G; 102 T; 0 other;

Alignment Scores:
Pred. No.: 1.6e-43 Length: 431
Score: 399.00 Matches: 78
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 21 Gaps: 0

US-09-092-296-15 (1-78) x AAZ98124 (1-431)
Qy 1 MetGlySerGlyLeuProLeuValLeuLeuThrLeuLeuGlySerSerHisGlyThr 20
Db 51 ATGGGGTCGGGGTCGCCCTGTCTCTCTGACCCCTCTTGGCAGCTCACATGGAACA 110

Qy 21 GlyProGlyMetThrLeuGlnLeuLysLeuLysGluSerPheLeuThrAsnSerSerTyr 40
Db 111 GGGCCGGGTATGACTTTGCAACTGAAGCTGAAGGAGTCTTTCTGCAAAATTCCTCTAT 170

Qy 41 GluSerSerPheLeuGluLeuLeuGluLysLeuCysLeuLeuHisLeuProSerGly 60
Db 171 GAGTCCAGCTTCTCGAATTGCTTGAAGAAGCTCTGCCTCTCTCCATCTCCCTTCAGGG 230

Qy 61 ThrSerValThrLeuHisHisAlaArgSerGlnHisHisValValCysAsnThr 78
Db 231 ACCAGGTCACCCCTCCACCTGCAAGTCTCAACACCATGTTGTGTGCAACACA 284

RESULT 6
AAV84366
ID AAV84366 standard; cDNA to mRNA; 439 BP.
AC
XX
AC AAV84366;
XX
30-MAR-1999 (first entry)
XX
DE Human stomach carcinoma cDNA clone HP10408.
XX
KW Transmembrane protein; HP10408; human; stomach cancer; ds.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 75..311
FT /tag= a
FT /note= "cDNA comprising the coding region (minus
FT the stop codon) is claimed (Claim 3)."
XX
PN WO9855508-A2.
XX
PD 10-DEC-1998.
XX
PF 03-JUN-1998; 98WO-JP02445.
XX
PR 03-JUN-1997; 97JP-0144948.
XX
PA (PROT-) PROTEGENE INC.
PA (SAGA ) SAGAMI CHEM RES CENTRE.
XX
PI Kato S, Sekine S, Yamaguchi T;
XX
DR WPI; 1999-045730/04.
DR P-PSDB; AAW88498.
XX
PT New human proteins containing transmembrane domains and their
PT encoding sequences - useful in the preparation of antibodies and
PT large-scale protein production, gene diagnosis, and gene therapy
XX
PS Claim 4; Page 135; 178pp; English.
XX
CC This is the nucleotide sequence of cDNA clone HP10408, which
CC includes a coding region (also claimed) for a novel human
CC transmembrane protein (see AAW88498). The clone was isolated from a
```

```
CC stomach cancer cDNA library using a signal sequence detection
CC method, and by protein synthesis by in vitro translation. The
CC encoded protein has a putative signal sequence and a putative
CC internal transmembrane domain. The invention provides nucleotide
CC sequences (see AAV84359-76) coding for 18 transmembrane proteins
CC (see AAW88491-508), vectors containing such polynucleotides, and
CC eukaryotic cells containing the vectors. The proteins can be
CC used as antigens or as compositions in the preparation of
CC antibodies against the proteins. The polynucleotides can be used
CC as probes for gene diagnosis, and as gene sources for gene therapy
CC and large-scale production of proteins encoded by the cDNA. The
CC host cells are used for the detection of ligands corresponding to
CC the expressed proteins, and the screening of low mol.wt. medicines.
XX
SQ Sequence 439 BP; 89 A; 137 C; 109 G; 104 T; 0 other;

Alignment Scores:
Pred. No.: 1.64e-43 Length: 439
Score: 399.00 Matches: 78
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 20 Gaps: 0

US-09-092-296-15 (1-78) x AAV84366 (1-439)
Qy 1 MetGlySerGlyLeuProLeuValLeuLeuThrLeuLeuGlySerSerHisGlyThr 20
Db 75 ATGGGGTCGGGGTCGCCCTGTCTCTCTTGGACCCCTCTTGGCAGCTCACATGGAACA 134

Qy 21 GlyProGlyMetThrLeuGlnLeuLysLeuLysGluSerPheLeuThrAsnSerTyr 40
Db 135 GGGCCGGGTATGACTTTGCAACTGAAGCTGAAGGAGTCTTTCTGCAAAATTCCTCTAT 194

Qy 41 GluSerSerPheLeuGluLeuLeuGluLysLeuCysLeuLeuHisLeuProSerGly 60
Db 195 GAGTCCAGCTTCTCGAATTGCTTGAAGAAGCTCTGCCTCTCTCCATCTCCCTTCAGGG 254

Qy 61 ThrSerValThrLeuHisHisAlaArgSerGlnHisHisValValCysAsnThr 78
Db 255 ACCAGGTCACCCCTCCACCATGCAAGTCTCAACACCATGTTGTGTGCAACACA 308

RESULT 7
ABK81818
ID ABK81818 standard; DNA; 624 BP.
XX
AC ABK81818;
XX
XX
XX 13-AUG-2002 (first entry)
XX
DE DNA representing lung specific gene #4.
XX
KW Lung specific gene; gene therapy; vaccine; lung cancer;
KW cancer staging; cancer monitoring; cancer diagnosis;
KW imaging lung cancer; metastases; gene; ss.
XX
OS Homo sapiens.
XX
PN WO200218576-A2.
XX
PD 07-MAR-2002.
XX
PF 27-AUG-2001; 2001WO-US26684.
XX
PR 28-AUG-2000; 2000US-228378P.
XX
PA (DIAD-) DIADEXUS INC.
XX
PI Chen S, Macina RA, Sun Y, Recipon H;
XX
DR WPI; 2002-434904/46.
XX
PT New lung specific genes and their encoded proteins, useful in gene
```


PT therapy or as a vaccine for treating lung cancer, as well as for
PT measuring metastases of lung cancer, or staging, monitoring, diagnosing
PT or imaging lung cancer -
XX
XX
XX Claim 1; Page 161; 206pp; English.
XX
XX The invention describes a new lung specific gene and it's variants. The
CC lung specific gene proteins and genes are useful in gene therapy or as a
CC vaccine for treating lung cancer. Lung specific genes are also useful for
CC staging, monitoring, diagnosing or imaging lung cancer, as well as for
CC measuring metastases of lung cancer. This sequence represents a lung
CC specific gene described in the invention.
XX
XX
SQ Sequence 624 BP; 129 A; 175 C; 182 G; 138 T; 0 other;

Alignment Scores:
Pred. No.: 1.13e-36 Length: 624
Score: 349.00 Matches: 78
Percent Similarity: 49.37% Conservative: 0
Best Local Similarity: 49.37% Mismatches: 0
Query Match: 87.47% Indels: 80
DB: 24 Gaps: 1

US-09-092-296-15 (1-78) x ABR81818 (1-624)

QY 1 MetGlySerGlyLeuProLeuValLeuLeuLeuThrLeuGlySerSerHisGlyThr 20
DB 16 ATGGGTCCTGGGCTGCCCCCTGTCTCTTGACCTCTCTGGCAGCTCAGATGAACA 75
QY 20 ----- 20
DB 76 GGTGAGGCTAGAGGGCAGGAGCTCTGGTCCCTGGCAAGAAGAGCCAGAGAAAGG 135
QY 20 ----- 20
DB 136 GGTGGAGCTTCATGTCCTCGAGAGTGACAGAGACACCCAGTCTGAGTTCAGAGAG 195
QY 20 ----- 20
DB 196 CTCTGAGGGGCAATTCCTGGGAAGAGGAAGTGTGCCGGGAGCGTGAGCAGGAAGTTC 255
QY 20 ----- 20
DB 256 TGTGCTCGGAGGAATCAGCCCTGACTGCTGGTGGCTCTAAGCTGACTTGGATCGCA 315
QY 21 GlyProGlyMetThrLeuGlnLeuLysLeuLysGluSerPheLeuThrAsnSerSerTyr 40
DB 316 GGGCGGGTATGACTTTGCCAACTGAAGCTGAAGGAGTCTTTTCTGACAAATTCCTCTAT 375
QY 41 GluSerSerPheLeuGlnLeuLeuGluLysLeuCysLeuLeuLeuHisLeuProSerGly 60
DB 376 GAGTCCAGCTCTCTGGAAATTCCTTGAAGCTCTGCCCTCTCTCTCTCTCTCTCAGGG 435
QY 61 ThrSerValThrLeuHisHisAlaArgSerGlnHisHisValValCysAsnThr 78
DB 436 ACCAGGGTCACCCCTCCACCATGCAAGATCTCAACACCATGTTGTCTGCAACACA 489

RESULT 8
NAS65519
ID AS65519 standard; cDNA; 729 BP.
XX
XX AC AS65519;
XX
XX 13-FEB-2002 (first entry)
XX
XX DNA encoding novel human diagnostic protein #1323.
XX
XX Human; chromosome mapping; gene mapping; gene therapy; forensic;
KW food supplement; medical imaging; diagnostic; genetic disorder; ss.
XX
XX Homo sapiens.
OS
XX WO200175067-A2.
PN

XX 11-OCT-2001.
PD
XX 30-MAR-2001; 2001WO-US08631.
PF
XX 31-NAR-2000; 2000US-0540217.
PR 23-AUG-2000; 2000US-0649167.
XX (HYSE-) HYSEQ INC.
PA
XX Drmanac RT, Liu C, Tang YT;
PI
XX WPI; 2001-639362/73.
DR P-PADB; ABG01332.
XX
XX New isolated polynucleotide and encoded polypeptides, useful in
PT diagnostics, forensics, gene mapping, identification of mutations
PT responsible for genetic disorders or other traits and to assess
PT biodiversity -
XX
XX Claim 1; SEQ ID No 1323; 103pp; English.
XX
XX The invention relates to isolated polynucleotide (I) and
CC polypeptide (II) sequences. (I) is useful as hybridisation probes,
CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome
CC and gene mapping, and in recombinant products of (II). The
CC polynucleotides are also used in diagnostics as expressed sequence tags
CC for identifying expressed genes (I) or to treat disease states involving
CC (II). (II) is useful for generating antibodies against it, detecting or
CC to restore normal activity of (II) or to treat disease states involving
CC quantitating a polypeptide in tissue, as molecular weight markers and as
CC a food supplement. (II) and its binding partners are useful in medical
CC imaging of sites expressing (II). (I) and (II) are useful for treating
CC disorders involving aberrant protein expression or biological activity.
CC The polypeptide and polynucleotide sequences have applications in
CC diagnostics, forensics, gene mapping, identification of mutations
CC responsible for genetic disorders or other traits to assess biodiversity
CC and to produce other types of data and products dependent on DNA and
CC amino acid sequences. AAS64197-AAS94584 represent novel human
CC diagnostic coding sequences of the invention.
CC Note: The sequence data for this patent did not appear in the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 729 BP; 187 A; 169 C; 152 G; 146 T; 75 other;

Alignment Scores:
Pred. No.: 9.77e-12 Length: 729
Score: 161.50 Matches: 37
Percent Similarity: 66.07% Conservative: 0
Best Local Similarity: 66.07% Mismatches: 2
Query Match: 40.48% Indels: 17
DB: 23 Gaps: 1

US-09-092-296-15 (1-78) x AAS65519 (1-729)

QY 1 MetGlySerGlyLeuProLeuValLeuLeuLeuThrLeuGlySerSerHisGlyThr 20
DB 25 ATGGGCTCTGGGCTGCCCTCTGTCTCTCTGACCTCTTGGCAGCTCAGATGAACA 84
QY 21 GlyProGlyMetThrLeuGlnLeuLysLeuLysGlu----- 32
DB 85 GGACCGGGTATGACTTTTGCAACTGAAGCTGANGGGGGTCAAGAGGACACAGGCTTC 144
QY 33 -----SerPheLeuThrAsnSerSer 39
DB 145 AATGGCTGCAATTTCAAGGAAGTCACTTCTCTCTTAACACAGCAGC 192
RESULT 9
AAH70861/c
ID AAH70861 standard; cDNA; 715 BP.
XX
XX AC AAH70861;

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XX 19-SEP-2001 (first entry)
XX Human cervical cancer marker nucleic acid 2135.
XX Cervical cancer; cytostatic; pre-malignant condition; gene therapy; ss.
XX Homo sapiens.
XX WO200142467-A2.
XX 14-JUN-2001.
XX 08-DEC-2000; 2000WO-US33312.
XX 08-DEC-1999; 99US-0169681.
XX 21-DEC-1999; 99US-0171350.
XX 14-MAR-2000; 2000US-0189315.
XX 12-MAY-2000; 2000US-0203791.
XX 09-JUN-2000; 2000US-0210600.
XX 21-JUL-2000; 2000US-0220114.
XX (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
XX Schlegel R, Deeds J, Berger A, Zhao X;
XX WPI; 2001-375006/39.
XX New isolated nucleic acid for diagnosing and treating cervical cancer
XX and for assessing and detecting compounds for treating the cancer -
XX Claim 1; Page 451-452; 1051pp; English.
XX The invention relates to novel genes (AH68727-AH73383) associated with
XX cervical cancer with cytostatic activity. The nucleic acids and encoded
XX polypeptides are useful: to assess if a patient is afflicted with
XX cervical cancer or has a pre-malignant condition; to monitor the
XX progression of cervical cancer or a premalignant condition in a patient;
XX and to select and/or assess the efficacy of a compound or therapy for
XX inhibiting cervical cancer in a patient. The nucleic acids may also be
XX useful for gene therapy.
XX Sequence 715 BP; 247 A; 151 C; 138 G; 179 T; 0 other;
XX
XX Alignment Scores:
XX Pred. No.: 2.73 Length: 715
XX Score: 75.00 Matches: 23
XX Percent Similarity: 53.03% Conservative: 12
XX Best Local Similarity: 34.85% Mismatches: 25
XX Query Match: 18.80% Indels: 6
XX DB: 22 Gaps: 2
XX
XX US-09-092-296-15 (1-78) x AH70861 (1-715)
XX
XX QY 6 ProLeuValLeuLeuLeuLeuGlySerSerHisGlyThrGlyProGlyMetThr 25
XX 594 CCCTAGTACCGCGCGCAGCTTTGTGGAATTCGCTTCGACGGGCGCGGAGGTA 535
XX
XX QY 26 LeuLeuLeuLysLeuLysGluSerPheLeuThrAsnSerSerTyrGluSerSerPheLeu 45
XX 534 CTCATTCTAAGTAAATTAAGTATTAGGCTTCAAAATCTGAGATAGCTGCCACATT 475
XX
XX QY 46 GluLeuLeuGluLysLeuCys-----LeuLeuLeuHisLeuProSerGly 60
XX 474 GAGTTAATACATGAGATTTCTATCTCTGGAAGCTACTGAATATATCTGTCCAACT--- 418
XX
XX QY 61 ThrSerValThrLeuHis 66
XX 417 TGCAGCATACCATCCAT 400
XX
XX RESULT 10
XX ABL20661/c
XX ID ABL20661 standard; DNA; 1248 BP.
```

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XX ABL20661;
XX 26-MAR-2002 (first entry)
XX Drosophila melanogaster genomic polynucleotide SEQ ID NO 13456.
XX Drosophila; developmental biology; cell signalling; insecticide;
XX pharmaceutical; gene; ds.
XX Drosophila melanogaster.
XX WO200171042-A2.
XX 27-SEP-2001.
XX 23-MAR-2001; 2001WO-US09231.
XX 23-MAR-2000; 2000US-191637P.
XX 11-JUL-2000; 2000US-0614150.
XX (PEKE ) PE CORP NY.
XX Venter JC, Adams M, Li PWD, Myers EW;
XX WPI; 2001-656860/75.
XX New isolated nucleic acid detection reagent for detecting 1000 or more
XX genes from Drosophila and for elucidating cell signalling and cell-cell
XX interactions -
XX Claim 1; SEQ ID NO 13456; 21pp + Sequence Listing; English.
XX The invention relates to an isolated nucleic acid detection reagent
XX capable of detecting 1000 or more genes from Drosophila. The invention is
XX useful in developmental biology and in elucidating cell signalling and
XX cell-cell interactions in higher eukaryotes for the development of
XX insecticides, therapeutics and pharmaceutical drugs. The invention
XX discloses genomic DNA sequences (AB16176-AB16351), expressed DNA
XX sequences (AB101840-AB10175) and the encoded proteins
XX (AB15737-AB172072).
XX The sequence data for this patent did not form part of the printed
XX specification, but was obtained in electronic format directly from WIPO
XX at ftp.wipo.int/pub/published_pct_sequences.
XX
XX Sequence 1248 BP; 285 A; 375 C; 335 G; 253 T; 0 other;
XX
XX Alignment Scores:
XX Pred. No.: 6.02 Length: 1248
XX Score: 75.00 Matches: 25
XX Percent Similarity: 47.37% Conservative: 11
XX Best Local Similarity: 32.89% Mismatches: 30
XX Query Match: 18.80% Indels: 10
XX DB: 23 Gaps: 3
XX
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XX
XX QY 1 MetGlySerGlyLeuProLeuValLeuLeuLeuThrLeu----LeuGlySerSerHisGly 19
XX 753 CTGGGCGCTGGCGCTGAGCTGCTGCGACCTGAGCTGCTGGCGCTGAGCTGGCG 694
XX
XX QY 20 ThrGlyProGlyMetThrLeuGlnLeuLysLeuLysGluSerPheLeuThrAsnSerSer 39
XX 693 CTGGGATTTGAGTTTGTGATTCACCTGACCTGGTTAGCTGCTAGCTGCTAGCTCGG 634
XX
XX QY 40 TyrGluSerSerPheLeuGluLeuLeuGluLysLeuCysLeuLeuHisLeuProSer 59
XX 633 TATGATTCGGGC-----TGTCAACAGCTGCTCGCTCATCTTCATCAAGAACGG 586
XX
XX QY 60 GlyThrSerValThrLeuHisHisAlaArgSerGlnHisHisValVal 75
XX 585 AGCACCAACCATAGCGCTCCAT-----CATCATATCGTC 553
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PR 08-SEP-2000; 2000US-0231413.
PR 08-SEP-2000; 2000US-0231414.
PR 08-SEP-2000; 2000US-0232080.
PR 08-SEP-2000; 2000US-0232081.
PR 12-SEP-2000; 2000US-0231968.
PR 14-SEP-2000; 2000US-0222337.
PR 14-SEP-2000; 2000US-0222338.
PR 14-SEP-2000; 2000US-0222339.
PR 14-SEP-2000; 2000US-0222400.
PR 14-SEP-2000; 2000US-0232401.
PR 14-SEP-2000; 2000US-0233063.
PR 14-SEP-2000; 2000US-0233064.
PR 14-SEP-2000; 2000US-0233065.
PR 21-SEP-2000; 2000US-0234223.
PR 21-SEP-2000; 2000US-0234274.
PR 25-SEP-2000; 2000US-0234997.
PR 25-SEP-2000; 2000US-0234998.
PR 26-SEP-2000; 2000US-0234999.
PR 27-SEP-2000; 2000US-0235484.
PR 27-SEP-2000; 2000US-0235834.
PR 27-SEP-2000; 2000US-0235836.
PR 29-SEP-2000; 2000US-0236327.
PR 29-SEP-2000; 2000US-0236327.
PR 29-SEP-2000; 2000US-0236367.
PR 29-SEP-2000; 2000US-0236368.
PR 29-SEP-2000; 2000US-0236369.
PR 29-SEP-2000; 2000US-0236370.
PR 02-OCT-2000; 2000US-0236802.
PR 02-OCT-2000; 2000US-0237037.
PR 02-OCT-2000; 2000US-0237038.
PR 02-OCT-2000; 2000US-0237039.
PR 02-OCT-2000; 2000US-0237040.
PR 13-OCT-2000; 2000US-0237040.
PR 13-OCT-2000; 2000US-0239335.
PR 20-OCT-2000; 2000US-0240960.
PR 20-OCT-2000; 2000US-0241221.
PR 20-OCT-2000; 2000US-0241785.
PR 20-OCT-2000; 2000US-0241786.
PR 20-OCT-2000; 2000US-0241787.
PR 20-OCT-2000; 2000US-0241808.
PR 20-OCT-2000; 2000US-0241809.
PR 20-OCT-2000; 2000US-0241826.
PR 01-NOV-2000; 2000US-0244617.
PR 08-NOV-2000; 2000US-0246474.
PR 08-NOV-2000; 2000US-0246475.
PR 08-NOV-2000; 2000US-0246476.
PR 08-NOV-2000; 2000US-0246477.
PR 08-NOV-2000; 2000US-0246478.
PR 08-NOV-2000; 2000US-0246523.
PR 08-NOV-2000; 2000US-0246524.
PR 08-NOV-2000; 2000US-0246525.
PR 08-NOV-2000; 2000US-0246526.
PR 08-NOV-2000; 2000US-0246527.
PR 08-NOV-2000; 2000US-0246528.
PR 08-NOV-2000; 2000US-0246532.
PR 08-NOV-2000; 2000US-0246609.
PR 08-NOV-2000; 2000US-0246610.
PR 08-NOV-2000; 2000US-0246611.
PR 08-NOV-2000; 2000US-0246613.
PR 17-NOV-2000; 2000US-0249207.
PR 17-NOV-2000; 2000US-0249208.
PR 17-NOV-2000; 2000US-0249209.
PR 17-NOV-2000; 2000US-0249210.
PR 17-NOV-2000; 2000US-0249211.
PR 17-NOV-2000; 2000US-0249212.
PR 17-NOV-2000; 2000US-0249213.
PR 17-NOV-2000; 2000US-0249214.
PR 17-NOV-2000; 2000US-0249215.
PR 17-NOV-2000; 2000US-0249216.
PR 17-NOV-2000; 2000US-0249217.
PR 17-NOV-2000; 2000US-0249218.
PR 17-NOV-2000; 2000US-0249244.
PR 17-NOV-2000; 2000US-0249245.
PR 17-NOV-2000; 2000US-0249264.
PR 17-NOV-2000; 2000US-0249265.

PR 17-NOV-2000; 2000US-0249297.
PR 17-NOV-2000; 2000US-0249299.
PR 17-NOV-2000; 2000US-0249300.
PR 01-DEC-2000; 2000US-0250160.
PR 01-DEC-2000; 2000US-0250391.
PR 05-DEC-2000; 2000US-0251030.
PR 05-DEC-2000; 2000US-0251988.
PR 06-DEC-2000; 2000US-0256719.
PR 06-DEC-2000; 2000US-0256719.
PR 08-DEC-2000; 2000US-0251856.
PR 08-DEC-2000; 2000US-0251868.
PR 08-DEC-2000; 2000US-0251869.
PR 08-DEC-2000; 2000US-0251989.
PR 11-DEC-2000; 2000US-0251990.
PR 05-JAN-2001; 2000US-0254097.
PR 05-JAN-2001; 2000US-0259678.
XX (HUMA-) HUMAN GENOME SCI INC.
XX Rosen CA, Barash SC, Ruben SM;
PI WPI; 2001-476224/51.
DR Isolated polypeptide for treating, preventing and/or prognosing
PT disorders related to the respiratory system including respiratory
XX cancers and also for testing and detection e.g. diagnosis -
PS Disclosure; SED ID No 990; 546pp; English.
XX The present invention relates to the isolation of novel human
CC respiratory antigens (AAU17685-AAU17975), and cDNA and genomic
CC sequences encoding for these polypeptides. The sequences of the
CC invention are useful for preventing, treating and/or prognosing
CC disorders related to the respiratory system including throat
CC disorders (e.g. vocal cord paralysis, tonsillitis, and laryngitis),
CC lung disorders e.g. pneumonia, allergic disorders e.g. asthma,
CC pleurisy, cystic fibrosis, emphysema, nose disorders and cancers of
CC the respiratory tissues e.g. lung cancer. The polynucleotide sequences
CC of the invention are useful in gene therapy and antisense therapy.
CC AAS28161-AAS28764 represent genomic sequences encoding for novel
CC human respiratory antigens.
CC Note: The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 23580 BP; 5938 A; 5961 C; 5927 G; 5754 T; 0 other;

Alignment Scores:
Pred. No.: 712 Length: 23580
Score: 73.00 Matches: 29
Percent Similarity: 44.71% Conservative: 9
Best Local Similarity: 34.12% Mismatches: 23
Query Match: 18.30% Indels: 24
Db: 22 Gaps: 5

US-09-092-296-15 (1-78) x AAS28556 (1-23580)

Qy 4 GlyLeuProLeuValLeuLeuLeuLeuGlySerSerHisGlyThr----- 20
Db 17157 GGTTTCCTCGAGTTCCTACTTTGCTGAGTCAGGTGACCTGAGAACCTGACATCT 17216
Qy 21 GlyPro-----GlyMetThrLeuGlnLeuLeuLeuGlySerGluSerPheLeuThr 36
Db 17217 GGGCCATGAGACATCTTGGGGATGACTTTCAACCTTCAGATGAAGAAGAGGT----- 17270
Qy 37 AsnSerSeryrGluSerSerPheLeuGluLeuLeuGlyLeuGlySerLeuLeuHis 56
Db 17271 -----CTAGAGAAGTGTTCCTTCCTACTCT 17297
Qy 57 LeuProSerGlyThrSerValThrLeuHisHisAla-----ArgSerGlnHisHis 73
Db 17298 GATCAATGGGGAGTCA---ACCAGGCACCGGGCTCAATCAACAGCAATAAATCAAC 17354

Qy	74 ValValCysasThr 78	08-SEP-2000; 2000US-0231414
Db	17355 TGTCTGAGGTCAACT 17369	PR 08-SEP-2000; 2000US-0230800
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AAK87248	17355 TGTCTGAGGTCAACT 17369	PR 12-SEP-2000; 2000US-0231968
ID	AAK87248 standard; DNA; 23580 BP.	PR 14-SEP-2000; 2000US-0232397
XX		PR 14-SEP-2000; 2000US-0232398
XX		PR 14-SEP-2000; 2000US-0232399
XX		PR 14-SEP-2000; 2000US-0232400
XX		PR 14-SEP-2000; 2000US-0232401
XX		PR 14-SEP-2000; 2000US-0233063
XX		PR 14-SEP-2000; 2000US-0233064
DE		PR 14-SEP-2000; 2000US-0233065
XX	Human Immune/haematopoietic antigen genomic sequence SEQ ID NO:42060.	PR 21-SEP-2000; 2000US-0234223
XX	Human; immune; haematopoietic; immune/haematopoietic antigen; cancer;	PR 21-SEP-2000; 2000US-0234274
KW	cytostatic; gene therapy; vaccine; metastasis; ds.	PR 25-SEP-2000; 2000US-0234997
KW		PR 25-SEP-2000; 2000US-0234998
OS	Homo sapiens.	PR 26-SEP-2000; 2000US-0235484
OS		PR 27-SEP-2000; 2000US-0235834
XX		PR 27-SEP-2000; 2000US-0235836
XX		PR 29-SEP-2000; 2000US-0236327
XX		PR 29-SEP-2000; 2000US-0236367
XX		PR 29-SEP-2000; 2000US-0236368
XX		PR 29-SEP-2000; 2000US-0236369
XX		PR 29-SEP-2000; 2000US-0236370
XX		PR 02-OCT-2000; 2000US-0236802
XX		PR 02-OCT-2000; 2000US-0237037
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XX		PR 20-OCT-2000; 2000US-0241826
XX		PR 01-NOV-2000; 2000US-0244617
XX		PR 08-NOV-2000; 2000US-0246474
XX		PR 08-NOV-2000; 2000US-0246475
XX		PR 08-NOV-2000; 2000US-0246476
XX		PR 08-NOV-2000; 2000US-0246477
XX		PR 08-NOV-2000; 2000US-0246478
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XX		PR 08-NOV-2000; 2000US-0246525
XX		PR 08-NOV-2000; 2000US-0246526
XX		PR 08-NOV-2000; 2000US-0246527
XX		PR 08-NOV-2000; 2000US-0246528
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XX		PR 08-NOV-2000; 2000US-0246530
XX		PR 08-NOV-2000; 2000US-0246531
XX		PR 08-NOV-2000; 2000US-0246532
XX		PR 17-NOV-2000; 2000US-0249210
XX		PR 17-NOV-2000; 2000US-0249211
XX		PR 17-NOV-2000; 2000US-0249212
XX		PR 17-NOV-2000; 2000US-0249213
XX		PR 17-NOV-2000; 2000US-0249214
XX		PR 17-NOV-2000; 2000US-0249215
XX		PR 17-NOV-2000; 2000US-0249216
XX		PR 17-NOV-2000; 2000US-0249217
XX		PR 17-NOV-2000; 2000US-0249218
XX		PR 17-NOV-2000; 2000US-0249244
XX		PR 17-NOV-2000; 2000US-0249245
XX		PR 17-NOV-2000; 2000US-0249264
XX		PR 17-NOV-2000; 2000US-0249265
XX		PR 17-NOV-2000; 2000US-0249297
XX		PR 17-NOV-2000; 2000US-0249299
XX		PR 17-NOV-2000; 2000US-0249313
XX		PR 17-NOV-2000; 2000US-0249314
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XX		PR 17-NOV-2000; 2000US-0249316
XX		PR 17-NOV-2000; 2000US-0249317
XX		PR 17-NOV-2000; 2000US-0249318
XX		PR 17-NOV-2000; 2000US-0249319
XX		PR 17-NOV-2000; 2000US-0249320
XX		PR 17-NOV-2000; 2000US-0249321
XX		PR 17-NOV-2000; 2000US-0249322
XX		PR 17-NOV-2000; 2000US-0249323
XX		PR 17-NOV-2000; 2000US-0249324
XX		PR 17-NOV-2000; 2000US-0249325
XX		PR 17-NOV-2000; 2000US-0249326
XX		PR 17-NOV-2000; 2000US-0249327
XX		PR 17-NOV-2000; 2000US-0249328
XX		PR 17-NOV-2000; 2000

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PR 17-NOV-2000; 2000US-0249299.
PR 17-NOV-2000; 2000US-0249300.
PR 01-DEC-2000; 2000US-0250160.
PR 01-DEC-2000; 2000US-0250160.
PR 01-DEC-2000; 2000US-0250391.
PR 05-DEC-2000; 2000US-0251030.
PR 05-DEC-2000; 2000US-0251988.
PR 05-DEC-2000; 2000US-0256719.
PR 06-DEC-2000; 2000US-0251479.
PR 08-DEC-2000; 2000US-0251856.
PR 08-DEC-2000; 2000US-0251868.
PR 08-DEC-2000; 2000US-0251869.
PR 08-DEC-2000; 2000US-0251989.
PR 08-DEC-2000; 2000US-0251990.
PR 11-DEC-2000; 2000US-0254097.
PR 05-JAN-2001; 2001US-0259678.
XX (HUMA-) HUMAN GENOME SCI INC.
PA
XX
XX Rosen CA, Barash SC, Ruben SM;
XX
XX WPI; 2001-483426/52.
XX
XX Nucleic acids encoding human immune/hematopoietic antigen polypeptides,
PT useful for preventing, diagnosing and/or treating cancers and
PT metastasis -
XX
XX Disclosure; SEQ ID NO 42060; 3071pp + Sequence Listing; English.
XX
XX AAK54951 to AAK64702 encode the human immune/hematopoietic antigen (I)
CC amino acid sequences given in AAK82170 to AAK91921. (I) have cytostatic
CC activity, and can be used in gene therapy and vaccine production. (I)
CC proteins and polynucleotides may be used in the prevention, diagnosis and
CC treatment of diseases associated with inappropriate (I) expression. For
CC example, they may be used to treat disorders associated with decreased
CC expression by rectifying mutations or deletions in a patient's genome
CC that affect the activity of (I) by expressing inactive proteins or to
CC supplement the patients own production of (I). Additionally, (I)
CC polynucleotides may be used to produce the secreted (I), by inserting
CC the nucleic acids into a host cell and culturing the cell to express the
CC protein. (I) proteins and polynucleotides may be used to prevent,
CC diagnose and treat immune/hematopoietic-related diseases, especially
CC cancers and cancer metastases of hematopoietic-derived cells. AAK64703
CC to AAK87694 represent human immune/hematopoietic antigen genomic
CC sequences from the present invention. AAK54942 to AAK54950 and AAK82169
CC represent sequences used in the exemplification of the present invention.
XX
XX SQ Sequence 23580 BP; 5938 A; 5961 C; 5927 G; 5754 T; 0 other;

Alignment Scores:
Pred No.: 712 Length: 23580
Score: 73.00 Matches: 29
Percent Similarity: 44.71% Conservative: 9
Best Local Similarity: 34.12% Mismatches: 23
Query Match: 18.30% Indels: 24
DB: 22 Gaps: 5

US-09-092-296-15 (1-78) x AAK87248 (1-23580)
QY 4 GlyLeuProLeuValLeuLeuThrLeuLeuGlySerSerHisGlyThr----- 20
Db 17157 GGTTCCCGAAGTTCACCTTTGCTGAGTCAGGCTGACCTTGAGGAACCCCTGACATCT 17216
QY 21 GlyPro-----GlyMetThrLeuGlnLeuLysLeuLysGluSerPheLeuThr 36
Db 17217 GGGCCATGAGACATCTTGGGGATGACTTTCACCTTCAGATGAAGACGAGGT----- 17270
QY 37 AsnSerSerTyrGluSerSerPheLeuGluLeuLeuGlyLeuLeuHis 56
Db 17271 -----CTAGAGAAGTGTTGCTTCCTCACTCT 17297
QY 57 LeuProSerGlyThrSerValThrLeuHisHsIala-----ArgSerGlnHisHs 73
Db 17298 GATCCAATGGGGAGTCA---ACCGAGCACCAGGGCTCAATCAACGCAATAAACATCAC 17354
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QY 74 ValValCysAsnThr 78
Db 17355 TGCTGAGGTCACACT 17369
RESULT 14
ABQ88164
ID ABQ88164 standard; cDNA; 86080 BP.
AC ABQ88164;
XX
XX 18-SEP-2002 (first entry)
DE Human osteoblast differentiation related cDNA SEQ ID NO 71.
XX
XX Human; osteoblast; stem cell differentiation; bone tissue deposition;
XX osteoporosis; osteopathic; ss.
XX
XX Homo sapiens.
XX
XX WO2002050301-A2.
XX
XX 27-JUN-2002.
XX
XX 18-DEC-2001; 2001WO-US48276.
XX
XX 18-DEC-2000; 2000US-255882P.
XX
XX 24-APR-2001; 2001US-285691P.
XX
XX (GENE-) GENE LOGIC INC.
XX
XX (PROC ) PROCTER & GAMBLE CO.
XX
XX JI D, Axelrod DW, Cook JS, Jaiswal N, Einstein R, Houghton A;
XX Mertz L;
XX
XX WPI; 2002-557663/59.
XX
XX Use of genes and their expression profiles associated with osteoblast
XX differentiation for screening modulators bone formation, for diagnosing
XX or treating e.g. osteoporosis, or as markers for the differentiation
XX process -
XX
XX Claim 1; SQ ID NO 71; 78pp + Sequence Listing; English.
XX
XX The invention relates to genes and their expression profiles are used
XX for:
XX
XX (a) screening modulators of precursor stem cell differentiation into
XX osteoblasts, or bone tissue deposition;
XX
XX (b) diagnosing abnormal deposition of bone tissue, abnormal rate of
XX osteoblast formation or osteoporosis; or
XX
XX (c) treating or monitoring treatment of the conditions cited in (b), or
XX monitoring the progression of bone tissue deposition.
XX
XX Specific conditions include postmenopausal osteoporosis, glucocorticoid
XX osteoporosis or male osteoporosis, osteopenia, osteodystrophy,
XX drug-induced abnormalities in bone formation or bone loss, conditions
XX that involve altered bone metabolism (e.g. idiopathic juvenile
XX osteoporosis), skeletal disease linked to breast cancer, mastocytosis,
XX Fanconi syndrome or fibrous dysplasia. The present sequence is that of an
XX osteoblast differentiation associated cDNA marker of the invention.
XX
XX Note: the sequence data for this patent did not form part of the printed
XX specification, but was obtained in electronic format directly from WIPO
XX at ftp.wipo.int/pub/published_pct_sequences.
XX
XX SQ Sequence 86080 BP; 21583 A; 21475 C; 21694 G; 21328 T; 0 other;

Alignment Scores:
Pred No.: 4.46e+03 Length: 86080
Score: 73.00 Matches: 29
Percent Similarity: 44.71% Conservative: 9
Best Local Similarity: 34.12% Mismatches: 23
Query Match: 18.30% Indels: 24
DB: 22 Gaps: 5
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GenCore version 5.1.5
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OM protein - nucleic search, using frame_plus.p2n model

Run on: May 1, 2003, 05:14:56 ; Search time 1151 Seconds

(without alignments)
1972.214 Million cell updates/sec

Title: US-09-092-296-15

Perfect score: 399

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Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Deltext 7.0

Searched: 2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:

-Q=/cgn2_1/USPTO_spool/US0902296/runat_30042003_133102_14403/app_query.fasta_1.263
-DB=GenEmbl -OPT=fastap -SUFFIX=p2n.rge -MINMATCH=0.1 -LOOPCL=0 -LOPEXT=0
-UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cd1 -LIST=45
-DOCALIGN=200 -THR_SCORE=opt -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFM=ptc -NORM=ext -HEA_SIZE=300 -MINLEN=0 -MAXLEN=2000000000
-USER=US0902296.cgn_1_1319.erunat_30042003_133102_14403 -NCPU=6 -ICPU=3
-NO_XLPXY -NO_MAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

- 1: gb_ba.*
- 2: gb_rtg.*
- 3: gb_in.*
- 4: gb_ov.*
- 5: gb_pat.*
- 6: gb_ph.*
- 7: gb_pl.*
- 8: gb_pr.*
- 9: gb_ro.*
- 10: gb_sts.*
- 11: gb_sy.*
- 12: gb_un.*
- 13: gb_un.*
- 14: gb_vi.*
- 15: em_ba.*
- 16: em_fun.*
- 17: em_hum.*
- 18: em_in.*
- 19: em_mu.*
- 20: em_mu.*
- 21: em_ov.*
- 22: em_ov.*
- 23: em_ph.*
- 24: em_pl.*
- 25: em_ro.*
- 26: em_ro.*
- 27: em_sts.*
- 28: em_un.*

- 29: em_vi.*
- 30: em_htg_hum.*
- 31: em_htg_inv.*
- 32: em_htg_other.*
- 33: em_htg_mus.*
- 34: em_htg_pln.*
- 35: em_htg_rtd.*
- 36: em_htg_nam.*
- 37: em_htg_vrt.*
- 38: em_sy.*
- 39: em_htgo_hum.*
- 40: em_htgo_mus.*
- 41: em_htgo_other.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	399	100.0	422	6	AX092334	Sequence
2	399	100.0	422	6	AX376174	Sequence
3	399	100.0	422	6	AX403475	Sequence
4	394	98.7	484	9	AX102070	Homo sapi
5	349	97.5	624	6	AX472955	Sequence
6	317	79.4	47323	9	AC005937	Homo sapi
7	317	79.4	104154	2	AL773541	Homo sapi
8	317	79.4	156272	9	AL669830	Human DNA
9	317	79.4	178688	2	AL713893	Homo sapi
10	317	79.4	192650	9	AB023048	Homo sapi
11	317	79.4	200000	9	AP000511	Homo sapi
12	312	78.2	84474	9	AL662854	Human DNA
13	203	50.9	34980	6	AX344553	Sequence
14	203	50.9	34980	6	AX344553	Sequence
15	121	30.3	132977	2	RN510020	Sequence
16	109.5	27.4	175345	2	AC022301	Rattus no
17	106	26.6	34980	6	AX344571	Mus muscu
18	99.5	24.9	337832	2	AC099175	Sequence
19	90	22.6	201296	10	AC115299	Rattus no
20	85.5	21.4	149078	2	AC117264	Mus muscu
21	83.5	20.9	176233	2	AC102885	Oryza sat
22	83.5	20.9	196980	2	AC122405	Mus muscu
23	82.5	20.7	185078	2	AC097616	Rattus no
24	82	20.6	96445	9	AC107397	Homo sapi
25	81.5	20.4	2182	10	BC019813	Mus muscu
26	80	20.1	168426	2	AC124357	Mus muscu
27	80	20.1	189175	2	AC121200	Rattus no
28	79.5	19.9	169241	2	AC129409	Rattus no
29	79.5	19.9	206168	10	AL672307	Mouse DNA
30	79	19.8	109238	9	AC004997	Homo sapi
31	79	19.8	158257	9	AC005585	Homo sapi
32	79	19.8	169281	2	AC098927	Rattus no
33	79	19.8	172811	2	AC103034	Rattus no
34	79	19.8	191111	2	AC114527	Rattus no
35	78.5	19.7	225924	2	AC074210	Mus muscu
36	78	19.5	11078	1	AE009918	Pyrobacul
37	78	19.5	171602	2	AC130212	Mus muscu
38	78	19.5	193567	2	AC102127	Rattus no
39	77.5	19.4	165402	2	AC128392	Rattus no
40	77.5	19.4	178676	2	AC087868	Mus muscu
41	77.5	19.4	226903	2	AC079272	Mus muscu
42	77	19.3	64607	9	AC005021	Homo sapi
43	77	19.3	172478	9	AC015844	Homo sapi
44	77	19.3	176630	2	AC109427	Rattus no
45	77	19.3	203827	10	AL669816	Mouse DNA

ALIGNMENTS


```
|||||
Db 118 GGGCGGGTATGACTTCAACTGAAGGAGTCTTTCTTGACAAATTCCTCTAT 177
QY 41 GluSerSerPheLeuLeuGluLeuLysLeuCysLeuLeuHisLeuProSerGly 60
Db 178 GAGTCCAGCTCTCGAATTCCTGAAAGAGCTCGCCCTCCCTCCATCTCCCTTCAGGG 237
QY 61 ThrSerValThrLeuHisHisAlaArgSerGlnHisHisValValCysAsnThr 78
Db 238 ACCAGCTCACCTCCACCATGCAAGATCTCAACACCATGTTGCTGCAACACA 291
RESULT 4
AY102070 484 bp mRNA linear PRI 18-JUN-2002
LOCUS Homo sapiens surfactant associated protein G mRNA, partial
DEFINITION sequence.
ACCESSION AY102070
VERSION AY102070.1 GI:21464498
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 484)
AUTHORS Walker M.G. and Spiro, P.
JOURNAL Unpublished
TITLE Genes co-expressed with pulmonary surfactants
REFERENCE 2 (bases 1 to 484)
AUTHORS Walker M.G. and Spiro, P.
JOURNAL Direct Submission
TITLE Submitted (07-MAY-2002) Incyte Genomics, 1475 Flamingo Way,
Sunnyvale, CA 94087-3405, USA
FEATURES
source
1..484
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="236582"
<1..>484
/gene="surfactant associated protein G"
/note="SFPFG"
BASE COUNT 124 a 149 c 110 g 101 t
ORIGIN
Alignment Scores:
Pred. No.: 1.99e-41 Length: 484
Score: 394.00 Matches: 77
Percent Similarity: 100.00% Conservative: 1
Best Local Similarity: 98.72% Mismatches: 0
Query Match: 98.75% Indels: 0
DB: 9 Gaps: 0
US-09-092-296-15 (1-78) x AY102070 (1-484)
QY 1 MetGlySerGlyLeuProLeuValLeuLeuThrLeuLeuGlySerSerHisGlyThr 20
Db 55 ATGGGCTCTGGGCTGCCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCAGGACA 114
QY 21 GlyProGlyMetThrLeuGlnLeuLysLeuLysGluSerPheLeuThrAsnSerSerTyr 40
Db 115 GGGCGGGTATGACTTCAACTGAAGCTGAAGGAGTCTTTCTGACAAATTCCTCTAT 174
QY 41 GluSerSerPheLeuLeuGluLysLeuCysLeuLeuHisLeuProSerGly 60
Db 175 GAGTCCAGCTCTCGAATTCCTGAAAGAGCTCGCCCTCCCTCCATCTCCCTTCAGGG 234
QY 61 ThrSerValThrLeuHisHisAlaArgSerGlnHisHisValValCysAsnThr 78
Db 235 ACCAGCTCACCTCCACCATGCAAGATCTCAACACCATGTTGCTGCAACACA 288
RESULT 5
AX472955 624 bp DNA linear PAT 09-AUG-2002
LOCUS Homo sapiens
DEFINITION Sequence 4 from Patent WO218576.
```

```
AX472955
VERSION AX472955.1 GI:22207742
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Chen, S. Y., Macina, R. A., Sun, Y., and Reclapon, H.
JOURNAL Compositions and methods relating to lung specific genes
Patent: WO 0218576-A 4 07-MAR-2002;
Diadexus, Inc. (US)
FEATURES
source
1..624
/organism="Homo sapiens"
/db_xref="taxon:9606"
BASE COUNT 129 a 175 c 182 g 138 t
ORIGIN
Alignment Scores:
Pred. No.: 1.61e-35 Length: 624
Score: 349.00 Matches: 78
Percent Similarity: 49.37% Conservative: 0
Best Local Similarity: 49.37% Mismatches: 0
Query Match: 87.47% Indels: 80
DB: 6 Gaps: 1
US-09-092-296-15 (1-78) x AX472955 (1-624)
QY 1 MetGlySerGlyLeuProLeuValLeuLeuThrLeuLeuGlySerSerHisGlyThr 20
Db 16 ATGGGCTCTGGGCTGCCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCAGGACA 75
QY 20 ----- 20
Db 76 GGTGAGGCTAGAGGGCAGGACTCTGGTCCCTGTGGCAAGAGAGCCAGCAAGAGG 135
QY 20 ----- 20
Db 136 GGTGGGACTTCATGTCCTCCCTGAGAGTGACAGAGACACCCAGTCTCTGAGCTTCCAAGAGG 195
QY 20 ----- 20
Db 196 CTCTGGAGGGCATTTGCTGGGAAGAGGAACTGTCCCGGGGAGCGTGACAGGAAGGTTTC 255
QY 20 ----- 20
Db 256 TGTGTCTCCGGAGGAATCAGCCCTGACTGCTGGGTCTTAAGCTGTACTTCTGGATCCGCA 315
QY 21 GlyProGlyMetThrLeuGlnLeuLysLeuLysGluSerPheLeuThrAsnSerSerTyr 40
Db 316 GGGCGGGTATGACTTTCGAACCTGAAGCTGAAGAGTCTTTCTGACAAATTCCTCTAT 375
QY 41 GluSerSerPheLeuGluLeuLeuGluLysLeuCysLeuLeuHisLeuProSerGly 60
Db 376 GAGTCCAGCTCTCGAATTCCTGAAAGAGTCTGCTGAAAAGCTCTGCCCTCCATCCCTTCAGGG 435
QY 61 ThrSerValThrLeuHisHisAlaArgSerGlnHisHisValValCysAsnThr 78
Db 436 ACCAGCTCACCTCCACCATGCAAGATCTCAACACCATGTTGCTGCAACACA 489
RESULT 6
AC005937 47323 bp DNA linear PRI 05-NOV-1998
LOCUS Homo sapiens clone UNGC:370M23.002 from 6p21, complete sequence.
DEFINITION
ACCESSION AC005937
VERSION AC005937.1 GI:3845393
KEYWORDS HTG.
SOURCE Homo sapiens.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 47323)
```


US-09-092-296-15 (1-78) x AC005937 (1-47323)

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QY 1 MetGlySerGlyLeuProLeuValLeuLeuLeuThrLeuLeuGlySerSerHisGlyThr 20
Db 35167 ATGGGCTCTGGGCTCCCTTGTCTTCCCTTGGACCTCTTGGCAGCTCAGATGGAA 35226
QY 20 ----- 20
Db 35227 GGTGAGGGCTAGAGGGCAGGACTCTGGTCCCTGTGCAAGAGAGCCAGAGAAAGG 35286
QY 20 ----- 20
Db 35287 GGTGGGACTTCATGCTCCTGAGAGTGCAGAGACACCCAGTCCTGAGCTTCCAGAGG 35346
QY 20 ----- 20
Db 35347 CTCGTGGAGGGGCATTGTGGGGAAGAGAACTGTGCCGGGAGCGTGAGCAGGAAGTTC 35406
QY 20 ----- 20
Db 35407 TGTCTCTCCGAGGAATCAGCCCTGACTGCTGGGTCTCTAGCTGTACTTGGATCCGCA 35466
QY 21 GlyProGlyMetThrLeuGlnLeuLysLeuLysGluSerPheLeuThrAsnSerSerTyr 40
Db 35467 GGGCCGGGATGACTTTGCAACTGAAGCTGAAGGAGTCTTTCTGACAAATTCCTCTAT 35526
QY 41 GluSerSerPheLeuGluLeuLys----- 50
Db 35527 GAGTCCAGCTCTCTGGAATGCTTGAAAGGTAGTTCTTTGGAGGGGAAGATGGGGCT 35586
QY 50 ----- 50
Db 35587 GTGTGTTGTGAGTCAGTTTGGGCTCTGCTGGGTCTGGATGCTCTCGTGGGGAATG 35646
QY 51 -----LeuCysLeuLeuHis 56
Db 35647 GAGAGCTCTTTACATCGGCCCTTTAACCCCTTTGTCGCCAGCTGCTCTCTCCAT 35706
QY 57 LeuProSerGlyThrSerValThrLeuHisHisAlaArgSerGlnHisHisValValCys 76
Db 35707 CTCCTTCAGGACGACGCGTCAACCCCTCACCATGCAAGATCTCAACACCATGTTGCTGC 35766
QY 77 AsnThr 78
Db 35767 AACACA 35772
```

```
RESULT 7
LOCUS AL773541
DEFINITION Homo sapiens chromosome 6 clone xxbac-11J22, linear HTG 09-AUG-2002
PROGRESS ***, in ordered pieces.
ACCESSION AL773541
VERSION AL773541.4 GI:22204637
KEYWORDS HTG: HTGS_PHASE2; HTGS_ACTIVEFIN; HTGS_DRAFT; HTGS_FULLTOP.
SOURCE human.
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
TITLE 1 (bases 1 to 104154)
JOURNAL Almeida, J.
Direct Submission
Submitted (31-JUL-2002) Wellcome Trust Sanger Institute, Hinxton,
Cambridgeshire, CB10 1SA, UK. E-mail enquiries:
humquerry@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
On Aug 11, 2002 this sequence version replaced gi:21621737.
----- Genome Center
Center: Wellcome Trust Sanger Institute
Center code: SC
Web site: http://www.sanger.ac.uk
Contact: humquerry@sanger.ac.uk
----- Project Information
Center project name: bQ11u22
----- Summary Statistics
```

Assembly program: XGAP4; version 4.5
Chemistry: Dye-terminator; 100% of reads
Consensus quality: 104135 bases at least Q40
Consensus quality: 104142 bases at least Q30
Consensus quality: 104145 bases at least Q20
Insert size: 110727; 1.1% error; agarose-fp
Quality coverage: 19.52x in Q20 bases; sum-of-contigs Quality
coverage: 18.64x in Q20 bases; agarose-fp

* NOTE: this is a 'working draft' sequence.
* this sequence will be replaced
* by the finished sequence as soon as it is available and
* the accession number will be preserved.

FEATURES

source
1..104154
/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="6"
/clone="XXbac-11J22"
/clone_lib="DNA-arts-BAC.1-QBL.1"
misc_feature
1..104154
/note="assembly_fragment:00090"
BASE COUNT 26560 a 25418 c 26093 g 26083 t
ORIGIN
Alignment Scores:
Pred. No.: 9.38e-29 Length: 104154
Score: 317.00 Matches: 78
Percent Similarity: 38.61% Conservative: 0
Best Local Similarity: 38.61% Mismatches: 0
Query Match: 79.45% Indels: 124
DB: 2 Gaps: 2

US-09-092-296-15 (1-78) x AL773541 (1-104154)

```
QY 1 MetGlySerGlyLeuProLeuValLeuLeuLeuThrLeuLeuGlySerSerHisGlyThr 20
Db 67548 ATGGGCTCTGGGCTCCCTTGTCTCTCTTGTACCTCTTGGCAGCTCAGATGGAA 67607
QY 20 ----- 20
Db 67608 GGTGAGGGCTAGAGGGCAGGACTCTCTGGTCCCTGTGGCAAGAGAGGCCAGAAAGG 67667
QY 20 ----- 20
Db 67668 GGTGGGACTTCATGCTCCTGAGAGTGCAGAGACACCCAGTCTCTGAGCTTCCAAGAGG 67727
QY 20 ----- 20
Db 67728 CTCGTGAGGGGCATTGCTGGGGGAAGGAGGACTGTCCGGGGAGCGTGAGCAGGAGGTTTC 67787
QY 20 ----- 20
Db 67788 TGTGTCTCCGAGGAATCAGCCCTGACTGCTGGTCTCTAAGCTGTACTTCTGGATCCGCA 67847
QY 21 GlyProGlyMetThrLeuGlnLeuLysLeuLysGluSerPheLeuThrAsnSerSerTyr 40
Db 67848 GGCCGGGTATGACTTTGCAACTGAAGCTGAAGGAGTCTTTCTGACAAATTCCTCTAT 67907
QY 41 GluSerSerPheLeuGluLeuLys----- 50
Db 67908 GAGTCCAGCTCTCTGGAATGCTTTGAAAGGTAGTTCTTTGGAAGGGGAAGATGGGGCT 67967
QY 50 ----- 50
Db 67968 GTGTGTTGTGAGTCAGTTTGGGCTCTGCTGGGTCTGGATGCTCCGTGGTGGGATG 68027
QY 51 -----LeuCysLeuLeuHis 56
Db 68028 GAGAGCTCTTTACATCGGCCCTTTAAACCCCTTTGTTCCAGCTCTGGCTCTCTCCAT 68087
QY 57 LeuProSerGlyThrSerValThrLeuHisHisAlaArgSerGlnHisHisValValCys 76
```

```
|||||
Db 68088 CTCCTTCAGGACGAGCGTCACCCCTCCACCATGCAAGATCTCAACACCATGTTGTCTGC 68147
|||||
QY 77 AsnThr 78
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Db 68148 AACACA 68153

RESULT 8
AL669830/c
LOCUS Human DNA sequence from clone XXbac-118E17 on chromosome 6,
DEFINITION complete sequence.
ACCESSION AL669830
VERSION AL669830.9 GI:20135762
KEYWORDS HTG.
SOURCE human.
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Johnson, C.
TITLE Direct Submission
JOURNAL Submitted (23-APR-2002) Wellcome Trust Sanger Institute, Hinxton,
Cambridgeshire, CB10 1SA, UK. E-mail enquiries:
humquerry@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
During sequence assembly data is compared from overlapping clones.
Where differences are found these are annotated as variations
together with a note of the overlapping clone name. Note that the
variation annotation may not be found in the sequence submission
corresponding to the overlapping clone, as we submit sequences with
only a small overlap as described above.
COMMENT This sequence was finished as follows unless otherwise noted: all
regions were either double-stranded or sequenced with an alternate
chemistry or covered by high quality data (i.e., phred quality >=
30); an attempt was made to resolve all sequencing problems, such
as compressions and repeats; all regions were covered by at least
one plasmid subclone or more than one M13 subclone; and the
assembly was confirmed by restriction digest. The following
abbreviations are used to associate primary accession numbers given
in the feature table with their source databases: Em, EMBL; Swi,
SWISSPROT; Tr, TrEMBL; Wp, WORMPEP; information on the WORMPEP
database can be found at
http://www.sanger.ac.uk/projects/C.elegans/wormpep
from a CHORI-501 human bac - PGF cell line library VECTOR:
PTARBAC2.1
This sequence was generated from part of bacterial clone contigs
constructed by the MHC Haplotype Consortium and collaborators.
Further information can be found at
http://www.sanger.ac.uk/HGP/Chr6/MHC.
FEATURES
source Location/Qualifiers
1..156272
/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="6"
/clone="XXbac-118E17"
/clone_lib="CHORI-501"
BASE COUNT 41135 a 37989 c 36907 g 40241 t
ORIGIN

Alignment Scores:
Pred. No.: 1.52e+28 Length: 156272
Score: 317.00 Matches: 78
Percent Similarity: 38.61% Conservative: 0
Best Local Similarity: 38.61% Mismatches: 0
Query Match: 79.45% Indels: 124
Db: 9 Gaps: 2

US-09-092-296-15 (1-78) x AL669830 (1-156272)
QY 1 MetGlySerGlyLeuProLeuValLeuLeuLeuThrLeuLeuGlySerSerHisGlyThr 20
|||||
Db 25856 ATGGGGGTGGGTGCCCTTGCTCTCTTGACCCCTCCCTTGGCAGCTCACATGGACA 25797
```

```
QY 20 ----- 20
Db 25796 GGTGAGGGCTAGAGGGCAGGACTCCTGGGTCCCTGTGGCAAGAGAGGCCAGAGAAAGG 25737
QY 20 ----- 20
Db 25736 GGTGGGACTTCATGGTCCCTGAGAGTGCACAGACACCCAGCTCCTGAGCTTCCAGAGG 25677
QY 20 ----- 20
Db 25676 CTCTGAGGGGCGATTCCTGGGGAGAGGAACTGTGCCGGGAGCGTGAGCAGGAAGGTTTC 25617
QY 20 ----- 20
Db 25616 TGTGCTCTCGGAGGAACACGCCCTGACTGGGGTCTTACGCTGTACTTCTGGATCCGCA 25557
QY 21 GLYProGlyMetThrLeuGlnLeuLysLeuLysGluSerPheLeuThrAsnSerSerTyr 40
|||||
Db 25556 GGCCGGGTATGACTTTGCAACTGAAGCTGAAGGAGTCTTTTCTGACAAATTCCTCTCTAT 25497
QY 41 GluSerSerPheLeuGluLeuLys----- 50
|||||
Db 25496 GAGTCAGCGTCTCTGGAATTCCTTGAAGAAGTAGTCTTTGGGAAGGGGAAGATGGGGCT 25437
QY 50 ----- 50
Db 25436 GTGTGTTCTGAGTCAAGTTTGGGCTCTGCTGGGGTCTGGATGCTCTCCGTGGTGAATG 25377
QY 51 -----LeuCysLeuLeuLeuHis 56
|||||
Db 25376 GAGAGCTCTTACATGGCGCCCTTTAACCCCTTGTTCACGAGCTGCTCCTCTCTCCAT 25317
QY 57 LeuProSerGlyThrSerValThrLeuHisHisAlaArgSerGlnHisHisValValCys 76
|||||
Db 25316 CTCCTCTAGGAGCAGCAGCGTCACCCCTCCACCATGCAAGATCTCAACACCATGTTGTCTGC 25257
QY 77 AsnThr 78
|||||
Db 25256 AACACA 25251

RESULT 9
AL713893
LOCUS Homo sapiens chromosome 6 clone XXbac-307M4, *** SEQUENCING IN
DEFINITION PROGRESS ***, 6 unordered pieces.
ACCESSION AL713893
VERSION AL713893.5 GI:19847952
KEYWORDS HTG: HTGS_PHASE1; HTGS_DRAFT; HTGS_FULLTOP.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Sims, S.
TITLE Direct Submission
JOURNAL Submitted (26-MAR-2002) Wellcome Trust Sanger Institute, Hinxton,
Cambridgeshire, CB10 1SA, UK. E-mail enquiries:
humquerry@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
On Mar 29, 2002 this sequence version replaced gi:19772907.
COMMENT ----- Genome Center
Center: Wellcome Trust Sanger Institute
Center code: SC
Web site: http://www.sanger.ac.uk
Contact: humquerry@sanger.ac.uk
----- Project Information
Center project name: bpg307M4
----- Summary Statistics
Assembly program: XGAP4; version 4.5
Chemistry: Dye-terminator Big Dye; 100% of reads
Consensus quality: 17727 bases at least Q40
Consensus quality: 17708 bases at least Q30
Consensus quality: 17795 bases at least Q20
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Insert size: 178188; sum-of-contigs
 Insert size: 192613; 0.9% error; agarose-fp
 Quality coverage: 8.57x in Q20 bases; agarose-fp
 coverage: 8.00x in Q20 bases; agarose-fp

* NOTE: This is a 'working draft' sequence. It currently
 * consists of 6 contigs. The true order of the pieces
 * is not known and their order in this sequence record is
 * arbitrary. Gaps between the contigs are represented as
 * runs of N, but the exact sizes of the gaps are unknown.
 * This record will be updated with the finished sequence
 * as soon as it is available and the accession number will
 * be preserved.

* 1 37410: contig of 37410 bp in length
 * 37411 37510: gap of 100 bp
 * 37511 82372: contig of 44862 bp in length
 * 82373 82472: gap of 100 bp
 * 82473 142457: contig of 59985 bp in length
 * 142458 142557: gap of 100 bp
 * 142558 152859: contig of 10302 bp in length
 * 152860 152959: gap of 100 bp
 * 152960 172054: contig of 19095 bp in length
 * 172055 172154: gap of 100 bp
 * 172155 178688: contig of 6534 bp in length.

FEATURES

source
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 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /chromosome="6"
 /clone="XXbac-307M4"
 /clone_lib="CHORI-501"
 1..37410
 /note="assembly_fragment:03218
 fragment_chain:1"
 37511..82372
 /note="assembly_fragment:00918
 fragment_chain:1"
 82473..142457
 /note="assembly_fragment:03231
 fragment_chain:1"
 142558..152859
 /note="assembly_fragment:03008
 fragment_chain:1"
 152960..172054
 /note="assembly_fragment:04309
 fragment_chain:1"
 172155..178688
 /note="assembly_fragment:03507
 fragment_chain:1"
 clone_end:r7
 vector_side:right"
 46316 a 40707 c 42186 g 48998 t 501 others

Alignment Scores:

Pred. No.: 1.79e-28 Length: 178688
 Score: 317.00 Matches: 78
 Percent Similarity: 38.61% Conservative: 0
 Best Local Similarity: 38.61% Mismatches: 0
 Query Match: 79.45% Indels: 124
 DB: 2 Gaps: 2

US-09-092-296-15 (1-78) x AL713893 (1-178688)

QY 1 MetGlySerGlyLeuProLeuValLeuLeuLeuThrLeuLeuGlySerHisGlyThr 20

Db 173497 ATGGGGTCTGGGCTGGCCCTGTGCTCTCTTGACCTCTCTGCACATGAACA 173556

QY 20 ----- 20

Db 173557 GGTGAGGGCTAGAGGGGAGGACTCTTGGGTCTCCCTGTGGCAGAGAGGCGCAGAAAGG 173616

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QY 51 -----LeuCysLeuLeuLeuHis 56

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QY 77 AsnThr 78

Db 174097 AACACA 174102

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AB023048 192650 bp DNA linear PRI 20-NOV-1999
 Homo sapiens genomic DNA, chromosome 6p21.3, HLA class I region,
 clone:5319, complete sequence.

AB023048

AB023048.1 GI:5672603

HTG.

Homo sapiens cell_line:978SK DNA, clone:53L9.

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

Shiina,T., Tamiya,G., Oka,A., Takishima,N., Yamagata,T.,

Kikkawa,E., Iwata,K., Tomizawa,M., Okuaki,N., Kuwano,Y.,

Watanabe,K., Eukuzumi,Y., Itakura,S., Sugawara,C., Ono,A.,

Yamazaki,M., Tashiro,H., Ando,A., Ikemura,T., Soeda,E., Kimura,M.,

Bahrani,S. and Inoko,H.

Molecular dynamics of MHC genesis unraveled by sequence analysis of

The 1,796,938-bp HLA class I region

Proc. Natl. Acad. Sci. U.S.A. 96 (23), 13282-13287 (1999)

2002539

2 (bases 1 to 192650)

Shiina,T. and Takishima,N.

Direct Submission

Submitted (29-JAN-1999) Takashi Shiina, Tokai University School of

Medicine, Department of Molecular Life Science 2; Bohseidai,

Isehara, Kanagawa 259-1193, Japan

(E-mail:tsushima@is.icc.u-tokai.ac.jp, Tel:81-463-93-1121,

Fax:81-463-94-8884)

Location/Qualifiers

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VERSION
  AL662854.7 GI:20068660
KEYWORDS
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SOURCE
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ORGANISM
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  Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
  1
  Tracey, A.
  Direct Submission
  Submitted (23-APR-2002) Wellcome Trust Sanger Institute, Hinxton,
  Cambridgeshire, CB10 1SA, UK. E-mail enquiries:
  humquerry@sanger.ac.uk Clone requests: clonerequests@sanger.ac.uk
  On Apr 7, 2002 this sequence version replaced gi:19031750.
  During sequence assembly data is compared from overlapping clones.
  Where differences are found these are annotated as variations
  together with a note of the overlapping clone name. Note that the
  variation annotation may not be found in the sequence submission
  corresponding to the overlapping clone, as we submit sequences with
  only a small overlap as described above.
  This sequence was finished as follows unless otherwise noted: all
  regions were either double-stranded or sequenced with an alternate
  chemistry or covered by high quality data (i.e., phred quality >=
  30); an attempt was made to resolve all sequencing problems, such
  as compressions and repeats; all regions were covered by at least
  one plasmid subclone or more than one M13 subclone; and the
  assembly was confirmed by restriction digest. The following
  abbreviations are used to associate primary accession numbers given
  in the feature table with their source databases: Em., ENBL; Sw.,
  SWISSPROT; Tr., TREMBL; Wp., WORMPEP; Information on the WDRMP
  database can be found at
  http://www.sanger.ac.uk/Projects/C.elegans/wormpep XXbac-105N19 is
  from a CHORI-502 human bac - COX cell line library VECTOR:
  PTABAC2.1
  This sequence was generated from part of bacterial clone contigs
  constructed by the MHC Haplotype Consortium and collaborators.
  Further information can be found at
  http://www.sanger.ac.uk/HGP/Chr6/MHC.
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BASE COUNT 19363 a 22004 c 21777 g 21330 t

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Score: 312.00 Matches: 77
Percent Similarity: 38.61% Conservatives: 1
Best Local Similarity: 38.12% Mismatches: 0
Query Match: 78.20% Indels: 124
DB: 9 Gaps: 2
US-09-092-296-15 (1-78) x AL662854 (1-84474)
QY 1 MetGlySerGlyLeuProLeuValLeuLeuLeuThrLeuLeuGlySerSerHisGlyThr 20
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QY 20 ----- 20
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QY 20 ----- 20
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QY 20 ----- 20
Db 56274 TGTGTCTCCGGAGGAATCAGCCCTGACTGTGGGTCTTAAGCTGTACTTCTGGATCCGA 56215
QY 21 GlyProGlyMetThrLeuGlnLeuLysLeuLysGluSerPheLeuThrAsnSerSerTyr 40
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Db 56214 GGGCCGGGTATGACTTTGCCAATGAAGCTGAAGAGTCTTTCTGCACAGTTCCTCTAT 56155
QY 41 GluSerSerPheLeuGluLeuLeuLys----- 50
|||||
Db 56154 GAGTCCAGCTTCTCGAATGTGCTTGAAAGGTAGTTCTTTTGAAGGGGAAGATGGGGCT 56095
QY 50 ----- 50
Db 56094 GTGTCTTTGTGAGTCACTTTGGCCCTCTGCTGGGCTGCGATGTCTCGTGGGAATG 56035
QY 51 -----LeuCysLeuLeuLeuHis 56
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Db 56034 GAGACTCTTACATCGCGCCCTTTAACCTTTGTTCACGCTCTGCCCTCTCTCCAT 55975
QY 57 LeuProSerGlyThrSerValThrLeuHisHisAlaArgSerGlnHisHisValValCys 76
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Db 55974 CTCCCTCAGGACCAAGCTCACCCTCCACCATGAAGATCTCAACACCATGTTGTCTGC 55915
QY 77 AsnThr 78
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DEFINITION
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ACCESSION
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VERSION
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KEYWORDS
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SOURCE
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  ORGANISM
    1
  REFERENCE
    1
    Dlek, A., Piepenbrock, C. and Berlin, K.
    Diagnosis of known genetic parameters within the mhc
    Patent: WO 0200932-A 4 03-JAN-2002;
    Epigenomics AG (DE)
  FEATURES
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;   LENGTH: 413 base pairs
;   TYPE: nucleic acid
;   STRANDEDNESS: single
;   TOPOLOGY: linear
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US-09-092-296-6

Query Match      100.0%; Score 234; DB 9; Length 413;
Best Local Similarity 100.0%; Pred. No. 2.6e-71;
Matches 234; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 61 GGGCGGGTATGACTTTCGAAGCTGAAGGAGTCTTTTCGACAAATTCCTCTAT 120
Db 107 GGGCGGGTATGACTTTCGAAGCTGAAGGAGTCTTTTCGACAAATTCCTCTAT 166
QY 121 GAGTCAGCTTCCTGGAATGCTTGAAGAGCTCTGCGCTCTCTCCATCTCCCTTCAGGG 180
Db 167 GAGTCAGCTTCCTGGAATGCTTGAAGAGCTCTGCGCTCTCTCCATCTCCCTTCAGGG 226
QY 181 ACCAGCGTCACCTCCACCATGCAAGATCTCAACACCATGTTGTCTGCAACACA 234
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RESULT 2
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; Sequence 362, Application US/09992598
; Patent No. US20020160384A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Kijavini, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tamas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2730PIC20
; CURRENT FILING DATE: 2001-11-14
; PRIOR APPLICATION NUMBER: US/09/992,598
; PRIOR FILING DATE: 1997-06-16
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/065186
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; PRIOR FILING DATE: 1998-07-01
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; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/091626
; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/091633
; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/091978
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/091982
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/092182
; PRIOR FILING DATE: 1998-07-09
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Query Match          100.0%; Score 234; DB 9; Length 422;
Best Local Similarity 100.0%; Pred. No. 2.6e-71;
Matches 234; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy 1 ATGGGCTCGGGCTGGCCCTTGTGCAACTGAAGCTGAAGAGCTCTTCTGACCTCTCTTGGCAGCTCACATGGAACA 60
Db 58 ATGGGCTCGGGCTGGCCCTTGTGCAACTGAAGCTGAAGAGCTCTTCTGACCTCTCTTGGCAGCTCACATGGAACA 117
Qy 61 GGGCCGGGTATGACTTTGCAACTGAAGCTGAAGAGCTCTTCTGACCTCTCTTGGCAGCTCACATGGAACA 120
Db 118 GGGCCGGGTATGACTTTGCAACTGAAGCTGAAGAGCTCTTCTGACCTCTCTTGGCAGCTCACATGGAACA 177
Qy 121 GAGTCAGCTTCCTTGGAAATGGCTTGAAGCTCTGCTCTCTCCATCTCCCTTCAGGG 180
Db 178 GAGTCAGCTTCCTTGGAAATGGCTTGAAGCTCTGCTCTCTCCATCTCCCTTCAGGG 237
Qy 181 ACCAGCGTCACCTCCACCATGCAAGATCTCAACACCATGTTGTCGCAACACA 234
Db 238 ACCAGCGTCACCTCCACCATGCAAGATCTCAACACCATGTTGTCGCAACACA 291
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RESULT 4

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; Sequence 65, Application US/10063547
; Publication No. US20020182638A1
; GENERAL INFORMATION:
; APPLICANT: Eaton, Dan L.
; APPLICANT: Flivaroff, Ellen
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3230R1C1
; CURRENT APPLICATION NUMBER: US/10/063,547
; CURRENT FILING DATE: 2002-05-02
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 170
; SEQ ID NO 65
; LENGTH: 422
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-063-547-65
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Query Match          100.0%; Score 234; DB 9; Length 422;
Best Local Similarity 100.0%; Pred. No. 2.6e-71;
Matches 234; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy 1 ATGGGCTCGGGCTGGCCCTTGTGCAACTGAAGCTGAAGAGCTCTTCTGACCTCTCTTGGCAGCTCACATGGAACA 60
Db 58 ATGGGCTCGGGCTGGCCCTTGTGCAACTGAAGCTGAAGAGCTCTTCTGACCTCTCTTGGCAGCTCACATGGAACA 117
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Qy 61 GGGCCGGGTATGACTTTGCAACTGAAGCTGAAGAGCTCTTCTGACCTCTCTTGGCAGCTCACATGGAACA 120
Db 118 GGGCCGGGTATGACTTTGCAACTGAAGCTGAAGAGCTCTTCTGACCTCTCTTGGCAGCTCACATGGAACA 177
Qy 121 GAGTCAGCTTCCTTGGAAATGGCTTGAAGCTCTGCTCTCTCCATCTCCCTTCAGGG 180
Db 178 GAGTCAGCTTCCTTGGAAATGGCTTGAAGCTCTGCTCTCTCCATCTCCCTTCAGGG 237
Qy 181 ACCAGCGTCACCTCCACCATGCAAGATCTCAACACCATGTTGTCGCAACACA 234
Db 238 ACCAGCGTCACCTCCACCATGCAAGATCTCAACACCATGTTGTCGCAACACA 291
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RESULT 5

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US-09-989-735-362
; Sequence 362, Application US/09989735
; Publication No. US20020193299A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2730P1C61
; CURRENT APPLICATION NUMBER: US/09/989,735
; CURRENT FILING DATE: 2001-11-19
; PRIOR APPLICATION NUMBER: 60/049787
; PRIOR FILING DATE: 1997-06-16
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/065186
; PRIOR FILING DATE: 1997-11-12
; PRIOR APPLICATION NUMBER: 60/065311
; PRIOR FILING DATE: 1997-11-13
; PRIOR APPLICATION NUMBER: 60/066770
; PRIOR FILING DATE: 1997-11-24
; PRIOR APPLICATION NUMBER: 60/075945
; PRIOR FILING DATE: 1998-02-25
; PRIOR APPLICATION NUMBER: 60/078910
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/083322
; PRIOR FILING DATE: 1998-04-28
; PRIOR APPLICATION NUMBER: 60/084600
; PRIOR FILING DATE: 1998-05-07
; PRIOR APPLICATION NUMBER: 60/087106
; PRIOR FILING DATE: 1998-05-28
; PRIOR APPLICATION NUMBER: 60/087607
; PRIOR FILING DATE: 1998-06-02
; PRIOR APPLICATION NUMBER: 60/087609
; PRIOR FILING DATE: 1998-06-02
; PRIOR APPLICATION NUMBER: 60/087759
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; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/091978
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/091982
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/092182
; PRIOR FILING DATE: 1998-07-09

Query Match          100.0%; Score 234; DB 9; Length 422;
Best Local Similarity 100.0%; Pred. No. 2.6e-71;
Matches 234; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGGGTCGCGCTGCCCTTGTCCCTCTCTTGACCCCTCTTGCGAGCTCATCGGACACA 60
    |||||
Db 58 ATGGGTCGCGCTGCCCTTGTCCCTCTCTTGACCCCTCTTGCGAGCTCATCGGACACA 117
    |||||

QY 61 GGCCGGGTATGACTTTCGAACCTGAAGCTGAAGGAGTCTTTCTGACAAATTCCTCCTAT 120
    |||||
Db 118 GGCCGGGTATGACTTTCGAACCTGAAGCTGAAGGAGTCTTTCTGACAAATTCCTCCTAT 177
    |||||

QY 121 GATCCAGCTTCCTGGAAATGCTTTGAAAGCTTGGCTCTCTCCATCTCCCTTCAGGG 180
    |||||
Db 178 GATCCAGCTTCCTGGAAATGCTTTGAAAGCTTGGCTCTCTCCATCTCCCTTCAGGG 237
    |||||

QY 181 ACCAGGCTCACCTCCACCATGCAAGATCTCAACACCATGTTGCTGCAACACA 234
    |||||
Db 238 ACCAGGCTCACCTCCACCATGCAAGATCTCAACACCATGTTGCTGCAACACA 291
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RESULT 8
US-09-990-436-362
; Sequence 362, Application US/09990436
; Publication No. US20020198148A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2730P1C14
; CURRENT APPLICATION NUMBER: US/09/990,436
; CURRENT FILING DATE: 2001-11-14
; PRIOR APPLICATION NUMBER: 60/049787
; PRIOR FILING DATE: 1997-06-16
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/065186
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; PRIOR APPLICATION NUMBER: 60/065311
; PRIOR FILING DATE: 1997-11-13
; PRIOR APPLICATION NUMBER: 60/066770
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; PRIOR FILING DATE: 1998-04-28
; PRIOR APPLICATION NUMBER: 60/084600
; PRIOR FILING DATE: 1998-05-07
; PRIOR APPLICATION NUMBER: 60/087106
; PRIOR FILING DATE: 1998-05-28
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; PRIOR FILING DATE: 1998-06-17
; PRIOR APPLICATION NUMBER: 60/089538
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; PRIOR FILING DATE: 1998-06-17
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; PRIOR FILING DATE: 1998-06-17
; PRIOR APPLICATION NUMBER: 60/089599
; PRIOR FILING DATE: 1998-06-17
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; PRIOR FILING DATE: 1998-06-17
; PRIOR APPLICATION NUMBER: 60/089653
; PRIOR FILING DATE: 1998-06-17
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; PRIOR FILING DATE: 1998-06-18
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; PRIOR APPLICATION NUMBER: 60/090355
; PRIOR FILING DATE: 1998-06-23
; PRIOR APPLICATION NUMBER: 60/090429
; PRIOR FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: 60/090431
; PRIOR FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: 60/090435
; PRIOR FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: 60/090444
; PRIOR FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: 60/090445
; PRIOR FILING DATE: 1998-06-24
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; PRIOR FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: 60/090676
; PRIOR FILING DATE: 1998-06-25
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; PRIOR FILING DATE: 1998-06-25
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; PRIOR APPLICATION NUMBER: 60/091360
; PRIOR FILING DATE: 1998-07-01
; PRIOR APPLICATION NUMBER: 60/091478
; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/091544
; PRIOR FILING DATE: 1998-07-01

; PRIOR APPLICATION NUMBER: 60/091519
; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/091626
; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/091633
; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/091978
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/091982
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/092182
; PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 234; DB 9; Length 422;
Best Local Similarity 100.0%; Pred. No. 2.6e-71;
Matches 234; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 ATGGGGTCTGGGCTGCCCTTGTCTCTCTCTGACCTCTTGACCTCTTGACGCTGACATGGGAACA 60
Db 58 ATGGGGTCTGGGCTGCCCTTGTCTCTCTCTGACCTCTTGACCTCTTGACGCTGACATGGGAACA 117
Qy 61 GGCGCGGTATGACTTTGCAACTGAAGCTGAAGAGTCTTTTCTGACAAATTCCTCTAT 120
Db 118 GGCGCGGTATGACTTTGCAACTGAAGCTGAAGAGTCTTTTCTGACAAATTCCTCTAT 177
Qy 121 GAGTCAGCTTCCTGGAATTCCTGAAAAGCTCTGAAAAGCTCTGCTCCTCCTCCTCCTTCAGGG 180
Db 178 GAGTCAGCTTCCTGGAATTCCTGAAAAGCTCTGAAAAGCTCTGCTCCTCCTCCTCCTTCAGGG 237
Qy 181 ACAGCGTCACCCCTCCACCATGCAAGATCTCAACACCATGTTGTCTGCAACACA 234
Db 238 ACCAGCGTCACCCCTCCACCATGCAAGATCTCAACACCATGTTGTCTGCAACACA 291

RESULT 9

US-09-991-181-362
; Sequence 362, Application US/09991181
; Publication No. US20020197615A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnovers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: ROY, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2730P1C53
; CURRENT APPLICATION NUMBER: US/09/991,181
; CURRENT FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/049787
; PRIOR FILING DATE: 1997-06-16
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/065186

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; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE OF INVENTION: Acids Encoding the Same
; CURRENT APPLICATION NUMBER: US/09/989,734
; CURRENT FILING DATE: 2001-11-19
; PRIOR APPLICATION NUMBER: 60/049787
; PRIOR FILING DATE: 1997-06-16
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;; PRIOR APPLICATION NUMBER: 60/091978
;; PRIOR FILING DATE: 1998-07-07
;; PRIOR APPLICATION NUMBER: 60/091982
;; PRIOR FILING DATE: 1998-07-07
;; PRIOR APPLICATION NUMBER: 60/092182
;; PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 234; DB 9; Length 422;

Best Local Similarity 100.0%; Pred. No. 2,6e-71; Mismatches 0; Indels 0; Gaps 0;

Matches 234; Conservative 0;

QY 1 ATGGGGTCTGGGCTGCCCTTGTCTCTCTTGACCCCTCTTGCGAGCTCACATGGAACA 60
Db 58 ATGGGGTCTGGGCTGCCCTTGTCTCTCTTGACCCCTCTTGCGAGCTCACATGGAACA 117
QY 61 GGGCGGGTATGACTTTCGAAGCTGAAGAGTCTTTCTGCAAAATTCCTCCAT 120
Db 118 GGGCGGGTATGACTTTCGAAGCTGAAGAGTCTTTCTGCAAAATTCCTCCAT 177
QY 121 GAGTCCAGTTCCTGGAATTCCTGAAAGCTCTGCGCTCCCTCCATCCTCCAGGG 180
Db 178 GAGTCCAGTTCCTGGAATTCCTGAAAGCTCTGCGCTCCCTCCATCCTCCAGGG 237
QY 181 ACCAGCGTCACCTCCACATGCAAGATCTCAACACCATGTTGCTGCAACACA 234
Db 238 ACCAGCGTCACCTCCACATGCAAGATCTCAACACCATGTTGCTGCAACACA 291

RESULT 12

US-09-997-653-362
; Sequence 362, Application US/09997653
; Publication No. US2003008297A1

GENERAL INFORMATION:

;; APPLICANT: Ashkenazi, Avi J.
;; APPLICANT: Baker, Kevin P.
;; APPLICANT: Botstein, David
;; APPLICANT: Desnoyers, Luc
;; APPLICANT: Eaton, Dan L.
;; APPLICANT: Ferrara, Napoleone
;; APPLICANT: Fong, Sherman
;; APPLICANT: Gerber, Hanspeter
;; APPLICANT: Gerritsen, Mary E.
;; APPLICANT: Goddard, Audrey
;; APPLICANT: Godowski, Paul J.
;; APPLICANT: Grimaldi, J. Christopher
;; APPLICANT: Gurney, Austin L.
;; APPLICANT: Kijavini, Ivar J.
;; APPLICANT: Napier, Mary A.
;; APPLICANT: Pan, James
;; APPLICANT: Paoni, Nicholas F.
;; APPLICANT: Roy, Margaret Ann
;; APPLICANT: Stewart, Timothy A.

;; APPLICANT: Tumas, Daniel
;; APPLICANT: Watanabe, Colin K.
;; APPLICANT: Williams, P. Mickey
;; APPLICANT: Wood, William I.
;; APPLICANT: Zhang, Zemin
;; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
;; TITLE OF INVENTION: Acids Encoding the Same
;; FILE REFERENCE: P2730PIC38
;; CURRENT APPLICATION NUMBER: US/09/997,653
;; CURRENT FILING DATE: 2001-11-15
;; PRIOR APPLICATION NUMBER: 60/049787
;; PRIOR FILING DATE: 1997-06-16
;; PRIOR APPLICATION NUMBER: 60/062250
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; PRIOR APPLICATION NUMBER: 60/091978
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/091982
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/092182
; PRIOR FILING DATE: 1998-07-09

Query Match 100.0% Score 234; DB 9; Length 422;

Best Local Similarity 100.0%; Pred. No. 2.6e-71; Matches 234; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 58 ATGGGGTCTGGGCTGCCCTTGCTCTCTTGACCCCTCTTGGCAGCTCACATGAACA 117
QY 61 GGGCGGGTATGACTTTGCAACTGAAGTGAAGAGTCTTTCTGACAAAATTCCTCTAT 120
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Db 118 GGGCGGGTATGACTTTGCAACTGAAGTGAAGAGTCTTTCTGACAAAATTCCTCTAT 177
QY 121 GAGTCCAGCTTCTCTGGAATGCTTGAAAAGCTTGCTCTCTCTCCATCTCCCTCAGG 180
|||||
Db 178 GAGTCCAGCTTCTCTGGAATGCTTGAAAAGCTTGCTCTCTCTCCATCTCCCTCAGG 237
QY 181 ACCAGCGTCACCTCCACCATGCAAGATCTCAACACCATGTTGTGCAACACA 234
|||||
Db 238 ACCAGCGTCACCTCCACCATGCAAGATCTCAACACCATGTTGTGCAACACA 291

RESULT 13

US-10-174-590-241
; Sequence 241, Application US/10174590
; Publication No. US20030008352A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Chen, Jian
; APPLICANT: Desnoyers, Luc
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Smith, Victoria
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3430R1C42

```
; CURRENT APPLICATION NUMBER: US/10/174,590
; CURRENT FILING DATE: 2002-06-18
; Prior application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 241
; LENGTH: 422
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-174-590-241
```

```
Query Match      100.0%; Score 234; DB 9; Length 422;
Best Local Similarity 100.0%; Pred. No. 2.6e-71;
Matches 234; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGGGCTGTGGCTGGCCCTTGTCTCTCTGTGACCCCTCTGGAGCTCAGCTGGAACA 60
    |||||||
Db 58 ATGGGCTGTGGCTGGCCCTTGTCTCTCTGTGACCCCTCTGGAGCTCAGCTGGAACA 117
    |||||||
QY 61 GGGCCGGGTATGACTTTGCAACTGAAAGCTGAAAGAGTCTTTTCTGACAAATTCCTCTAT 120
    |||||||
Db 118 GGGCCGGGTATGACTTTGCAACTGAAAGCTGAAAGAGTCTTTTCTGACAAATTCCTCTAT 177
    |||||||
QY 121 GAGTCAGCTTCCTGGAAATGCTTGAAGAGCTTGGCTCTCTCCATCTCCCTTCAGGG 180
    |||||||
Db 178 GAGTCAGCTTCCTGGAAATGCTTGAAGAGCTTGGCTCTCTCCATCTCCCTTCAGGG 237
    |||||||
QY 181 ACCAGCGTCACCCCTCCACCATGCAAGATCTCAACACCATGTTGTCTGCAACACA 234
    |||||||
Db 238 ACCAGCGTCACCCCTCCACCATGCAAGATCTCAACACCATGTTGTCTGCAACACA 291
    |||||||
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RESULT 14
US-10-176-758-241
; Sequence 241, Application US/10176758
; Publication NO. US20030008353A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Chen, Jian
; APPLICANT: Desnoyers, Luc
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Smith, Victoria
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3430R1C104
; CURRENT APPLICATION NUMBER: US/10/176,758
; CURRENT FILING DATE: 2002-06-21
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 241
; LENGTH: 422
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-176-758-241
```

```
Query Match      100.0%; Score 234; DB 9; Length 422;
Best Local Similarity 100.0%; Pred. No. 2.6e-71;
Matches 234; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGGGCTGTGGCTGGCCCTTGTCTCTCTGTGACCCCTCTGGAGCTCAGCTGGAACA 60
    |||||||
Db 58 ATGGGCTGTGGCTGGCCCTTGTCTCTCTGTGACCCCTCTGGAGCTCAGCTGGAACA 117
    |||||||
QY 61 GGGCCGGGTATGACTTTGCAACTGAAAGCTGAAAGAGTCTTTTCTGACAAATTCCTCTAT 120
    |||||||
Db 118 GGGCCGGGTATGACTTTGCAACTGAAAGCTGAAAGAGTCTTTTCTGACAAATTCCTCTAT 177
    |||||||
QY 121 GAGTCAGCTTCCTGGAAATGCTTGAAGAGCTTGGCTCTCTCCATCTCCCTTCAGGG 180
    |||||||
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```
Db 178 GAGTCAGCTTCCTGGAAATGCTTGAAGAGCTTGGCTCTCTCCATCTCCCTTCAGGG 237
    |||||||
QY 181 ACCAGCGTCACCCCTCCACCATGCAAGATCTCAACACCATGTTGTCTGCAACACA 234
    |||||||
Db 238 ACCAGCGTCACCCCTCCACCATGCAAGATCTCAACACCATGTTGTCTGCAACACA 291
    |||||||

RESULT 15
US-10-063-616-65
; Sequence 65, Application US/10063616
; Publication NO. US20030013855A1
; GENERAL INFORMATION:
; APPLICANT: Eaton, Dan L.
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3230R1C1
; CURRENT APPLICATION NUMBER: US/10/063,616
; CURRENT FILING DATE: 2002-05-03
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 170
; SEQ ID NO 65
; LENGTH: 422
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-063-616-65

Query Match      100.0%; Score 234; DB 9; Length 422;
Best Local Similarity 100.0%; Pred. No. 2.6e-71;
Matches 234; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGGGCTGTGGCTGGCCCTTGTCTCTCTCTGTGACCCCTCTGTGAGCTCAGCTGGAACA 60
    |||||||
Db 58 ATGGGCTGTGGCTGGCCCTTGTCTCTCTCTGTGAGCTCAGCTGGAACA 117
    |||||||
QY 61 GGGCCGGGTATGACTTTGCAACTGAAAGCTGAAAGAGTCTTTTCTGACAAATTCCTCTAT 120
    |||||||
Db 118 GGGCCGGGTATGACTTTGCAACTGAAAGCTGAAAGAGTCTTTTCTGACAAATTCCTCTAT 177
    |||||||
QY 121 GAGTCAGCTTCCTGGAAATGCTTGAAGAGCTTGGCTCTCTCCATCTCCCTTCAGGG 180
    |||||||
Db 178 GAGTCAGCTTCCTGGAAATGCTTGAAGAGCTTGGCTCTCTCCATCTCCCTTCAGGG 237
    |||||||
QY 181 ACCAGCGTCACCCCTCCACCATGCAAGATCTCAACACCATGTTGTCTGCAACACA 234
    |||||||
Db 238 ACCAGCGTCACCCCTCCACCATGCAAGATCTCAACACCATGTTGTCTGCAACACA 291
    |||||||

Search completed: May 1, 2003, 05:17:14
Job time : 64.8775 secs
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Best Local Similarity 3.5%; Pred. No. 2; Indels 0; Caps 0

Matches 75; Conservative 0; Mismatches 90; Gaps 60

Query 1 ATGGGCTGTGGCGTCCCTTCCTCCTTGACCCCTCTGGCAGCTCACATGGGAACA 60
||||| |||| :||||: ||:::|| |:
Db 1053 AGGCAGCTTGGCATYNYNNYYNYYYNYNYNYNYNYNYNYNYNYNYNYNYNYNY 1112

Qy 61 GGCGGGGTATGACTTTGCCAATGAAGCTGAAGGAGTCTTTTTGTGACAAATTCTCCTAT 120
||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
Db 1113 YY 1172

Qy 121 GAGTCAGCTTCCTGGAAATGGTGTGAAGAAGCTCGCTCCTCCTCAATCCTTCAGG 180
:: :::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: :::::
Db 1173 YY 1232

Qy 181 ACCAGGCTCACCTCCCACCATCAAGATCTCAAACCATGTGTCT 226
:: :::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: :::::
Db 1233 YY 1278

RESULT 3
US-09-484-970B-38/c
Sequence 38, Application US/09484970B
Patent NO. 6426186
GENERAL INFORMATION:
APPLICANT: Jones, Karen A.
APPlicant: Volkmutz, Wayne
ApplicAnT: Walker, Michael G.
TITLE OF INVENTION: BONE REMODELING GENES
FILE REFERENCE: PB-0014 US
CURRENT APPLICATION NUMBER: US/09/484,970B
CURRENT FILING DATE: 2000-01-18
NUMBER OF SEQ ID NOS: 172
SOFTWARE: PERL Program
SEQ ID NO 38
LENGTH: 1956
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc-feature
OTHER INFORMATION: Incyte ID NO.. 6426186 247608.ICBI
US-09-484-970B-38

Query Match 13.1%; Score 30.6; DB 4; Length 1956;
Best local similarity 50.3%; pred. no. 1.4; indels 0; caps 0;
Matches 75; conservative 0; mismatches 74;

Qy 72 GACITTTGCAACTGAAGCTGAAGGAGTCTTTCTGACAAAATTCCTCTATGAGTCAGCTT 131
||||| |||| |||| |||| |||| |||| |||| |||| |||| |||| ||||
Db 399 GATTTTCTTCTTAAGTCTACTCTTGACAGAGATCTTCAAGTGTGTGTTGAGTT 340

Qy 132 CTGGAATTCCTTGAAGAGCTGCTCCTCCTCCAATTCCTTCAGGGACCAGGCTCAC 191
||| |||| |||| |||| |||| |||| |||| |||| |||| |||| ||||
Db 339 CUAACACTGATTAAGTCTGTTTTTCCICCACTTCCACTTGATTTTCAGCATCAA 280

Qy 192 CCTCCACATGCAAGATCAACACCATG 220
||| |||| || |||| || |||| || |||| || |||| || |||| || ||||
Db 279 CTGCATCATGTGCAGCATTCATCATCTTG 251

RESULT 4
US-09-128-155-17/c
Sequence 17, Application US/09128155
Patent NO. 6117654
GENERAL INFORMATION:
APPLICANT: Pan, Yang
TITLE OF INVENTION: NOVEL MOLECULES OF TANGO-77 RELATED PROTEIN FAMILY
FILE REFERENCE: 09404/052001
CURRENT APPLICATION NUMBER: US/09/128.155
CURRENT FILING DATE: 1998-08-03
EARLIER APPLICATION NUMBER: US 60/091.650
EARLIER FILING DATE: 1998-07-02

EARLIER APPLICATION NUMBER: US 60/054,646
; EARLIER FILING DATE: 1997-08-04
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 17
; LENGTH: 176373
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc.feature
; LOCATION: (1)..(176373)
; OTHER INFORMATION: n = A,T,C or G
US-09-128-155-17

Query Match 12.8%; Score 30; DB 3; Length 176373;
Best Local Similarity 55.9%; Pred. No. 16;
Matches 57; Conservative 0; Mismatches 45; Indels 0; Gaps 0;
QY 73 ACTTTCGAAGCTGAAGGAGCTCTTTCTGACAAATCCTCCTATGAGTCCAGCTC 132
Db 137160 ACTTACAGCTGAGGTAAGTGAATGCTATGGAATGAGCCCTCTCAGCCTCTGCTAC 137101
QY 133 CTGGAATGCTTGAAGCTCTGCGCCCTCCCTCCATCCCT 174
Db 137100 CACTTATCCAGAACACCACTCTCTCCCGGCCCATCCCT 137059

RESULT 5
US-09-219-194-2
; Sequence 2, Application US/09219194
; Patent No. 6410230
; GENERAL INFORMATION:
; APPLICANT: MCGILL UNIVERSITY
; TITLE OF INVENTION: GLYCERALDEHYDE-3-PHOSPHATE
DEHYDROGENASE AND NUCLEAR RESTORATION OF CYTOPLASMIC MALE
STERILITY
; NUMBER OF SEQUENCES: 3
; CORRESPONDENCE ADDRESS:
STREET: 1981 McGill College Ave. - Suite 1600
CITY: Montreal
STATE: QC
COUNTRY: Canada
ZIP: H3A 2Y3
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/219,194
FILING DATE: 23-Dec-1998
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/020,553
FILING DATE: 26-JUN-1996
ATTORNEY/AGENT INFORMATION:
NAME: Cote, France
REGISTRATION NUMBER: 4166
REFERENCE/DOCKET NUMBER: 1770-152*PCT* FC
TELECOMMUNICATION INFORMATION:
TELEPHONE: 514 845-7126
TELEFAX: 514-288-8389
TELEX: <Unknown>
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 1091 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-219-194-2

Query Match 12.7%; Score 29.8; DB 4; Length 1091;
Best Local Similarity 51.9%; Pred. No. 2;
Matches 67; Conservative 0; Mismatches 62; Indels 0; Gaps 0;
QY 39 CTTGGCAGCTCACATGGAACAGGCGCGGTATGACTTTGCAACTGAAGCTGAAGAGTC 98
Db 263 CCTGAGGATATCCATGGGTGAGGCGCGAGCTGACTTTCTTGTGACTACTGGTGC 322
QY 99 TTTTCTGACAAATTCCTCCTATGAGTCCAGCTTCTCTGGAATTGCTTGAAGAGCTCTGCT 158
Db 323 TTCACCTGACAAGGACAAGGCTGCTCTCACTTGAAGGTGGTGGCCAAAGTGTCTATC 382
QY 159 CTTCTCCA 167
Db 383 TCTGCACCA 391

RESULT 6
US-09-081-345-1/c
; Sequence 1, Application US/09081345
; Patent No. 6228641
; GENERAL INFORMATION:
; APPLICANT: Bahija Jallal
; APPLICANT: Gregory D. Plowman
; TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF
TITLE OF INVENTION: PTP04 RELATED DISORDERS
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
ADDRESS: Lyon & Lyon
STREET: 633 West Fifth Street
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071-2066
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: FastSeq for Windows 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/081,345
FILING DATE: Herewith
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/047,222
FILING DATE: May 20, 1997
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 234/253
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 3580 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-09-081-345-1

Query Match 12.4%; Score 29; DB 4; Length 3580;
Best Local Similarity 48.0%; Pred. No. 6.1;
Matches 83; Conservative 0; Mismatches 90; Indels 0; Gaps 0;
QY 23 TCTCTCTTGAACCCCTTCGTCAGCTCACATGGAACAGGCGCGGTATGACTTTGCAAC 82
Db 642 TCATGGTCTGCCAATCTTGTATGAAGTGTAGTAGTTCGAGTTTCACATTGAC 583

83	QY	TGAAGCTGAAGGAGTCTTTCTTGACAAATTCCTCTATGAGTCACGCTTCCTGGAATTGC	142
582	Db	TTAACTTTTATAGATCCTGATTTATATATACAGATTTCTCTTTTTCAGCTTCACAGGATACA	523
143	QY	TTGAAAAGCTCTGCCTCTCTCCATCTCCCTTCAGGAGCACGGTCACCCCTC	195
522	Db	GAGAAAGGGCGCAATTTCCAGCTGCATCTCTCTGGCTCAGCGCCAGTAGGGCTC	470

RESULT 7
US-08-750-357-8/c
; Sequence 8, Application US/08750357
; Patent No. 6008437
; GENERAL INFORMATION:
; APPLICANT: KREBBERS, Enno
; APPLICANT: WILLIAMS, Mark
; APPLICANT: LEBMANS, Jan
; TITLE OF INVENTION: USE OF ANTHOCYANIN GENES TO MAINTAIN
; TITLE OF INVENTION: MALE STERILE PLANTS
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS. L.L.P.
; STREET: P.O. Box 1404
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: United States
; ZIP: 22313-1404

	Query Match	12.2%	Score 28.6;	DB 3;	Length 2660;
	Best Local Similarity	61.3%	Pred. No. 7.2;		
	Matches 46;	Conservative	Mismatches 0;	Indels 29;	Gaps 0;
QY	157	CTCCTTCCTCATCTCCCTTCAGGAGACCGAGTCAACCTCCACATGCAGAGATCTCAACAC	216		
DB	1212	CTCTTTCTTCGACCGGTTTCAGGTCGCGGACGCGACACCAACGAGCGCTCCACAA	1153		
QY	217	CATGTTGTCTGCAAC	231		
DB	1152	AAACGGCGACGCAAC	1138		

RESULT 8
US-09-369-364A-6/c
; Sequence 6, Application US/09369364A
; Patent No. 6391610
; GENERAL INFORMATION:
; APPLICANT: Apte, Suneel
; APPLICANT: Huuskainen, Tiina L.
; APPLICANT: Hirohata, Setsoshi

```

; TITLE OF INVENTION: Nucleic Acids Encoding Zinc Metalloproteases
;
; FILE REFERENCE: 26473/4007/10-30-00
; CURRENT APPLICATION NUMBER: US/09/369,364A
; CURRENT FILING DATE: 1999-08-06
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
; LENGTH: 3218
; TYPE: DNA
; ORGANISM: Homo sapiens ADAMTS-7
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (13)..(3003)
; US-09-369-364A-6

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	Query Match	12.1%	Score 28.4;	DB 4;	Length 3218;
	Best Local Similarity	48.7%;	Pred. No. 9.1;		
	Matches	77;	Conservative	0;	Mismatches 81;
				Indels	0;
				Gaps	
Qy	4	GGGTCTGGGCTCCCCCTGCTCCTCTTGACCTCTCTGGCAGCTCACATGGAACAGGG	63		
Db	2838	GGGGCTGTGCTGCTGCCCACTTCTCACTCTGCGGAGTGACTGTGCACCTGGTCCAGGG	2779		
Qy	64	CGGGGTATGACTTTGCAACTGAAGCTGAAGGAGCTTTTCTGACAAATTCCTCTCATGAG	123		
Db	2778	CCCATATGCCAGGACACGGCGGGGACCTCTGCTGGCCACCTGCCTCCCTGTG	2719		
Qy	124	TCCAGCTTCCTGAANTGCTTGAAGACTCTGCCCTCT	161		
Db	2718	GATGGTGTACTCTAGTGCACCCCGGGTTGCTCTCT	2681		

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RESULT 9
US-09-368-590-1/c
; Sequence 1, Application US/09368590
; Patent No. 6187563
; GENERAL INFORMATION:
; APPLICANT: Solimena, Michele
; TITLE OF INVENTION: INTERACTING POLYPEPTIDES FOR
; FILE OF INVENTION: AUTOANTIGENS OF AUTOIMMUNE DISEASES
; FILE REFERENCE: 101918-200 (OCR-941)
; CURRENT APPLICATION NUMBER: US/09/368,590
; CURRENT FILING DATE: 1999-08-04
; EARLIER APPLICATION NUMBER: 60/095,657
; EARLIER FILING DATE: 1998-08-07
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 7812
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(6879)
; NAME/KEY: unsure
; LOCATION: (100)...(102)
; NAME/KEY: unsure
; LOCATION: (1021)...(1023)
; NAME/KEY: unsure
; LOCATION: (2266)...(2268)
UC-09-368-590-1

```

Query Match	12.1%	Score 28.4;	DB 4;	Length 7812;
Best Local Similarity	62.9%	Pred. No. 13;		
4.4-bp	44.0	Mismatches	26;	Indels
Conservative	0;	Gaps	0;	Gaps

	159	186	218
QY	CCTCCTCCATCTCCCTTTCAGGACCCAGCGTCACTCCACCATGCGAAGATCTCAACACCA		
Db	CTTCCACCGCTCGCTCTGGGGGCAATGTCTCCCTCCAGCAGTCCATGCTTCTGCACCA	827	
QY	TTGTTGCTGC	228	
Db	GGTCTGCTGC	817	

```
RESULT 10
US-09-360-186-4/c
; Sequence 4, Application US/09360186
; Patent No. 6262343
; GENERAL INFORMATION:
; APPLICANT: Staskawicz, et al.
; TITLE OF INVENTION: Bs2 Resistance Gene
; FILE REFERENCE: 50687
; CURRENT APPLICATION NUMBER: US/09/360,186
; EARLIER APPLICATION NUMBER: 1999-07-23
; EARLIER FILING DATE: 1998-07-23
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
; LENGTH: 2718
; TYPE: DNA
; ORGANISM: Capsicum annuum
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(2718)
US-09-360-186-4

Query Match      12.1%; Score 28.2; DB 4; Length 2718;
Best Local Similarity 50.4%; Pred. No. 9.9;
Matches 69; Conservative 0; Mismatches 68; Indels 0; Gaps 0;

QY 96 GTCCTTTCTGACAAATTCCTCTATGAGTCAGCTTCCTGGAATTCCTTGAAGAGCTCTG 155
DB 1390 GACTCTCTCTGTCGAGGAGGACTAGACATCTATCGAAGCTCTTGCAAAACACTTCTCAA 1331

QY 156 CCTCTTCCTCCATCTCTCCCTCAGGAGGACCAAGCTCCACCTCCACATGCGAAGCTCTCA 215
DB 1330 CCTCTCTCTCCAAATCATTTTCCAACTTCAGGAGCCCTCAGCCATCATCTCATCA 1271

QY 216 CCATGTGTGCTGCAACA 232
DB 1270 AATTCCTCACTGGAATA 1254

RESULT 11
US-09-360-186-2/c
; Sequence 2, Application US/09360186
; Patent No. 6262343
; GENERAL INFORMATION:
; APPLICANT: Staskawicz, et al.
; TITLE OF INVENTION: Bs2 Resistance Gene
; FILE REFERENCE: 50687
; CURRENT APPLICATION NUMBER: US/09/360,186
; EARLIER APPLICATION NUMBER: 1999-07-23
; EARLIER FILING DATE: 1998-07-23
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 3099
; TYPE: DNA
; ORGANISM: Capsicum annuum
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (93)..(2810)
US-09-360-186-2

Query Match      12.1%; Score 28.2; DB 4; Length 3099;
Best Local Similarity 50.4%; Pred. No. 10;
Matches 69; Conservative 0; Mismatches 68; Indels 0; Gaps 0;

QY 96 GTCCTTTCTGACAAATTCCTCTATGAGTCAGCTTCCTGGAATTCCTTGAAGAGCTCTG 155
DB 1482 GACTCTCTCTGAGGAGGACTAGACATCTATCGAAGCTCTTGCAAAACACTTCTCAA 1423
```

```
QY 156 CCTCTCTCTCCATCTCTCCCTCAGGAGGACCAAGCTTCACCTCCACCATGCAAGATCTCAACA 215
DB 1422 CCTCTCTCTCCAAATCAATTTTCCAACTTCAGGAGCCCTCAGCCATCCATGATCTCATCA 1363

QY 216 CCATGTGTGCTGCAACA 232
DB 1362 AATTCCTCACTGGAATA 1346

RESULT 12
US-09-360-186-1/c
; Sequence 1, Application US/09360186
; Patent No. 6262343
; GENERAL INFORMATION:
; APPLICANT: Staskawicz, et al.
; TITLE OF INVENTION: Bs2 Resistance Gene
; FILE REFERENCE: 50687
; CURRENT APPLICATION NUMBER: US/09/360,186
; EARLIER APPLICATION NUMBER: 1999-07-23
; EARLIER FILING DATE: 1998-07-23
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 31491
; TYPE: DNA
; ORGANISM: Capsicum annuum
US-09-360-186-1

Query Match      12.1%; Score 28.2; DB 4; Length 31491;
Best Local Similarity 50.4%; Pred. No. 29;
Matches 69; Conservative 0; Mismatches 68; Indels 0; Gaps 0;

QY 96 GTCCTTTCTGACAAATTCCTCTATGAGTCAGCTTCCTGGAATTCCTTGAAGAGCTCTG 155
DB 2869 GACTCTCTCTGTCGAGGAGGACTAGACATCTATCGAAGCTCTTGCAAAACACTTCTCAA 2810

QY 156 CCTCTCTCTCCATCTCTCCCTCAGGAGGACCAAGCTTCACCTCCACCATGCAAGATCTCAACA 215
DB 2809 CCTCTCTCTCCAAATCATTTTCCAACTTCAGGAGCCCTCAGCCATCCATGATCTCATCA 2750

QY 216 CCATGTGTGCTGCAACA 232
DB 2749 AATTCCTCACTGGAATA 2733

RESULT 13
US-08-188-582-10/c
; Sequence 10, Application US/08188582
; Patent No. 5534410
; GENERAL INFORMATION:
; APPLICANT: Tjian, Robert
; APPLICANT: Comai, Lucio
; APPLICANT: Dynlacht, Brian D.
; APPLICANT: Hoey, Timothy
; APPLICANT: Ruppert, Siegfried
; APPLICANT: Tanese, Naoko
; APPLICANT: Wang, Edith
; APPLICANT: Weinzierl, Robert O.J.
; TITLE OF INVENTION: TATA-BINDING PROTEIN ASSOCIATED FACTORS.
; TITLE OF INVENTION: NUCLEIC ACIDS ENCODING TAFs AND METHODS OF USE
; NUMBER OF SEQUENCES: 36
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FLEHR, HOEBACH, TEST, ALBRITTON & HERBERT
; STREET: 4 Embarcadero Center, Suite 3400
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-4187
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
```



```

; TELEFAX: (650) 343-4342
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2782 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
US-08-937-466-1

Query Match      11.9%; Score 27.8; DB 2; Length 2782;
Best Local Similarity 53.2%; Pred. No. 14;
Matches 59; Conservative 0; Mismatches 52; Indels 0; Gaps 0;

QY 56 GAACAGGCGCGGTATGACTTTGCACTGAGCTGAGGAGTCTTTCTGACAAATTCCT 115
Db 2101 GAAACCTCGAGAGAGAGCGAGAGAGCTGTCTCTGCTTCCCTAAGGTGGAG 2042

QY 116 CCTATGAGTCCAGCTTCTCGAATTGCTTGAAAGCTCTGCCTCCTCCTCC 166
Db 2041 ATTCTGAGTCTCTGCTTTGAACTGATGAGCAGGCGAGTGCCTCCCTCC 1991

Search completed: May 1, 2003, 05:14:21
Job time : 99.449 secs

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GenCore version 5.1.5
Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: May 1, 2003, 03:08:45 ; Search time 1171.86 Seconds
(without alignments)
3233.964 Million cell updates/sec

Title: US-09-092-296-7_copy_51_284

Perfect score: 234

Sequence: 1 ATGGGGCTGGGTGCCCCCTACCATGTTGTGTCACACACA 234

Scoring table: IDENTITY_NUC

Gapop 10.0, Gapext 1.0

Searched: 16154066 seqs, 8097743376 residues

Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

EST: *

1: em_estba:*

2: em_esthm:*

3: em_estin:*

4: em_estmu:*

5: em_estov:*

6: em_estpl:*

7: em_estro:*

8: em_hic:*

9: qb_estl:*

10: qb_est2:*

11: qb_hic:*

12: qb_est3:*

13: qb_est4:*

14: qb_est5:*

15: em_estfun:*

16: em_estom:*

17: qb_gss:*

18: em_gss_hum:*

19: em_gss_inv:*

20: em_gss_pin:*

21: em_gss_vrt:*

22: em_gss_fun:*

23: em_gss_mam:*

24: em_gss_mus:*

25: em_gss_other:*

26: em_gss_pro:*

27: em_gss_rod:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	234	100.0	456	12	BG506690 601861290
c	2	232.4	99.3	449	10 AW293443
	3	232.4	99.3	830	13 BI759796
c	4	221	94.4	422	12 BF002050
	5	194.2	83.0	895	13 BI820029
	6	181.2	77.4	865	13 BI820110

c	7	175	74.8	404	9	AI857998
	8	117	50.0	361	12	BF521842
	9	113.8	48.6	521	10	BB533837
	10	113.8	48.6	522	10	BB664284
c	11	93.2	39.8	328	9	AI136523
c	12	81.4	34.8	244	12	BF511043
c	13	75.8	32.4	552	17	AQ718761
c	14	47.6	20.3	633	17	AZ079350
c	15	47.4	20.3	506	17	AZ241329
c	16	37	15.8	496	12	BF920882
c	17	36.4	15.6	331	9	AA282040
c	18	36.4	15.6	365	10	AA263952
c	19	36.4	15.6	402	9	AA936790
c	20	36.4	15.6	424	9	AA741185
c	21	36.4	15.6	494	9	AA534569
c	22	36.4	15.6	529	9	AI018775
c	23	36.4	15.6	606	10	AA970327
c	24	36.4	15.6	719	10	AA970246
c	25	36.4	15.6	797	14	BQ775963
c	26	36.2	15.5	600	12	BG803137
c	27	35.2	15.0	458	13	BJ231120
	28	35.2	15.0	574	13	BJ254868
	29	35.2	15.0	729	13	BJ254605
c	30	34.8	14.9	451	9	AI829206
	31	34.8	14.9	639	17	AG048646
c	32	34.6	14.8	281	10	BB411111
	33	34.2	14.6	863	12	BG698056
c	34	34	14.5	190	9	AI010074
c	35	34	14.5	575	17	BH729561
	36	34	14.5	919	14	BQ28365
c	37	33.8	14.4	826	13	BI080794
	38	33.6	14.3	791	17	CNS03JMS
	39	33.4	14.3	545	14	T41524
c	40	33.4	14.3	550	12	BF779666
c	41	33.2	14.2	252	9	AA991822
c	42	33.2	14.2	597	10	AW013553
c	43	33.2	14.2	740	17	AG135659
c	44	33	14.1	803	17	BH440024
	45	33	14.1	827	17	BH712332

ALIGNMENTS

RESULT 1
BG506690
LOCUS 601861290f1 NIH_MGC_77 Homo sapiens cDNA clone IMAGE:4070759 5',
DEFINITION mRNA sequence.
ACCESSION BG506690.1 GI:13468207
VERSION BG506690
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 456)
AUTHORS NIH-MGC <http://mgc.uci.nih.gov/>
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: CLONTECH Laboratories, Inc.
CDNA Library Preparation: CLONTECH Laboratories, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
Plate: LLCM915 row: d column: 24
High quality sequence stop: 401.
Location/Qualifiers
1. .456

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/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:4070759"
/clone_lib="NIH_MGC_77"
/lab_host="DH10B (T1 phage-resistant)"
/notes="Organ: lung; Vector: pDNR-LIB (Clontech); Site:1:
SfiI (ggcgctcgcc); Site:2: SfiI (ggccattatggc); 5' and
3' adaptors were used in cloning as follows: 5' adaptor
sequence: 5'-CACGCCATATGGCC-3' and 3' adaptor sequence:
5'-ATTCTAGAGCCGAGCGCGGACATG-dT(30)BN-3' (where B = A,
C, or G and N = A, C, G, or T). Average insert size 1.9
kb (range 0.5-4.0 kb). 12/15 colonies contained inserts
by PCR. This library was enriched for full-length clones
and was constructed by Clontech Laboratories (Palo Alto,
CA). Note: this is a NIH_MGC Library."
BASE COUNT 109 a 137 c 106 g 103 t 1 others
ORIGIN
Query Match 100.0%; Score 234; DB 12; Length 456;
Best Local Similarity 100.0%; Pred. No. 5.3e-55;
Matches 234; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ATGGGGTCTGGGCTGCCCTTGCTCTTGACCTCTGCGAGCTCACATGGAACA 60
|||||
Db 45 ATGGGGTCTGGGCTGCCCTTGCTCTTGACCTCTGCGAGCTCACATGGAACA 104
|||||
QY 61 GGGCCGGATGACATTTGCAACTGAAGCTGAAGGAGTCTTTCTGACAAATTCCTCTAT 120
|||||
Db 105 GGGCCGGATGACATTTGCAACTGAAGCTGAAGGAGTCTTTCTGACAAATTCCTCTAT 164
|||||
QY 121 GAGTCCAGCTTCCTGGAATTCCTTGAAGAGCTCTGCTCTCTCTCCATCCTCCTTCAGGG 180
|||||
Db 165 GAGTCCAGCTTCCTGGAATTCCTTGAAGAGCTCTGCTCTCTCTCCATCCTCCTTCAGGG 224
|||||
QY 181 ACCAGCTCACCTCCACATGAAGATCTCAACACCATGTGTCGCAACACA 234
|||||
Db 225 ACCAGCTCACCTCCACATGAAGATCTCAACACCATGTGTCGCAACACA 278
|||||
RESULT 2
AW293443/c 449 bp mRNA linear EST 16-JAN-2000
LOCUS UI-H-B12-abm-c-08-0-UI.s1 NCI_CGAP_Sub4 Homo sapiens cDNA clone
DEFINITION IMAGE:2727182 3', mRNA sequence.
ACCESSION AW293443
VERSION 1
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 449)
NCI-CCGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cyapbs@mail.nih.gov
The sequence contained an oligo-dT track that was present in the
oligonucleotide that was used to prime the synthesis of first
strand cDNA and therefore this may represent a bonafide poly A
tail. cDNA Library Preparation: M.B. Soares Lab Clone distribution:
NCI-CCGAP clone distribution information can be found through the
I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
Seq primer: M13 Forward
POLYA=Yes.
Location/Qualifiers
1. .449
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:2727182"
/clone_lib="NCI_CGAP_Sub4"
```

```
/lab_host="DH10B (Life Technologies)"
/notes="Vector: pT73D-Pac (Pharmacia) with a modified
polylinker; Site:1: Not I; Site:2: Eco RI; The
NCI_CGAP_Sub4 library is a subtracted library derived from
the NCI_CGAP_Sub2 library which is a subtracted library
derived from the NCI_CGAP_Sub1 library, which is a
subtracted library derived from BI. BI constitutes a
mixture of 21 normalized or subtracted NCI_CGAP
libraries: NCI_CGAP_Co4, NCI_CGAP_Pr22, NCI_CGAP_Pr28,
NCI_CGAP_Co10, NCI_CGAP_Co16, NCI_CGAP_Kid5,
NCI_CGAP_Kid12, NCI_CGAP_Kid3, NCI_CGAP_Kid11,
NCI_CGAP_Lym2, NCI_CGAP_Br2, NCI_CGAP_Co8, NCI_CGAP_CLL1,
NCI_CGAP_Le12, NCI_CGAP_Brn23, NCI_CGAP_Lu5,
NCI_CGAP_Lu24, NCI_CGAP_Lu19, NCI_CGAP_GC4, NCI_CGAP_GC6,
NCI_CGAP_Brn25. These 21 libraries were pooled and a
single-stranded DNA preparation of the resulting mixture
was used as a tracer in a subtractive hybridization with
a driver whose composition is detailed below:
NCI_CGAP_Kid3 pool 1 : LLAM 3334-3337, 3682-3683,
3798-3803 (IMAGE Clones 1322376-1323911,
1456008-1456775, 1500552-1502853) NCI_CGAP_Kid5 pool 1 :
LLAM 3338-3342, 3722-3725, 3776-3778 (IMAGE Clones
1323912-1325831, 1471368-1472903, 1492104-1493253)
NCI_CGAP_Lu5 pool 1 : LLAM 3575-3582, 3851-3854 (IMAGE
Clones 1414920-1417991, 1520904-1522439) NCI_CGAP_GC4
pool 1 : LLAM 3164-3167, 3716-3720, 3733-3735 (IMAGE
Clones 1257096-1258631, 1469064-1470983, 1475592-1476743)
NCI_CGAP_Pr22 pool 1 : LLAM 2457-2459, 2758-2759,
3062-3068 (IMAGE Clones 985608-986759, 1101192-1101959,
1217928-1220615) NCI_CGAP_Co10 pool 1 : LLAM 2644-2653,
2871-2872 (IMAGE Clones 1057416-1061255, 1144584-1145351)
) Subtraction was performed as previously described
(Bonaldi, Lennon & Soares (1996): Normalization and
Subtraction: Two Approaches To Facilitate Gene Discovery.
Genome Research 6, 791-806.)
TAG_LIB=NCI_CGAP_Co4
TAG_TISSUE=Colon
TAG_SEQ=CTTCG"
BASE COUNT 104 a 108 c 134 g 103 t
ORIGIN
Query Match 99.3%; Score 232.4; DB 10; Length 449;
Best Local Similarity 99.6%; Pred. No. 1.5e-54;
Matches 233; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 ATGGGGTCTGGGCTGCCCTTGCTCTTGACCTCTGCGAGCTCACATGGAACA 60
|||||
Db 387 ATGGGGTCTGGGCTGCCCTTGCTCTTGACCTCTGCGAGCTCACATGGAACA 328
|||||
QY 61 GGGCCGGATGACATTTGCAACTGAAGCTGAAGGAGTCTTTCTGACAAATTCCTCTAT 120
|||||
Db 327 GGGCCGGATGACATTTGCAACTGAAGCTGAAGGAGTCTTTCTGACAAATTCCTCTAT 268
|||||
QY 121 GAGTCCAGCTTCCTGGAATTCCTTGAAGAGCTCTGCTCTCTCTCCATCCTCCTTCAGGG 180
|||||
Db 267 GAGTCCAGCTTCCTGGAATTCCTTGAAGAGCTCTGCTCTCTCTCCATCCTCCTTCAGGG 208
|||||
QY 181 ACCAGCTCACCTCCACATGAAGATCTCAACACCATGTGTCGCAACACA 234
|||||
Db 207 ACCAGCTCACCTCCACATGAAGATCTCAACACCATGTGTCGCAACACA 154
|||||
RESULT 3
BI759796 830 bp mRNA linear EST 25-SEP-2001
LOCUS 603045679F1 NIH_MGC_116 Homo sapiens cDNA clone IMAGE:5186107 5',
DEFINITION mRNA sequence.
ACCESSION BI759796
VERSION BI759796.1 GI:15751374
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
```

REFERENCE
 AUTHORS
 TITLE
 JOURNAL
 COMMENT

Mammalia; Euthera; Primates; Catarrhini; Hominiidae; Homo.
 1 (bases 1 to 830)
 NIH-MGC <http://mgi.nci.nih.gov/>.
 National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished (1999)
 Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-remail.nih.gov
 Tissue Procurement: Life Technologies, Inc.
 cDNA Library Preparation: Life Technologies, Inc.
 DNA Sequencing by: The I.M.A.G.E. Consortium (LLNL)
 Clone Distribution: Incyte Genomics, Inc.
 found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
 Plate: LLAM11464 row: m column: 20
 High quality sequence stop: 432.
 Location/Qualifiers
 1. 830
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="IMAGE:5186107"
 /clone_lib="NIH_MGC_116"
 /lab_host="PH108"
 /note="Organ: pooled colon, kidney, stomach; Vector:
 pCW-SF0R6; Site:1: NotI; Site:2: EcoRV (destroyed); RNA
 source anonymous pool of 3 colons, age 26 yo male, 49 yo
 female, 71 yo male colon; 46 yo male kidney, and pool of 2
 stomachs, 62 yo male and 70 yo female. Library is
 oligo-dT primed and directionally cloned (EcoRV site is
 destroyed upon cloning). Average insert size 1.4 kb,
 insert size range 1-3 kb. Library is normalized and
 enriched for full-length clones and was constructed by C.
 Gruber (Invitrogen). Research Genetics tracking code
 023. Note: this is a NIH_MGC Library."

BASE COUNT 175 a 276 c 210 g 168 t 1 others
 ORIGIN

Query Match 99.3%; Score 232.4; DB 13; Length 830;
 Best Local Similarity 99.6%; Pred. No. 2e-54;
 Matches 233; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ATGGGCTGGGCTGCCCTTGTCTCTTGACCTCTCTGGCAGCTCACATGGAACA 60
 Db 81 ATGGGCTGGGCTGCCCTTGTCTCTTGACCTCTCTGGCAGCTCACATGGAACA 140
 QY 61 GGCCCGGTATGACTTTGCACTGAAGCTGAAGAGTCTTTTCTGACAAATTCCTCTAT 120
 Db 141 GGACCGGTATGACTTTGCACTGAAGCTGAAGAGTCTTTTCTGACAAATTCCTCTAT 200
 QY 121 GAGTCCAGCTTCCTGGAATGCTTGAAGCTGAGCTGCTCCTCCATCTCCCTTCAGG 180
 Db 201 GAGTCCAGCTTCCTGGAATGCTTGAAGCTGAGCTGCTCCTCCATCTCCCTTCAGG 260
 QY 181 ACCAGGCTACCCCTCCACCATCAAGATCTCAACACCATGTTGTTCTGCAACACA 234
 Db 261 ACCAGGCTACCCCTCCACCATCAAGATCTCAACACCATGTTGTTCTGCAACACA 314

RESULT 4
 BF002050/c
 LOCUS
 DEFINITION 799811.x1 NCI_CGAP_Col6 422 bp mRNA linear EST 06-OCT-2000
 mRNA sequence.
 ACCESSION BF002050
 VERSION BF002050
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Euthera; Primates; Catarrhini; Hominiidae; Homo.
 1 (bases 1 to 422)
 NIH-MGC <http://www.ncbi.nlm.nih.gov/ncicgap>.
 National Cancer Institute, Cancer Genome Anatomy Project (CGAP),

REFERENCE
 AUTHORS
 TITLE

Tumor Gene Index
 Unpublished (1997)
 Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-remail.nih.gov
 Tissue Procurement: Ilan Kirsch, M.D., Michael R. Emmert-Buck, M.D.,
 Ph.D.
 cDNA Library Preparation: M. Bento Soares, Ph.D.
 DNA Sequencing by: Greg Lennon, Ph.D.
 Clone Distribution: NCI-CGAP clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL, send email to:
infoimage.llnl.gov
 Seq primer: -400P from Gibco.
 Location/Qualifiers
 1. 422
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="IMAGE:3314516"
 /clone_lib="NCI_CGAP_Col6"
 /tissue_type="colon tumor, RER+"
 /lab_host="DH108"
 /note="Organ: colon; Vector: p773D-Pac (Pharmacia) with a
 modified polylinker; Site:1: Not I; Site:2: Eco RI;
 Plasmid DNA from the normalized library NCI_CGAP_Col6 was
 prepared, and ss circles were made in vitro. Following HAP
 purification, this DNA was used as tracer in a subtractive
 hybridization reaction. The driver was PCR-amplified cDNAs
 from a pool of 5,000 clones made from the same library
 (clonoids 1057416-1061255, and 1144584-1145351).
 Subtraction by Bento Soares and M. Fatima Bonaldo. *
 BASE COUNT 102 a 99 c 130 g 88 t 3 others
 ORIGIN

Query Match 94.4%; Score 221; DB 12; Length 422;
 Best Local Similarity 98.7%; Pred. No. 2.2e-51;
 Matches 232; Conservative 0; Mismatches 2; Indels 1; Gaps 1;

QY 1 ATGGGGCTGGGCTGCCCTTGTCTCTTGACCTCTCTGGCAGCTCACATGGAACA 60
 Db 377 ATGGGGCTGGGCTGCCCTTGTCTCTTGACCTCTCTGGCAGCTCACATGGAACA 318
 QY 61 GGCCCGGTATGACTTTGCACTGAAGCTGAAGAGTCTTTTCTGACAAATTCCTCTAT 120
 Db 317 GGCCCGGTATGACTTTGCACTGAAGCTGAAGAGTCTTTTCTGACAAATTCCTCTAT 258
 QY 121 GAGTCCAGCTTCCTGGAATGCTTGAAGCTGAGCTGCTCCTCCATCTCCCTTCAGG 179
 Db 257 GAGTCCAGCTTCCTGGAATGCTTGAAGCTGAGCTGCTCCTCCATCTCCCTTCAGG 198
 QY 180 GACCAGCTCACCTCCACCATCAAGATCTCAACACCATGTTGTTCTGCAACACA 234
 Db 197 GACCAGCTCACCTCCACCATCAAGATCTCAACACCATGTTGTTCTGCAACACA 143

RESULT 5
 B1820029
 LOCUS
 DEFINITION B1820029.1 N1H_MGC_115 895 bp mRNA linear EST 04-OCT-2001
 mRNA sequence.
 ACCESSION B1820029
 VERSION B1820029.1
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Euthera; Primates; Catarrhini; Hominiidae; Homo.
 1 (bases 1 to 895)
 NIH-MGC <http://mgi.nci.nih.gov/>.
 National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished (1999)
 Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-remail.nih.gov
 Tissue Procurement: Life Technologies, Inc.

cDNA Library Preparation: Life Technologies, Inc.
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
 Plate: LHAM1444 row: c column: 04
 High quality sequence start: 5
 High quality sequence stop: 422.
 Location/Qualifiers
 1. .895
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="IMAGE:5178171"
 /clone_lib="NIH_MGC_115"
 /lab_host="DH10B"
 /note="Organ: pooled brain, lung, testis; Vector:
 pCMT-SPORT6; Site: 1: NotI; Site 2: EcoRV (destroyed); RNA
 source anonymous pool of 6 male brains, age range 23-27; 1
 male lung, age 27; and 1 male testis, age 59. Library is
 oligo-dT primed and directionally cloned (EcoRV site is
 destroyed upon cloning). Average insert size 1.8 kb,
 insert size range 1-3 kb. Library is normalized and
 enriched for full-length clones and was constructed by C.
 Gruber (Invitrogen). Research Genetics tracking code
 021. Note: this is a NIH_MGC Library."

FEATURES

source

BASE COUNT 349 a 229 c 202 g 115 t
 ORIGIN
 Query Match 83.0%; Score 194.2; DB 13; Length 895;
 Best Local Similarity 98.5%; Pred. No. 9.7e-44;
 Matches 196; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 36 CCTCTTGGCAGCTCACATGGACAGGCGGGGTATGACTTTGCAACTGAAGCTGAAGGA 95
 |||
 Db 6 CCTCTTGGCAGCTCACATGGACAGGCGGGGTATGACTTTGCAACTGAAGCTGAAGGA 65
 QY 96 GTCTTTTCTGCAAAATTCCTCCTATGAGTCCAGCTTCCTGGAATTCCTTGAAGAGCTCTG 155
 |||
 Db 66 GTCTTTTCTGCAAAATTCCTCCTATGAGTCCAGCTTCCTGGAATTCCTTGAAGAGCTCTG 125
 QY 156 CCTCTCTCCATCTCCCTTCAGGACAGCCTCACCTCCACCATGCAAGATCTCAACA 215
 |||
 Db 126 CCTCTCTCCATCTCCCTTCAGGACAGCCTCACCTCCACCATGCAAGATCTCAACA 185

QY 216 CCATGTGTCTGCAACACA 234
 |||
 Db 186 CCATGTGTCTGCAACACA 204

RESULT 6
 BI820110
 LOCUS 603037110F1 NIH_MGC_115 Homo sapiens cDNA clone IMAGE:5178170 5',
 DEFINITION mRNA sequence.
 BI820110 865 bp mRNA linear EST 04-OCT-2001
 BI820110.1 GI:59315660
 ACCESSION
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM
 Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 865)
 NIH-MGC <http://mgc.nci.nih.gov/>
 National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished (1999)
 Contact: Robert Strausberg, Ph.D.
 Email: cgabbs-r@mail.nih.gov

REFERENCE
 AUTHORS
 TITLE
 JOURNAL
 COMMENT
 NIH-MGC <http://mgc.nci.nih.gov/>
 Unpublished (1999)
 Contact: Robert Strausberg, Ph.D.
 Email: cgabbs-r@mail.nih.gov
 Tissue Procurement: Life Technologies, Inc.
 cDNA Library Preparation: Life Technologies, Inc.
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
 Plate: LHAM1444 row: c column: 03
 High quality sequence stop: 417.
 Location/Qualifiers
 1. .865

FEATURES

source

/organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="IMAGE:5178170"
 /clone_lib="NIH_MGC_115"
 /lab_host="DH10B"
 /note="Organ: pooled brain, lung, testis; Vector:
 pCMT-SPORT6; Site: 1: NotI; Site 2: EcoRV (destroyed); RNA
 source anonymous pool of 6 male brains, age range 23-27; 1
 male lung, age 27; and 1 male testis, age 59. Library is
 oligo-dT primed and directionally cloned (EcoRV site is
 destroyed upon cloning). Average insert size 1.8 kb,
 insert size range 1-3 kb. Library is normalized and
 enriched for full-length clones and was constructed by C.
 Gruber (Invitrogen). Research Genetics tracking code
 021. Note: this is a NIH_MGC Library."

BASE COUNT 330 a 219 c 198 g 117 t
 ORIGIN

Query Match 77.4%; Score 181.2; DB 13; Length 865;
 Best Local Similarity 97.5%; Pred. No. 4.1e-40;
 Matches 194; Conservative 0; Mismatches 4; Indels 1; Gaps 1;

QY 36 CCTCTTGGCAGCTCACATGGACAGGCGGGGTATGACTTTGCAACTGAAGCTGAAGGA 95
 |||
 Db 6 CCTCTTGGCAGCTCACATGGACAGGCGGGGTATGACTTTGCAACTGAAGCTGAAGGA 65
 QY 96 GTCTTTTCTGCAAAATTCCTCCTATGAGTCCAGCTTCCTGGAATTCCTTGAAGAGCTCTG 155
 |||
 Db 66 GTCTTTTCTGCAAAATTCCTCCTATGAGTCCAGCTTCCTGGAATTCCTTGAAGAGCTCTG 124
 QY 156 CCTCTCTCCATCTCCCTTCAGGACAGCCTCACCTCCACCATGCAAGATCTCAACA 215
 |||
 Db 125 CCTCTCTCCATCTCCCTTCAGGACAGCCTCACCTCCACCATGCAAGATCTCAACA 184
 QY 216 CCATGTGTCTGCAACACA 234
 |||
 Db 185 CCATGTGTCTGCAACACA 203

RESULT 7
 AI857998/c
 LOCUS w169b01.x1 NCL_CGAP_Lu19 Homo sapiens cDNA clone IMAGE:2408041 3',
 DEFINITION mRNA sequence.
 AI857998
 AI857998.1 GI:5511614
 ACCESSION
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM
 Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 404)
 NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>
 National Cancer Institute, Cancer Genome Anatomy Project (CGAP).
 Tumor Gene Index
 Unpublished (1997)
 Contact: Robert Strausberg, Ph.D.
 Email: cgabbs-r@mail.nih.gov

REFERENCE
 AUTHORS
 TITLE
 JOURNAL
 COMMENT
 NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>
 National Cancer Institute, Cancer Genome Anatomy Project (CGAP).
 Unpublished (1997)
 Contact: Robert Strausberg, Ph.D.
 Email: cgabbs-r@mail.nih.gov
 Tissue Procurement: Christopher Moskalko, M.D., Ph.D., Michael R.
 Emmert-Buck, M.D., Ph.D.
 cDNA Library Preparation: M. Bento Soares, Ph.D.
 cDNA Library Arrayed by: Greg Lennon, Ph.D.
 DNA Sequencing by: Washington University Genome Sequencing Center
 Clone distribution: NCI-CGAP clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
www.bio.llnl.gov/bbrp/image/image.html
 Insert Length: 629 Std Error: 0.00

Seq primer: -40UP from Gibco
High quality sequence stop: 395.
Location/Qualifiers
1. .404
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:2408041"
/clone_lib="NCI_CGAP_Lu19"
/tissue_type="squamous cell carcinoma, poorly
differentiated (4 pooled tumors, including primary and
metastatic)"
/dev_stage="adult"
/lab_host="DH10B (phage-resistant)"
/note="Organ: lung; Vector: p773D-Pac (Pharmacia) with a
modified polylinker; 1st strand cDNA was prepared from
pooled lung tumor tissue, and was then primed with a Not I
- oligo(dT) primer. Double-stranded cDNA was ligated to
Eco RI adaptors (Pharmacia), digested with Not I and
cloned into the Not I and Eco RI sites of the modified
p773 vector. Library went through one round of
normalization. Library constructed by Bento Soares and M.
Fatima Bonaldo."

BASE COUNT 97 a 105 c 117 g 84 t 1 others
ORIGIN

Query Match 74.8%; Score 175; DB 9; Length 404;
Best Local Similarity 99.4%; Pred. No. 1.6e-38;
Matches 175; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 59 CAGGGCGGATGACCTTTCGAACCTGAAGGAGTCTTTTCGACAAATTCCTCT 118
Db 311 CAGGGCGGATGACCTTTCGAACCTGAAGGAGTCTTTTCGACAAATTCCTCT 252

QY 119 ATGAGTCCAGCTTCGTGAATTCCTTGAAGAGCTTCGCTCCCTCCCTCCCTTCAG 178
Db 251 ATGAGTCCAGCTTCGTGAATTCCTTGAAGAGCTTCGCTCCCTCCCTTCAG 192

QY 179 GGACCGAGTCCAGCTCCAGGATCTCAACACCATGTGTCTGCAACACA 234
Db 191 GGACCGAGTCCAGCTCCAGGATCTCAACACCATGTGTCTGCAACACA 136

RESULT 8
BF521842
LOCUS
DEFINITION
UI-R-C2p-nq-e-02-0-UI.r1 UI-R-C2p Rattus norvegicus cDNA clone
BF521842
BF521842.1 GI:11629809
VERSION
KEYWORDS
SOURCE
ORGANISM
Rattus norvegicus
Norway rat.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.

REFERENCE
AUTHORS
TITLE
Normalization and subtraction: two approaches to facilitate gene
discovery
JOURNAL
MEDLINE
Genome Res. 6 (9), 791-806 (1996)
COMMENT
Contact: Soares, MB
Program for Rat Gene Discovery and Mapping
University of Iowa
451 Eckstein Medical Research Building Iowa City, IA 52242, USA
Tel: 319 335 8250
Fax: 319 335 9565
Email: msoares@blue.wesg.uiowa.edu
cDNA Library Preparation: M.B. Soares Lab Clone distribution:
clones will be available through Research Genetics (www.resgen.com)
This clone is also available through the I.M.A.G.E. Consortium at
LLNL (info@image.llnl.gov). IMAGE ID= 1792770
Seq primer: M13 Forward.

Seq primer: -40UP from Gibco
High quality sequence stop: 395.
Location/Qualifiers
1. .361
/organism="Rattus norvegicus"
/strain="Sprague-Dawley"
/db_xref="taxon:10116"
/clone="UI-R-C2p-nq-e-02-0-UI"
/clone_lib="UI-R-C2p"
/dev_stage="adult"
/lab_host="DH10B (Life Technologies)"
/note="Vector: p773D-Pac (Pharmacia) with a modified
polylinker; Site_1: Not I; Site_2: Eco RI; The UI-R-C2p
library is a subtracted library derived from the UI-R-C1
library, which is a subtracted library derived from the
UI-R-C0 library. The UI-R-C0 library consisted of a
mixture of individually tagged normalized libraries
constructed from rat placenta, adult lung, brain, liver,
kidney, heart, spleen, ovary, muscle, 8, 12 and 18-day
embryo. The tag is a string of 3-5 nucleotides present
between the Not I site and the oligo-dT track which allows
identification of the library of origin of a clone within
the mixture. The subtracted library (UI-R-C2p) was
constructed as follows: PCR amplified cDNA inserts from
UI-R-C1 clones from which 3' ESTs had been derived was
used as a driver in a hybridization with the UI-R-C1
library in the form of single-stranded circles. The
remaining single-stranded circles (subtracted library) was
purified by hydroxyapatite column chromatography,
converted to double-stranded circles and electroporated
into DH10B bacteria (Life Technologies) to generate the
UI-R-C2p library. This procedure has been previously
described (Bonaldo, Lennon and Soares, Genome Research 6:
791-806, 1996)"

BASE COUNT 79 a 121 c 91 g 70 t
ORIGIN

Query Match 50.0%; Score 117; DB 12; Length 361;
Best Local Similarity 69.4%; Pred. No. 2.5e-22;
Matches 159; Conservative 0; Mismatches 70; Indels 0; Gaps 0;

QY 1 ATGGGCTGTGGGTCGCCCTTGTCTTGGACCTCTGGCAGCTCAGTGAACA 60
Db 22 ATGGAGCTTCGATGTGCTCTCTCTGACCTCTCTGCGAGCTCAGTGAAGG 81

QY 61 GGCGCGGTATGACCTTTCGAACCTGAAGGAGTCTTTTCGACAAATTCCTCTAT 120
Db 82 CCAACAAGAGTGTGCTTTCGAAGTAAACTGACCGAGCATCTCAGCCAGACCTCCCA 141

QY 121 GAGTCAGCTTCCTGGAATGCTTGAAGGCTTGCTCTCTCTCTCTCTCTCTCAGGG 180
Db 142 GACTCGGCTTCTGGACATGCTCCAAAGATCTGCTCTCTCTCTCTCTCTCTCAGGG 201

QY 181 ACCAGCTCACCCTCCACCATGCAAGATCTCAACACCATGTGTCTGCA 229
Db 202 ACCAATGTACCCCTTCATCATATAAAGGCCACACCATCTTACCTGCA 250

RESULT 9
BF533837
LOCUS
DEFINITION
BF533837 RIKEN full-length enriched, 0 day neonate lung Mus
musculus cDNA clone E030032D13 3', mRNA sequence.
BF533837
BF533837.2 GI:1646306
VERSION
KEYWORDS
SOURCE
ORGANISM
Mus musculus
house mouse.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 521)
REFERENCE
AUTHORS
Arakawa,T., Carninci,P., Fukuda,S., Furuno,M., Hanagaki,T., Hara,A.,
Hiramoto,K., Hori,F., Ishii,Y., Ito,M., Kawai,J., Konno,H., Kouda
M., Koya,S., Matsuyama,T., Miyazaki,A., Nomura,K., Ohno,M.,
Okazaki,Y., Okido,T., Salto,K., Sakai,C., Sano,H., Sasaki

FEATURES source

Location/Qualifiers
1. .361
/organism="Rattus norvegicus"
/strain="Sprague-Dawley"
/db_xref="taxon:10116"
/clone="UI-R-C2p-nq-e-02-0-UI"
/clone_lib="UI-R-C2p"
/dev_stage="adult"
/lab_host="DH10B (Life Technologies)"
/note="Vector: p773D-Pac (Pharmacia) with a modified
polylinker; Site_1: Not I; Site_2: Eco RI; The UI-R-C2p
library is a subtracted library derived from the UI-R-C1
library, which is a subtracted library derived from the
UI-R-C0 library. The UI-R-C0 library consisted of a
mixture of individually tagged normalized libraries
constructed from rat placenta, adult lung, brain, liver,
kidney, heart, spleen, ovary, muscle, 8, 12 and 18-day
embryo. The tag is a string of 3-5 nucleotides present
between the Not I site and the oligo-dT track which allows
identification of the library of origin of a clone within
the mixture. The subtracted library (UI-R-C2p) was
constructed as follows: PCR amplified cDNA inserts from
UI-R-C1 clones from which 3' ESTs had been derived was
used as a driver in a hybridization with the UI-R-C1
library in the form of single-stranded circles. The
remaining single-stranded circles (subtracted library) was
purified by hydroxyapatite column chromatography,
converted to double-stranded circles and electroporated
into DH10B bacteria (Life Technologies) to generate the
UI-R-C2p library. This procedure has been previously
described (Bonaldo, Lennon and Soares, Genome Research 6:
791-806, 1996)"

BASE COUNT 79 a 121 c 91 g 70 t
ORIGIN

Query Match 50.0%; Score 117; DB 12; Length 361;
Best Local Similarity 69.4%; Pred. No. 2.5e-22;
Matches 159; Conservative 0; Mismatches 70; Indels 0; Gaps 0;

QY 1 ATGGGCTGTGGGTCGCCCTTGTCTTGGACCTCTGGCAGCTCAGTGAACA 60
Db 22 ATGGAGCTTCGATGTGCTCTCTCTGACCTCTCTGCGAGCTCAGTGAAGG 81
QY 61 GGCGCGGTATGACCTTTCGAACCTGAAGGAGTCTTTTCGACAAATTCCTCTAT 120
Db 82 CCAACAAGAGTGTGCTTTCGAAGTAAACTGACCGAGCATCTCAGCCAGACCTCCCA 141
QY 121 GAGTCAGCTTCCTGGAATGCTTGAAGGCTTGCTCTCTCTCTCTCTCTCAGGG 180
Db 142 GACTCGGCTTCTGGACATGCTCCAAAGATCTGCTCTCTCTCTCTCTCTCAGGG 201
QY 181 ACCAGCTCACCCTCCACCATGCAAGATCTCAACACCATGTGTCTGCA 229
Db 202 ACCAATGTACCCCTTCATCATATAAAGGCCACACCATCTTACCTGCA 250

RESULT 9
BF533837
LOCUS
DEFINITION
BF533837 RIKEN full-length enriched, 0 day neonate lung Mus
musculus cDNA clone E030032D13 3', mRNA sequence.
BF533837
BF533837.2 GI:1646306
VERSION
KEYWORDS
SOURCE
ORGANISM
Mus musculus
house mouse.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 521)
REFERENCE
AUTHORS
Arakawa,T., Carninci,P., Fukuda,S., Furuno,M., Hanagaki,T., Hara,A.,
Hiramoto,K., Hori,F., Ishii,Y., Ito,M., Kawai,J., Konno,H., Kouda
M., Koya,S., Matsuyama,T., Miyazaki,A., Nomura,K., Ohno,M.,
Okazaki,Y., Okido,T., Salto,K., Sakai,C., Sano,H., Sasaki


```

VERSION      BF511043.1  GI:11594341
KEYWORDS     EST.
SOURCE       human.
ORGANISM     Homo sapiens
             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
             Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE    1 (bases 1 to 244)
AUTHORS      NCI-CCGAP http://www.ncbi.nlm.nih.gov/ncicgap.
             National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
             Tumor Gene Index
TITLE        Unpublished (1997)
JOURNAL      Contact: Robert Strausberg, Ph.D.
COMMENT      Email: cgapbs-remail.nih.gov
             The sequence contained an oligo-dT track that was present in the
             oligonucleotide that was used to prime the synthesis of first
             strand cDNA and therefore this may represent a bonafide poly A
             tail. cDNA library Preparation: M.B. Soares Lab Clone distribution:
             NCI-CCGAP clone distribution/Information can be found through the
             I.M.A.G.E. Consortium/LLNL at:
             www.bio.llnl.gov/bbrp/image/image.html
             Seq primer: M13 Forward
             POLYA=Yes.

FEATURES             Location/Qualifiers
     source           1..244
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:3087887"
                     /lab_host="NCI CGAP Sub8"
                     /note="Vector: pT73D-Pac (Pharmacia) with a modified
                     polylinker; Site_1: Not 1; Site_2: Eco RI; NCI_CGAP_Sub8
                     is a subtracted library derived from NCI_CGAP_Sub5. The
                     NCI_CGAP_Sub8 library had 2.5 million recombinants. A
                     single-stranded DNA preparation of NCI_CGAP_Sub5 was used
                     as a tracer in a subtractive hybridization with a driver
                     comprising: a pool of clones from NCI_CGAP_Sub5 (IMAGE
                     clone ids 2732833-2737415, 3068040-3069191; 25% of the
                     driver population), a pool of clones from NCI_CGAP_Sub4
                     (IMAGE clone ids 272592-2729326; 25% of the driver
                     population), NCI_CGAP_Sub6 (pool AIF-AuJ, IMAGE ids
                     2728969-2733190; 25% of the driver population), and
                     NCI_CGAP_Sub7 (IMAGE ids 3069192-3072238, 3081864-3084550
                     ; 25% of the driver population). Subtraction was
                     performed as previously described [Bonaldo, Lennon &
                     Soares (1996): Normalization and Subtraction: Two
                     Approaches to Facilitate Gene Discovery. Genome Research
                     6: 791-806.
                     TAG_LIB=NCI_CGAP_C04
                     TAG_ISSUE=colon
                     TAG_SEQ=CFTGC"
     BASE COUNT      51 a 54 c 68 g 71 t
     ORIGIN
Query Match      34.8%; Score 81.4; DB 12; Length 244;
Best Local Similarity 93.4%; Pred. No. 1.9e-12;
Matches 85; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 144 TGAAGACTCGCTCCCTCCGATCTCCCTTCAGGACAGCGTCACCTCCACCATGC 203
||||| 1 | ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 244 TGAAGACTGTATACCTCGCTCCGATCTCCCTTCAGGACAGCGTCACCTCCACCATGC 185
||||| 1 | ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 204 AAGATCTCAACACCATGTGTCTGCAACACA 234
||||| 1 | ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 184 AAGATCTCAACACCATGTGTCTGCAACACA 154
||||| 1 | ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

RESULT 13
AQ718761/c
LOCUS          AQ718761          552 bp      DNA      linear      GSS 13-JUL-1999
DEFINITION    HS.5511.B2_F09_77A RPCI-11 Human Male BAC Library Homo sapiens
               genomic clone Plate=1087 Col=18 Row=L, DNA sequence.
ACCESSION     AQ718761
VERSION       AQ718761.1  GI:5468077

KEYWORDS      GSS.
SOURCE        house mouse.
ORGANISM      Mus musculus
             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
             Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae; Mus.
             1 (bases 1 to 633)
REFERENCE     Zhao,S., Nierman,W., Feldblyum,T., Malek,J., Shatsman,S., Aklnret
             ,B., Levins,M., McGann,S., Tsegaye,G., Geer,K., Kroll,M., de Jong,P.
             ,

KEYWORDS      GSS.
SOURCE        human.
ORGANISM      Homo sapiens
             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
             Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE    1 (bases 1 to 552)
AUTHORS      Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T., and
             Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D., and
             Hood,L.
TITLE        Sequence-tagged connectors: A sequence approach to mapping and
             scanning the human genome
JOURNAL      PROC. Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999)
COMMENT      99380589
             Contact: Mahairas GG, Wallace JC, Hood L
             High Throughput Sequencing Center
             University of Washington
             401 Queen Anne Avenue North, Seattle, WA 98109, USA
             Tel: (206) 616-3618
             Fax: (206) 616-3887
             Email: jwallace@u.washington.edu
             Clones are derived from the human BAC library RPCI-11. For BAC
             library availability, please contact Pieter de Jong
             (pieter@dejong.med.buffalo.edu). Clones may be purchased from
             BACPAC Resources (http://bacpac.med.buffalo.edu/ordering.bac.htm)
             or from Resear h Genetics (info@resgen.com). BAC end Web Server:
             http://www.htsc.washington.edu
             Plate: 1087 row: L column: 18
             Seq primer: T7
             Class: BAC ends
             High quality sequence stop: 552.
             Location/Qualifiers
     source           1..552
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="Plate=1087 Col=18 Row=L"
                     /clone_lib="RPCI-11 Human Male BAC Library"
                     /sex="male"
                     /notes="Vector: pBAC3.6; Site_1: EcoRI; Site_2: EcoRI;
                     Male blood DNA was isolated from one randomly chosen donor
                     and partially digested with a combination of EcoRI and
                     EcoRI Methylase. Size selected DNA was cloned into the
                     pBAC3.6 vector at EcoRI sites"
     BASE COUNT      141 a 153 c 124 g 117 t 17 others
     ORIGIN
Query Match      32.4%; Score 75.8; DB 17; Length 552;
Best Local Similarity 86.5%; Pred. No. 1e-10;
Matches 83; Conservative 0; Mismatches 13; Indels 0; Gaps 0;

QY 57 AHCAGGCGCGGTATGACTTTGCACTGAAGCTGAAGGAGTCTTTTTCACAAATTCCTC 116
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 474 AGCATGGCGAGGTATGACTTTGCANCTGAAGCTGAAGGAGTCTATTAGACAAATTCGTC 415
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 117 CTATGAGTCCAGCTTCCTGGGAATTCGTTGAAAAGCT 152
||||| 1 | ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 414 TTATGAGTCCAGCTTCCTGGGAATTCGTTGAAAAGGT 379
||||| 1 | ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

RESULT 14
AQ79350/c
LOCUS          AQ79350          633 bp      DNA      linear      GSS 31-MAR-2000
DEFINITION    RPCI-23-438H19.TV RPCI-23 Mus musculus genomic clone RPCI-23-438H19
               , DNA sequence.
ACCESSION     AQ79350
VERSION       AQ79350.1  GI:7372249
KEYWORDS      GSS.
SOURCE        house mouse.
ORGANISM      Mus musculus
             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
             Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae; Mus.
             1 (bases 1 to 633)
REFERENCE     Zhao,S., Nierman,W., Feldblyum,T., Malek,J., Shatsman,S., Aklnret
             ,B., Levins,M., McGann,S., Tsegaye,G., Geer,K., Kroll,M., de Jong,P.
             ,
```


TITLE Mouse BAC End Sequences from Library RPCI-23
JOURNAL Unpublished (1999)
COMMENT other GSSES: RPCI-23-438H19 TJ
and Fraser, C.M.

The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fax: 301 838 0208

Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fax: 301 838 0208

email: szhaoetigr.org
Clones are derived from the mouse BAC library RPCI-23. For BAC library availability, please contact Pieter de Jong (pieterdejong.med.buffalo.edu). Clones may be purchased from BACPAC Resources (<http://bacpac.med.buffalo.edu/orderingframe.htm>) or from Resea ch Genetics (info@resgen.com). BAC end page: http://www.tigr.org/tdb/bac Ends/mouse/bac_end_intro.html

Clones are derived from the mouse BAC library RPCI-23. For BAC library availability, please contact Pieter de Jong (pieterdejong.med.buffalo.edu). Clones may be purchased from BACPAC Resources (<http://bacpac.med.buffalo.edu/orderingframe.htm>) or from Resea ch Genetics (info@resgen.com). BAC end page: http://www.tigr.org/tdb/bac_ends/mouse/bac_end_intro.html

```

http://www.tigr.org/tdb/bac_ends/mouse/bac_end_intro.html
plate: 75  row: C  column: 13
Seq primer: SP6
Class: BAC ends.
FEATURES             Location/Qualifiers
     1..506
        /organism="Mus musculus"
        /strain="C57BL/6J"
        /db_xref="taxon:10090"
        /clone="RPC1-23-75C13"
        /clone_lib="RPC1-23"
        /sex="Female"
        /lab_host="DH10B"
        /notes="Organ: Kidney/Brain; Vector: pBACE3.6; Site_1:
ECORI; Site_2: EORI; Female C57BL/6J mouse kidney and/or
brain genomic DNA was isolated and partially digested
with a combination of EORI and EORI Methylase. Size
selected DNA was cloned into the pBACE3.6 vector at the
ECORI sites. The ligation products were transformed into
DH10B electrocompetent cells (BRL Life Technologies)."

```

ECORI; site_2: EcoRI; Female C57BL/6J mouse kidney and/or brain genomic DNA was isolated and partially digested with a combination of EcoRI and EcoRI Methylase. Size selected DNA was cloned into the pBAC3.6 vector at the EcoRI sites. The ligation products were transformed into DH10B electrocompetent cells (BRL Life Technologies).
138 a 191 c 161 g 143 t
BASE COUNT

BASE COUNT	116 a	145 c	138 g	107 t	DNA9 electrocompetent cells (BRL Life Technologies).
ORIGIN					
Query Match					
				20.3%; Score 47.4; DB 17; Length 506;	

Qy	144	TGAAAAGTGTGCTCTCTCTCCATCTCCTCAGGACCAAGGTCACCCCTCCACCATGC	203
Db	179	TACCAAGATCTGCGCTCTCTCCATCTGCATCAGGACCAATGTCACCTTCTTCAAA	120
Qy	204	AAGATCTCAACACCATTGTTGTGCA	229
Db	119	AGGACCACCACTACTCTTACTTCA	94

Db 114 CACCACCTACCTTACTTGCA 94

Search completed: May 1, 2003, 05:10:13
Job time : 1177.36 secs

[illegible]

SOURCE	ORGANISM
house mouse	
Mus musculus	
	Eukaryota; Metazoa; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 506)	
REFERENCE	
AUTHORS	Zhao, S., Nierman, W., Feldblyum, T., Malek, J., Shatsman, S., Akınret, B., Levins, M., McGann, S., Tsengaye, G., Geer, K., Kroll, M., de Jong, P. and Fraser, C. W.

TITLE Mouse BAC End Sequences from Library RPCI-23
JOURNAL Unpublished (1999)
COMMENT Other GSSs: RPCI-23-75C13.TV
Contact: Shaying Zhao
Department of Eukaryotic Genomics

GenCore version 5.1.5
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OM nucleic - nucleic search, using sw model

Run on: May 1, 2003, 02:59:25 ; Search time 765,143 Seconds
(without alignments)
8900.373 Million cell updates/sec

Title: US-09-092-296-7_COPY_51_284
Perfect score: 234
Sequence: 1 ARGGGCTGCTGGCTCCCT.....ACCATGTTGCTGCAACACA 234

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2054640 seqs, 14551402878 residues
Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

- GenEmbl.*
- 1: gb_ba.*
- 2: gb_hgt.*
- 3: gb_in.*
- 4: gb_om.*
- 5: gb_ov.*
- 6: gb_pat.*
- 7: gb_ph.*
- 8: gb_pl.*
- 9: gb_pr.*
- 10: gb_ro.*
- 11: gb_sts.*
- 12: gb_sy.*
- 13: gb_un.*
- 14: gb_vi.*
- 15: em_ba.*
- 16: em_fun.*
- 17: em_hum.*
- 18: em_in.*
- 19: em_mu.*
- 20: em_om.*
- 21: em_or.*
- 22: em_ov.*
- 23: em_pat.*
- 24: em_ph.*
- 25: em_pl.*
- 26: em_ro.*
- 27: em_sts.*
- 28: em_un.*
- 29: em_vi.*
- 30: em_htg_hum.*
- 31: em_htg_inv.*
- 32: em_htg_other.*
- 33: em_htg_mus.*
- 34: em_htg_pln.*
- 35: em_htg_rtd.*
- 36: em_htg_mam.*
- 37: em_htg_vrt.*
- 38: em_sy.*
- 39: em_htg_hum.*
- 40: em_higo_mus.*
- 41: em_higo_other.*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	234	100.0	422	6	AX092334	Sequence
2	234	100.0	422	6	AX376174	Sequence
3	234	100.0	422	6	AX403475	Sequence
4	232.4	99.3	484	9	AY102070	Homo sapi
5	176	75.2	624	6	AX472955	Sequence
6	92.4	39.5	47323	9	AC005937	Homo sapi
7	92.4	39.5	104154	2	AL773541	Homo sapi
8	92.4	39.5	156272	9	AL669830	Human DNA
9	92.4	39.5	178688	2	AL713893	Human DNA
10	92.4	39.5	192650	9	AB023048	Homo sapi
11	92.4	39.5	200000	9	AP000511	Homo sapi
12	90.8	38.8	84474	9	AL662854	Homo sapi
13	68.4	29.2	349980	6	AX344553	Sequence
14	68.4	29.2	349980	6	AX344554	Sequence
15	62.6	26.8	349980	6	AX344571	Sequence
16	48.4	20.7	152977	2	RN510020	Sequence
17	48.4	20.7	337832	2	AC099175	Rattus no
18	46	19.7	175345	2	AC022301	Mus muscu
19	37.8	16.2	185154	2	AC127110	Rattus no
20	37	15.8	168145	9	AL159171	Human DNA
21	36.8	15.7	2649	5	AF282675	Danio rer
22	36.4	15.6	118276	9	AC004148	Homo sapi
23	36	15.4	155406	2	AC105514	Rattus no
24	35.6	15.2	187533	2	AC125827	Rattus no
25	35.4	15.1	145253	9	AC006329	Homo sapi
26	35	15.0	67243	2	AC100215	Mus muscu
27	35	15.0	289157	2	AC103283	Rattus no
28	34.8	14.9	157104	9	AC108686	Homo sapi
29	34.8	14.9	161973	2	AC115067	Mus muscu
30	34.8	14.9	172421	2	AL683803	Mus muscu
31	34.8	14.9	182199	2	AC095097	Rattus no
32	34.8	14.9	193110	2	AC109311	Mus muscu
33	34.8	14.9	196491	9	AC092832	Rattus no
34	34.6	14.8	88176	2	AL390202_09	Continuation (10 o
35	34.6	14.8	110275	10	AL663028	Mouse DNA
36	34.6	14.8	152502	2	AC012583	Human DNA
37	34.6	14.8	170970	9	AL354707	D86631 Mus sp. DNA
38	34.2	14.6	3626	10	D86631	AC115874 Mus muscu
39	34.2	14.6	169197	2	AC115874	AC110539 Mus muscu
40	34.2	14.6	190180	2	AC110539	AC122764 Mus muscu
41	34	14.5	54472	2	AC122764	AC073752 Mus muscu
42	34	14.5	211118	2	AC073752	AC102934 Mus muscu
43	33.8	14.4	166991	2	AC102934	AL591373 Mouse DNA
44	33.8	14.4	174264	10	AL591373	AC122589 Rattus no
45	33.8	14.4	175279	2	AC122589	

ALIGNMENTS

RESULT 1
AX092334
LOCUS AX092334
DEFINITION Sequence 65 from Patent WO0116318.
ACCESSION AX092334
VERSION AX092334.1
KEYWORDS GI:13444481
SOURCE human
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 422)
AUTHORS Eaton,D.L., Filvaroff,E., Gerritsen,M.E., Goddard,A.,
Godovskii,P.J., Grimaldi,C.J., Gurney,A.L., Watanabe,C.K. and
Wood,W.I.

TITLE Secreted and transmembrane polypeptides and nucleic acids encoding
the same
JOURNAL Patent: WO 0116318-A 65 08-MAR-2001;
Genentech, Inc. (US)
FEATURES Location/Qualifiers
source
1. .422
/organism="Homo sapiens"
/db_xref="taxon:9606"
BASE COUNT 84 a 134 c 104 g 100 t
ORIGIN

Query Match 100.0%; Score 234; DB 6; Length 422;
Best Local Similarity 100.0%; Pred. No. 4.7e-62;
Matches 234; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGGGCTCTGGGCTGGCCCTTGTCTCTTGTGACCCCTCTTGGCAGCTCAGATGGAACA 60
Db 5B ATGGGCTCTGGGCTGGCCCTTGTCTCTTGTGACCCCTCTTGGCAGCTCAGATGGAACA 117
QY 61 GGGCCGGGTATGACCTTTCACACTGAAGCTGAAGAGTCTTTCTGACAAATTCCTCTAT 120
Db 118 GGGCCGGGTATGACCTTTCACACTGAAGCTGAAGAGTCTTTCTGACAAATTCCTCTAT 177
QY 121 GAGTCCAGCTTCTCGAATTCCTGAAAGCTTGTGAAAGCTTCTCTCCATCTCCCTTCAGGG 180
Db 178 GAGTCCAGCTTCTCGAATTCCTGAAAGCTTGTGAAAGCTTCTCTCCATCTCCCTTCAGGG 237
QY 181 ACCAGGCTCACCTCCACATGCAAGATCTCAACACCATGTTGTCTGCAACACA 234
Db 238 ACCAGGCTCACCTCCACATGCAAGATCTCAACACCATGTTGTCTGCAACACA 291

RESULT 2
AX376174 422 bp DNA linear PAT 01-MAR-2002
LOCUS AX376174
DEFINITION Sequence 241 from Patent WO0168848.
ACCESSION AX376174
VERSION AX376174.1 GI:19170479
KEYWORDS human.
SOURCE
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1
AUTHORS Baker, K.P., Chen, J., Desnoyers, L., Goddard, A., Godowski, P.J.,
Gurney, A.L., Pan, J., Smith, V., Watanabe, C.K., Wood, W.I. and
Zhang, Z.
TITLE Secreted and transmembrane polypeptides and nucleic acids encoding
the same
JOURNAL Patent: WO 0168848-A 241 20-SEP-2001;
Genentech, Inc. (US)
FEATURES Location/Qualifiers
source
1. .422
/organism="Homo sapiens"
/db_xref="taxon:9606"
BASE COUNT 84 a 134 c 104 g 100 t
ORIGIN

Query Match 100.0%; Score 234; DB 6; Length 422;
Best Local Similarity 100.0%; Pred. No. 4.7e-62;
Matches 234; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGGGCTCTGGGCTGGCCCTTGTCTCTTGTGACCCCTCTTGGCAGCTCAGATGGAACA 60
Db 58 ATGGGCTCTGGGCTGGCCCTTGTCTCTTGTGACCCCTCTTGGCAGCTCAGATGGAACA 117
QY 61 GGGCCGGGTATGACCTTTCACACTGAAGCTGAAGAGTCTTTCTGACAAATTCCTCTAT 120
Db 118 GGGCCGGGTATGACCTTTCACACTGAAGCTGAAGAGTCTTTCTGACAAATTCCTCTAT 177
QY 121 GAGTCCAGCTTCTCGAATTCCTGAAAGCTTGTGAAAGCTTCTCTCCATCTCCCTTCAGGG 180
Db 178 GAGTCCAGCTTCTCGAATTCCTGAAAGCTTGTGAAAGCTTCTCTCCATCTCCCTTCAGGG 237

QY 181 ACCAGGCTCACCTCCACATGCAAGATCTCAACACCATGTTGTCTGCAACACA 234
Db 238 ACCAGGCTCACCTCCACATGCAAGATCTCAACACCATGTTGTCTGCAACACA 291

RESULT 3
AX403475 422 bp DNA linear PAT 14-JUN-2002
LOCUS AX403475
DEFINITION Sequence 362 from Patent WO0073454.
ACCESSION AX403475
VERSION AX403475.1 GI:21436973
KEYWORDS human.
SOURCE
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1
AUTHORS Ashkenazi, A.J., Baker, K.P., Botstein, D., Desnoyers, L., Eaton, D.,
Ferrara, N., Gerber, H., Gernitsen, M., Goddard, A., Godowski, P.,
Grimaldi, C.J., Gurney, A.L., Klijavik, I., Napier, M.A., Pan, J.,
Paoni, N.F., Roy, M., Stewart, T.A., Tumas, D., Watanabe, C.K.,
Williams, P., Wood, W.I. and Zhang, Z.
TITLE Secreted and transmembrane polypeptides and nucleic acids encoding
the same
JOURNAL Patent: WO 0073454-A 362 07-DEC-2000;
Genentech Inc. (US)
FEATURES Location/Qualifiers
source
1. .422
/organism="Homo sapiens"
/db_xref="taxon:9606"
BASE COUNT 84 a 134 c 104 g 100 t
ORIGIN

Query Match 100.0%; Score 234; DB 6; Length 422;
Best Local Similarity 100.0%; Pred. No. 4.7e-62;
Matches 234; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGGGCTCTGGGCTGGCCCTTGTCTCTTGTGACCCCTCTTGGCAGCTCAGATGGAACA 60
Db 58 ATGGGCTCTGGGCTGGCCCTTGTCTCTTGTGACCCCTCTTGGCAGCTCAGATGGAACA 117
QY 61 GGGCCGGGTATGACCTTTCACACTGAAGCTGAAGAGTCTTTCTGACAAATTCCTCTAT 120
Db 118 GGGCCGGGTATGACCTTTCACACTGAAGCTGAAGAGTCTTTCTGACAAATTCCTCTAT 177
QY 121 GAGTCCAGCTTCTCGAATTCCTGAAAGCTTGTGAAAGCTTCTCTCCATCTCCCTTCAGGG 180
Db 178 GAGTCCAGCTTCTCGAATTCCTGAAAGCTTGTGAAAGCTTCTCTCCATCTCCCTTCAGGG 237
QY 181 ACCAGGCTCACCTCCACATGCAAGATCTCAACACCATGTTGTCTGCAACACA 234
Db 238 ACCAGGCTCACCTCCACATGCAAGATCTCAACACCATGTTGTCTGCAACACA 291

RESULT 4
AY102070 484 bp mRNA linear PRI 18-JUN-2002
LOCUS AY102070
DEFINITION Homo sapiens surfactant associated protein G mRNA, partial
sequence.
ACCESSION AY102070
VERSION AY102070.1 GI:21464498
KEYWORDS human.
SOURCE
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 484)
AUTHORS Walker, M.G. and Spiro, P.
TITLE Genes co-expressed with pulmonary surfactants
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 484)
AUTHORS Walker, M.G. and Spiro, P.

Best Local Similarity 98.9%; Pred. No. 9.7e-18;
Matches 93; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 59 CAGGCGGGTATGACTTTCGAACTGAAGCTGAAGAGTCTTTCTGACAAATTCCTCCT 118
Db 67846 CAGGCGGGTATGACTTTCGAACTGAAGCTGAAGAGTCTTTCTGACAAATTCCTCCT 67905

QY 119 ATGAGTCCAGCTTCTCTGAAATTCCTTGAAGAGCT 152

Db 67906 ATGAGTCCAGCTTCTCTGAAATTCCTTGAAGAGCT 67939

RESULT 8
AL669830/c
LOCUS
DEFINITION Human DNA sequence from clone XXbac-118E17 on chromosome 6,
complete sequence.

ACCESSION AL669830
VERSION AL669830.9 GI:20135762

KEYWORDS HTG.

SOURCE human.

ORGANISM

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 Johnson,C.

Direct Submission

Submitted (23-APR-2002) Wellcome Trust Sanger Institute, Hinxton,

Cambridgeshire, CB10 1SA, UK. E-mail enquiries:

humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk

On Apr 10, 2002 this sequence version replaced gi:20067510.

During sequence assembly data is compared from overlapping clones.

Where differences are found these are annotated as variations

together with a note of the overlapping clone name. Note that the

variation annotation may not be found in the sequence submission

corresponding to the overlapping clone, as we submit sequences

only a small overlap as described above.

This sequence was finished as follows unless otherwise noted: all

regions were either double-stranded or sequenced with an alternate

chemistry or covered by high quality data (i.e., phred quality >=

30); an attempt was made to resolve all sequencing problems, such

as compressions and repeats; all regions were covered by at least

one plasmid subclone or more than one M13 subclone; and the

assembly was confirmed by restriction digest. The following

abbreviations are used to associate primary accession numbers given

in the feature table with their source databases: Em., EMBL; Sw.,

SWISSPROT; Tr., TrEMBL; Wp., WORMPEP; Information on the WORMPEP

database can be found at

http://www.sanger.ac.uk/Projects/C_elegans/wormpep

from a CHORI-501 human bac - PGF cell line library VECTOR:

PTARBAC2.1

This sequence was generated from part of bacterial clone contigs

constructed by the MHC Haplotype Consortium and collaborators.

Further information can be found at

http://www.sanger.ac.uk/HGP/Chr6/MHC.

Location/Qualifiers

1. .156272

/organism="Homo sapiens"

/db_xref="taxon:9606"

/chromosome="6"

/clone="XXbac-118E17"

/clone_lib="CHORI-501"

BASE COUNT 41135 a 37989 c 36907 g 40241 t

Query Match 39.5%; Score 92.4; DB 9; Length 156272;
Best Local Similarity 98.9%; Pred. No. 9.9e-18;
Matches 93; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 59 CAGGCGGGTATGACTTTCGAACTGAAGCTGAAGAGTCTTTCTGACAAATTCCTCCT 118
Db 25558 CAGGCGGGTATGACTTTCGAACTGAAGCTGAAGAGTCTTTCTGACAAATTCCTCCT 25499

QY 119 ATGAGTCCAGCTTCTCTGAAATTCCTTGAAGAGCT 152
Db 25498 ATGAGTCCAGCTTCTCTGAAATTCCTTGAAGAGCT 25465

RESULT 9

AL713893

LOCUS

DEFINITION Homo sapiens chromosome 6 clone xxbac-307M4, *** SEQUENCING IN

PROGRESS ***, 6 unordered pieces.

ACCESSION AL713893

VERSION AL713893.5 GI:19847952

KEYWORDS HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_FULLTOP.

SOURCE human.

ORGANISM

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1

Direct Submission

Submitted (26-MAR-2002) Wellcome Trust Sanger Institute, Hinxton,

Cambridgeshire, CB10 1SA, UK. E-mail enquiries:

humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk

On Mar 29, 2002 this sequence version replaced gi:19772907.

----- Genome Center

Center: Wellcome Trust Sanger Institute

Center code: SC

Web site: http://www.sanger.ac.uk

Contact: humquery@sanger.ac.uk

----- Project Information

Center project name: bpg307M4

----- Summary Statistics

Assembly program: XGAP4; version 4.5

Chemistry: Dye-terminator Big Dye; 100% of reads

Consensus quality: 177277 bases at least Q40

Consensus quality: 177708 bases at least Q30

Consensus quality: 177956 bases at least Q20

Insert size: 178188; sum-of-contigs

Insert size: 192613; 0.9% error; agarose-fp

Quality coverage: 8.57x in Q20 bases; sum-of-contigs Quality

coverage: 8.00x in Q20 bases; agarose-fp

* NOTE: this is a 'working draft' sequence. It currently

* consists of 6 contigs. The true order of the pieces

* is not known and their order in this sequence record is

* arbitrary. Gaps between the contigs are represented as

* runs of N, but the exact sizes of the gaps are unknown.

* This record will be updated with the finished sequence

* as soon as it is available and the accession number will

* be preserved.

1 37410: contig of 37410 bp in length

37411 37510: gap of 100 bp

37511 82372: contig of 44862 bp in length

82373 82472: gap of 100 bp

82473 142457: contig of 59985 bp in length

142458 142557: gap of 100 bp

142558 152859: contig of 10302 bp in length

152860 152959: gap of 100 bp

152960 172054: contig of 19095 bp in length

172055 172154: gap of 100 bp

172155 178688: contig of 6534 bp in length.

FEATURES

source

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/organism="Homo sapiens"

/db_xref="taxon:9606"

/chromosome="6"

/clone="XXbac-307M4"

/clone_lib="CHORI-501"

1. .37410

/note="assembly_fragment:03218

fragment_chain:1"

37511. 82372

/note="assembly_fragment:00918

misc_feature

misc_feature

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misc_feature      fragment_chain:1"
82473..142457
/Note="assembly_fragment:03231
fragment_chain:1"
142558..152859
/Note="assembly_fragment:03008
fragment_chain:1"
152960..172054
/Note="assembly_fragment:04309
fragment_chain:1"
172155..178688
/Note="assembly_fragment:03507
fragment_chain:1"
vector_side:right"
clone_end:r7
BASE COUNT      46316 a 40707 c 42166 g 48998 t 501 others
ORIGIN
Query Match      39.5%; Score 92.4; DB 2; Length 178688;
Best Local Similarity 98.9%; Pred. No. 1e-17;
Matches 93; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 59 CAGGCGCGGTATGACTTTCGAAGTGAAGTGAAGTCTTTCTGACAAATTCCTCCT 118
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Db 173795 CAGGCGCGGTATGACTTTCGAAGTGAAGTGAAGTCTTTCTGACAAATTCCTCCT 173854
|||||

QY 119 ATGAGTCCAGCTTCCTGGAATTCGTTGAAAAGCT 152
|||||
Db 173855 ATGAGTCCAGCTTCCTGGAATTCGTTGAAAAGCT 173888
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RESULT 10
AB023048 192650 bp DNA linear PRI 20-NOV-1999
LOCUS Homo sapiens genomic DNA, chromosome 6p21.3, HLA class I region,
DEFINITION clone:53L9, complete sequence.
ACCESSION AB023048
VERSION AB023048.1 GI:5672603
KEYWORDS HTG.
SOURCE Homo sapiens cell_line:978SK DNA, clone:53L9.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (sites)
AUTHORS Shilina,T., Tamiya,G., Oka,A., Takishima,N., Yamagata,T.,
Kikkawa,E., Iwata,K., Tonizawa,M., Okuaki,N., Kuwano,Y.,
Watanabe,K., Fukuzumi,Y., Itakura,S., Sugawara,C., Ono,A.,
Yamazaki,M., Tashiro,H., Ando,A., Ikemura,T., Soeda,E., Kimura,M.,
Bahran,S. and Inoko,H.
TITLE Molecular dynamics of MHC genesis unraveled by sequence analysis of
the 1,796,938-bp HLA class I region
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 96 (23), 13282-13287 (1999)
MEDLINE 20027539
REFERENCE 2 (bases 1 to 192650)
AUTHORS Shilina,T. and Takishima,N.
TITLE Direct Submission
JOURNAL Submitted (29-JAN-1999) Takashi Shilina, Tokai University School of
Medicine, Department of Molecular Life Science 2; Bohseidai,
Isehara, Kanagawa 259-1193, Japan
(E-mail:tsushina@is.icc.u-tokai.ac.jp, Tel:81-463-93-1121,
Fax:81-463-94-8884)
FEATURES
Location/Qualifiers
1..192650
/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="6"
/clone="53L9"
/cell_line="978SK"
BASE COUNT      49862 a 44743 c 45833 g 52212 t
ORIGIN
Query Match      39.5%; Score 92.4; DB 9; Length 192650;

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Best Local Similarity 98.9%; Pred. No. 1e-17;
Matches 93; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 59 CAGGCGCGGTATGACTTTCGAAGTGAAGTGAAGTCTTTCTGACAAATTCCTCCT 118
|||||
Db 177979 CAGGCGCGGTATGACTTTCGAAGTGAAGTGAAGTCTTTCTGACAAATTCCTCCT 178038
|||||

QY 119 ATGAGTCCAGCTTCCTGGAATTCGTTGAAAAGCT 152
|||||
Db 178039 ATGAGTCCAGCTTCCTGGAATTCGTTGAAAAGCT 178072
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RESULT 11
AF000511 200000 bp DNA linear PRI 22-AUG-2001
LOCUS Homo sapiens genomic DNA, chromosome 6p21.3, HLA class I region,
DEFINITION section 10/20.
ACCESSION AP000511 BA000025
VERSION AP000511.1 GI:5926698
KEYWORDS Homo sapiens DNA.
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1
AUTHORS Shilina,S., Tamiya,G., Oka,A. and Inoko,H.
TITLE Homo sapiens 2,229,817bp genomic DNA of 6p21.3 HLA class I region
JOURNAL Published Only in Database (1999)
REFERENCE 2 (bases 1 to 200000)
AUTHORS Hirakawa,M., Yamaguchi,H., Imai,K. and Shimada,J.
TITLE Direct Submission
JOURNAL Submitted (21-SEP-1999) Mika Hirakawa, Japan Science and Technology
Corporation (JST), Advanced Databases Department, 5-3, Yonbancho,
Chiyoda-ku, Tokyo 102-0081, Japan (E-mail:mika@tokyo.jst.go.jp,
URL:http://www-alls.tokyo.jst.go.jp/, Tel:81-3-5214-8491,
Fax:81-3-5214-8470)
COMMENT This sequence is conducted by Tokai University as a JST sequencing
Team.
Principal Investigator: Hidetoshi Inoko Ph.D
Phone:+81-463-93-1121, Fax:+81-463-94-8884.
The sequence is submitted by Human Genome Sequencing in ALIS
project of JST
Japan Science and Technology Corporation (JST)
5-3, Yonbancho, Chiyoda-ku, Tokyo, 102-0081 Japan
For further information about this sequences, please visit our
sequence archive Web site (http://www-alls.tokyo.jst.go.jp/HGS/top.
html) or send email to webmaster@www-alls.tokyo.jst.go.jp.
FEATURES
Location/Qualifiers
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/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="6"
/map="6p21.3"
108774..108864
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/Note="SHGC-12985:The location is between each flanking
site of PCR primers."
/db_xref="GDB:735268"
115648..115906
/standard_name="D6S1898"
/Note="WI-9418:The location is between each flanking site
of PCR primers."
/db_xref="GDB:678272"
complement(115665..115896)
/Note="Cda0vhl0:The location is between each flanking site
of PCR primers."
/db_xref="GDB:443382"
join(127993..128284,128708..128786,128938..128985,
129637..129767,129949..130081,130328..130411,
130596..130664,130826..130937,131154..131242,
131334..131430,132032..132163,132556..132660,
132922..133061,133692..133813)
/gene="TFIIH"

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gene	complement(join(128112..128284,128708..128786, 128938..128985,129637..129767,129949..130081, 130328..130411,130596..130664,130826..130937, 131154..131242,131334..131430,132032..132163, 132556..132660,132922..133058)) /gene="TFIIH"	STS	/note="SHGC-16870:The location is between each flanking site of PCR primers." /db_xref="GDB:741215"
CDS	complement(join(128112..128284,128708..128786, 128938..128985,129637..129767,129949..130081, 130328..130411,130596..130664,130826..130937, 131154..131242,131334..131430,132032..132163, 132556..132660,132922..133058)) /gene="TFIIH"	STS	/note="SHGC-16870:The location is between each flanking site of PCR primers." /db_xref="GDB:4573021"
exon	128708..128786 /gene="TFIIH"	gene	/note="SHGC-10808:The location is between each flanking site of PCR primers." /db_xref="GDB:675281"
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Matches 93; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 59 CAGGCGGGTATGACCTTGAACCTGAAGAGTCTTTCTTCTGACAAATTCCTCT 118
 Db 110306 CAGGCGGGTATGACCTTGAACCTGAAGAGTCTTTCTTCTGACAAATTCCTCT 110365

QY 119 ATGAGTCCAGCTTCCTGGAATTCCTTGAAGAGCT 152
 Db 110366 ATGAGTCCAGCTTCCTGGAATTCCTTGAAGAGT 110399

RESULT 12
 LOCUS AL662854 84474 bp DNA linear PRI 24-APR-2002
 DEFINITION Human DNA sequence from clone Xbac-105N19 on Chromosome 6,
 complete sequence.
 ACCESSION AL662854
 VERSION AL662854.7 GI:20068660
 KEYWORDS HTG.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1
 AUTHORS Tracey A.
 TITLE Direct Submission
 JOURNAL Submitted (23-APR-2002) Wellcome Trust Sanger Institute, Hinxton,
 Cambridgeshire, CB10 1SA, UK. E-mail enquiries:
 humquerry@sanger.ac.uk Clone requests: clonerequests@sanger.ac.uk
 On Apr 7, 2002 this sequence version replaced gi:19031750.
 During sequence assembly data is compared from overlapping clones.
 Where differences are found these are annotated as variations
 together with a note of the overlapping clone name. Note that the
 variation annotation may not be found in the sequence submission
 corresponding to the overlapping clone, as we submit sequences with
 only a small overlap as described above.
 This sequence was finished as follows unless otherwise noted: all
 regions were either double-stranded or sequenced with an alternate
 chemistry or covered by high quality data (i.e., phred quality >=
 30); an attempt was made to resolve all sequencing problems, such
 as compressions and repeats; all regions were covered by at least
 one plasmid subclone or more than one M13 subclone; and the
 assembly was confirmed by restriction digest. The following
 abbreviations are used to associate primary accession numbers given
 in the feature table with their source databases: Em, EMBL; SW,
 SWISSPROT; Tr, TREMBL; Wp, WORMPEP; Information on the WORMPEP
 database can be found at
 http://www.sanger.ac.uk/Projects/C_elegans/wormpep
 from a CHORI-502 human bac - COX cell line library VECTOR:
 PTARBAC2.1
 This sequence was generated from part of bacterial clone conigs
 constructed by the MHC haplotype Consortium and collaborators.
 Further information can be found at
 http://www.sanger.ac.uk/HGP/Chr6/MHC.

FEATURES
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 ORIGIN

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 Best Local Similarity 97.9%; Pred. No. 3e-17; Indels 0; Gaps 0;
 Matches 92; Conservative 0; Mismatches 2

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 Db 56216 CAGGCGGGTATGACCTTGAACCTGAAGAGTCTTTCTTCTGACAAATTCCTCT 56157

QY 119 ATGAGTCCAGCTTCCTGGAATTCCTTGAAGAGCT 152
 Db 56156 ATGAGTCCAGCTTCCTGGAATTCCTTGAAGAGT 56123

RESULT 13
 LOCUS AX344553/C 349980 bp DNA linear PAT 01-FEB-2002
 DEFINITION Sequence 4 from Patent WO0200932.
 ACCESSION AX344553
 VERSION AX344553.1 GI:18492439
 KEYWORDS synthetic construct.
 SOURCE synthetic construct.
 ORGANISM artificial sequences.

REFERENCE 1
 AUTHORS Olek, A., Piepenbrock, C. and Berlin, K.
 TITLE Diagnosis of known genetic parameters within the mhc
 JOURNAL Patent: WO 0200932-A 4 03-JAN-2002;
 Epigenomics AG (DE)
 FEATURES Location/Qualifiers
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 /organism="synthetic construct"
 /db_xref="taxon:32630"
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 BASE COUNT 86882 a 5859 c 85073 g 172166 t
 ORIGIN

Query Match 29.2%; Score 58.4; DB 6; Length 349980;
 Best Local Similarity 87.4%; Pred. No. 3.2e-10; Indels 0; Gaps 0;
 Matches 75; Conservative 0; Mismatches 11

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 Db 319291 AACTCTACCTCTCTCCATCTCCCTCAAAAACCAACGTCACCTCCACCATCAAAAT 319232

QY 209 CTCACACCATGTTGCTGCAACACA 234
 Db 319231 CTCACACCATATTATCTACACACA 319206

RESULT 14
 LOCUS AX344554/C 349980 bp DNA linear PAT 01-FEB-2002
 DEFINITION Sequence 5 from Patent WO0200932.
 ACCESSION AX344554
 VERSION AX344554.1 GI:18492440
 KEYWORDS synthetic construct.
 SOURCE synthetic construct.
 ORGANISM artificial sequences.

REFERENCE 1
 AUTHORS Olek, A., Piepenbrock, C. and Berlin, K.
 TITLE Diagnosis of known genetic parameters within the mhc
 JOURNAL Patent: WO 0200932-A 5 03-JAN-2002;
 Epigenomics AG (DE)
 FEATURES Location/Qualifiers
 source 1..349980
 /organism="synthetic construct"
 /db_xref="taxon:32630"

GenCore version 5.1.5
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: May 1, 2003, 02:55:40 ; Search time 160.776 seconds
(without alignments)
3277.661 Million cell updates/sec

Title: US-09-092-296-7_COPY_51_284

Perfect score: 234

Sequence: 1 ATGGGGTCGCGCTCCCT.....ACCAATGTGTCGCAACA 234

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 2185239 seqs, 112599159 residues

Total number of hits satisfying chosen parameters: 4370478

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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- 24: /SID52/gcgdata/geneseq/geneseq-emb1/NA2002.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	234	100.0	422	21	AAZ65087
2	234	100.0	422	21	AAZ65087
3	234	100.0	422	22	AAZ65087
4	234	100.0	422	22	AAZ65087
5	234	100.0	422	22	AAZ65087
6	234	100.0	422	22	AAZ65087
7	234	100.0	422	22	AAZ65087
8	234	100.0	422	22	AAZ65087
9	234	100.0	422	22	AAZ65087

c	10	36.4	15.6	1611	22	AAK86283	Human immune/haema
c	11	34.8	14.9	1146	21	AAC63412	Human secreted pro
c	12	33.4	14.3	550	21	AAC93727	Cat flea hindgut a
c	13	32.6	13.9	4885	22	AAS44656	Human full-length
c	14	32.2	13.8	27082	22	AAK70447	Human immune/haema
c	15	32	13.7	13216	22	AAK05122	Human reproductive
c	16	32	13.7	13216	22	ABL98014	Human testicular a
c	17	32	13.7	29163	23	AAK05121	Human reproductive
c	18	32	13.7	29163	23	ABL98013	Human testicular a
c	19	31.8	13.6	1997	22	AAS27006	cDNA encoding nove
c	20	31.8	13.6	1997	22	AAS27432	cDNA encoding nove
c	21	31.8	13.6	6855	24	ABN83971	Human gene sequenc
c	22	31.4	13.4	761	23	ABL07573	Drosophila melanog
c	23	31.4	13.4	1318	21	AAK04640	Arabidopsis thalia
c	24	31.2	13.3	2902	22	AAK89424	Human digestive sy
c	25	31.2	13.3	2902	22	AAS31927	Human liver associ
c	26	31.2	13.3	2902	24	ABN90282	Human liver antige
c	27	31	13.2	398	24	ABL77487	Human ovarian canc
c	28	31	13.2	1850	21	AAAS1383	Chromosome 16q tum
c	29	31	13.2	4824	24	ABK70289	Human lung cancer
c	30	31	13.2	6457	24	ABN96892	Gene #3390 used to
c	31	30.8	13.2	513	22	ABA61532	Human foetal liver
c	32	30.8	13.2	513	22	AAK09832	Human brain expres
c	33	30.8	13.2	513	22	AAK35726	Human bone marrow
c	34	30.8	13.2	513	22	AAI41441	Probe #10127 used
c	35	30.8	13.2	2693	24	ABK65374	Arabidopsis cDNA e
c	36	30.6	13.1	437	24	ABL37309	Human colon tumour
c	37	30.6	13.1	464	21	AAZ96747	Nuclear transport
c	38	30.6	13.1	467	24	ABL77906	Human ovarian canc
c	39	30.6	13.1	565	21	AAF16146	Human prostate can
c	40	30.6	13.1	830	22	AAH07574	Human CDNA clone (
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c	42	30.2	12.9	445	21	AAC00697	Human secreted pro
c	43	30.2	12.9	590	22	ABA60879	Human foetal liver
c	44	30.2	12.9	590	22	ABA60879	Human brain expres
c	45	30.2	12.9	590	22	AAK34852	Human bone marrow

ALIGNMENTS

RESULT 1	
AAZ65087	
ID	AAZ65087 standard; cDNA; 422 BP.
XX	
AC	AAZ65087;
XX	
DT	05-APR-2000 (first entry)
XX	
DE	Membrane-bound protein PRO1098 encoding cDNA.
XX	
KW	Membrane-bound polypeptide; PRO polypeptide; LDL receptor; TIE ligand;
KW	pharmaceutical; receptor immunoadhesin; gene mapping; ss.
XX	
OS	Homo sapiens.
XX	
PN	W09963088-A2.
XX	
PD	09-DEC-1999;
XX	
PF	02-JUN-1999; 99WO-US12252.
XX	
PR	02-JUN-1998; 98US-0087607.
PR	02-JUN-1998; 98US-0087609.
PR	02-JUN-1998; 98US-0087609.
PR	03-JUN-1998; 98US-0087827.
PR	04-JUN-1998; 98US-0088021.
PR	04-JUN-1998; 98US-0088025.
PR	04-JUN-1998; 98US-0088026.
PR	04-JUN-1998; 98US-0088029.
PR	04-JUN-1998; 98US-0088030.
PR	04-JUN-1998; 98US-0088033.
PR	04-JUN-1998; 98US-0088326.

CC employed for screening of potential peptide or small molecule inhibitors
CC of the relevant receptor/ligand interaction. The PRO encoding sequences
CC are useful as hybridization probes, in chromosome and gene mapping and in
CC the generation of antisense RNA and DNA. PRO nucleic acid sequences
CC will also be useful for the preparation of PRO polypeptides, especially
CC by recombinant techniques.

XX Sequence 422 BP; 84 A; 134 C; 104 G; 100 T; 0 other;

Query Match 100.0%; Score 234; DB 21; Length 422;
Best Local Similarity 100.0%; Pred. No. 2.5e-65;
Matches 234; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 61 GGGCCGGGTATGACTTTGCAACTGAAGCTGAAGGAGTCTTTCTGACAAATTCCTCTAT 120
Db 118 GGGCCGGGTATGACTTTGCAACTGAAGCTGAAGGAGTCTTTCTGACAAATTCCTCTAT 177
QY 121 GAGTCCAGCTTCTCGAATTCCTTGAAGCTTGAAGCTTGAAGCTTGAAGCTTGAAGCTTGAAGCT 180
Db 178 GAGTCCAGCTTCTCGAATTCCTTGAAGCTTGAAGCTTGAAGCTTGAAGCTTGAAGCTTGAAGCT 237
QY 191 ACCAGCTCACCTCCACCATGCAAGATCTCAACACCATGCTTGTCTGCAACACA 234
Db 238 ACCAGCTCACCTCCACCATGCAAGATCTCAACACCATGCTTGTCTGCAACACA 291

RESULT 2

AAS46045
ID AAS46045 standard; cDNA; 422 BP.

XX AAS46045;

DT 18-DEC-2001 (first entry)

XX Human DNA encoding PRO polypeptide sequence #121.

XX PRO polypeptide; mammal; tumour; cancer; human; cattle; horse; sheep; ss;
KW dog; cat; pig; goat; rabbit; tumour necrosis factor alpha; TNF-alpha;
KW blood; chondrocyte cell; cell proliferation; cell differentiation; colon;
KW adrenal; lung; breast; prostate; rectum; cervix; liver; genetic disorder;
KW PCR primer.

XX Homo sapiens.

XX W0200168848-A2.

XX 20-SEP-2001.

XX 28-FEB-2001; 2001WO-US06520.

XX 01-MAR-2000; 2000WO-US05601.

XX 02-MAR-2000; 2000WO-US05841.

XX 03-MAR-2000; 2000US-187202P.

XX 06-MAR-2000; 2000US-186968P.

XX 14-MAR-2000; 2000US-189320P.

XX 15-MAR-2000; 2000US-189328P.

XX 21-MAR-2000; 2000WO-US06884.

XX 21-MAR-2000; 2000US-130828P.

XX 21-MAR-2000; 2000US-191007P.

XX 21-MAR-2000; 2000US-191048P.

XX 28-MAR-2000; 2000US-191314P.

XX 29-MAR-2000; 2000US-192655P.

XX 29-MAR-2000; 2000US-193032P.

XX 30-MAR-2000; 2000US-193053P.

PR 11-APR-2000; 2000US-196187P.
PR 11-APR-2000; 2000US-196690P.
PR 11-APR-2000; 2000US-196820P.
PR 18-APR-2000; 2000US-198121P.
PR 18-APR-2000; 2000US-198585P.
PR 25-APR-2000; 2000US-199397P.
PR 25-APR-2000; 2000US-199550P.
PR 25-APR-2000; 2000US-199654P.
PR 03-MAY-2000; 2000US-201516P.
PR 17-MAY-2000; 2000WO-US13705.
PR 22-MAY-2000; 2000WO-US14042.
PR 30-MAY-2000; 2000WO-US14941.
PR 02-JUN-2000; 2000WO-US15264.
PR 05-JUN-2000; 2000US-209832P.
PR 28-JUL-2000; 2000WO-US20710.
PR 22-AUG-2000; 2000US-064848.
PR 24-AUG-2000; 2000WO-US23328.
PR 08-NOV-2000; 2000WO-US30952.
PR 01-DEC-2000; 2000WO-US32678.
PR 20-DEC-2000; 2000WO-US34956.

XX (GETH) GENENTECH INC.

PI Baker KP, Chen J, Desnoyers L, Goddard A, Godowski PJ, Gurney AL;

PI Pan J, Smith V, Watanabe CK, Wood WL, Zhang Z;

XX WPI; 2001-602746/68.

DR P-PSDB; AA029144.

XX Novel nucleic acids encoding PRO polypeptides, used to diagnose the
PT presence of tumours, such as prostate and breast tumours, in mammals and
PT to screen for modulators of the compounds -

XX Claim 2; Fig 241; 774pp; English.

XX Sequences AAS45925-AAS46231 represent DNA molecules encoding and PCR
CC primers for PRO polypeptides of the invention. The sequences of the
CC invention can be used to detect the presence of a tumour in a mammal by
CC comparing the level of expression of a PRO polypeptide in a test sample
CC of cells from the animal and a control sample of normal cells, whereby a
CC higher level of expression in the test sample indicates the presence of a
CC tumour in the mammal. Mammals include dogs, cats, cattle, horses, sheep,
CC pigs, goats and rabbits but are preferably human. The polypeptides can be
CC used to stimulate tumour necrosis factor (TNF) alpha release from human
CC blood, when contacted with it. A specific polypeptide can be used to
CC stimulate the proliferation or differentiation of chondrocyte cells. The
CC PRO proteins can be used to determine the presence of tumours and also
CC susceptibility to tumour development, particularly adrenal, lung, colon,
CC breast, prostate, rectal, cervical, or liver tumours, in mammalian
CC subjects. The oligonucleotide probes specific for the PRO nucleic acids
CC can be used for genetic analysis of individuals with genetic disorders.

SQ Sequence 422 BP; 84 A; 134 C; 104 G; 100 T; 0 other;

Query Match 100.0%; Score 234; DB 22; Length 422;
Best Local Similarity 100.0%; Pred. No. 2.5e-65;
Matches 234; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGGGGTCTGGCTGCCCTTGTCTCTCTCTGACCTCTCTTGACCTCTCTGGCAGCTACATGGAACA 60

Db 58 ATGGGGTCTGGCTGCCCTTGTCTCTCTCTGACCTCTCTTGACCTCTCTGGCAGCTACATGGAACA 117

QY 61 GGGCCGGGTATGACTTTGCAACTGAAGCTGAAGGAGTCTTTCTGACAAATTCCTCTAT 120

Db 118 GGGCCGGGTATGACTTTGCAACTGAAGCTGAAGGAGTCTTTCTGACAAATTCCTCTAT 177

QY 121 GAGTCCAGCTTCTCGAATTCCTTGAAGCTTGAAGCTTGAAGCTTGAAGCTTGAAGCT 180

Db 178 GAGTCCAGCTTCTCGAATTCCTTGAAGCTTGAAGCTTGAAGCTTGAAGCTTGAAGCT 237

QY 181 ACCAGCTCACCTCCACCATGCAAGATCTCAACACCATGCTTGTCTGCAACACA 234

Db 238 ACCAGCTCACCTCCACCATGCAAGATCTCAACACCATGCTTGTCTGCAACACA 291

RESULT 3
ID AAF92090 standard; cDNA; 422 BP.

XX AC AAF92090;
XX 15-MAY-2001 (first entry)
XX Human PRO1098 cDNA.
XX Human; PRO protein; mapping; ss.

XX OS Homo sapiens.
XX PN WO200116318-A2.
XX PD 08-MAR-2001.

XX PF 24-AUG-2000; 2000WO-US23328.

XX XX 01-SEP-1999; 99WO-US20111.

XX PR 15-SEP-1999; 99WO-US21090.

XX PR 07-DEC-1999; 99US-0169495.

XX PR 09-DEC-1999; 99US-0170262.

XX PR 11-JAN-2000; 2000US-0175481.

XX PR 18-FEB-2000; 2000WO-US04341.

XX PR 18-FEB-2000; 2000WO-US04342.

XX PR 22-FEB-2000; 2000WO-US04414.

XX PR 01-MAR-2000; 2000WO-US05601.

XX PR 03-MAR-2000; 2000US-0187202.

XX PR 25-APR-2000; 2000US-0199397.

XX PR 22-MAY-2000; 2000WO-US14042.

XX PR 05-JUN-2000; 2000US-0209832.

XX PA (GETH) GENENTECH INC.

XX PI Eaton DL, Flivaroff E, Gerritsen ME, Goddard A, Godowski PJ;

XX PI Grimaldi CJ, Gurney AL, Watanabe CK, Wood WI;

XX XX WPI; 2001-183260/18.

XX DR P-FSDB; AAB87558.

XX XX Eighty four nucleic acids encoding PRO polypeptides, useful in

XX PT molecular biology, including use as hybridization probes, and in

XX PT chromosome and gene mapping.

XX XX Claim 2; Fig 65; 278pp; English.

XX CC The present sequence is the coding sequence for a human PRO polypeptide

XX CC (secreted and transmembrane). The PRO protein, and PRO agonists, PRO

XX CC antagonists or anti-PRO antibodies are useful for preparation of a

XX CC medicament useful in the treatment of a condition which is responsive to

XX CC the PRO protein, agonists, antagonists or anti-PRO antibodies. The PRO

XX CC protein may also be employed as molecular weight markers for protein

XX CC electrophoresis. The PRO coding sequence has applications in molecular

XX CC biology, including use as hybridisation probes, and in chromosome and

XX CC gene mapping.

XX XX Query Match 100.0%; Score 234; DB 22; Length 422;
XX XX Best Local Similarity 100.0%; Pred. No. 2.5e-65;
XX XX Matches 234; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGGGGTCTGGGTGCGCCCTTGTCTCTCTTGGACCTCTTGGCAGCTCACATGGACA 60

Db 58 ATGGGGTCTGGGTGCGCCCTTGTCTCTCTTGGACCTCTTGGCAGCTCACATGGACA 117

QY 61 GGGCGGGGTATGACTTTGCAACTGAAGCTGAAGGAGICTTTCTGTGACAAATTCCTCTAT 120

Db 118 GGGCGGGGTATGACTTTGCAACTGAAGCTGAAGGAGICTTTCTGTGACAAATTCCTCTAT 177

QY 121 GAGTCCAGCTTCCTGGAAATGCTTGAAGAAGCTGTGCTCTCTCATCTCCCTTCAGGG 180
Db 178 GAGTCCAGCTTCCTGGAAATGCTTGAAGAAGCTGTGCTCTCTCATCTCCCTTCAGGG 237
QY 181 ACCAGGTCACCCCTCCACCACATGCAAGATCTCAACACCATGTGTCTGCAACACA 234
Db 238 ACCAGGTCACCCCTCCACCACATGCAAGATCTCAACACCATGTGTCTGCAACACA 291

RESULT 4

AAF44233

ID AAF44233 standard; cDNA; 422 BP.

XX AC AAF44233;

XX XX 02-APR-2001 (first entry)

XX DE Human PRO1098 (UNQ541) nucleotide sequence SEQ ID NO:362.

XX KW Human; secreted and transmembrane protein; PRO; cytostatic;

XX KW cell death; cancer; chromosomal mapping; gene mapping; tissue typing;

XX OS Homo sapiens.

XX XX WO200073454-A1.

XX PD 07-DEC-2000.

XX PF 30-MAR-2000; 2000WO-US08439.

XX XX 02-JUN-1999; 99WO-US12252.

XX PR 23-JUN-1999; 99US-0141037.

XX PR 07-JUL-1999; 99US-0143048.

XX PR 20-JUL-1999; 99US-0144758.

XX PR 26-JUL-1999; 99US-0145698.

XX PR 28-JUL-1999; 99US-0146222.

XX PR 17-AUG-1999; 99US-0149396.

XX PR 15-SEP-1999; 99WO-US21090.

XX PR 15-SEP-1999; 99WO-US21547.

XX PR 08-OCT-1999; 99US-0158663.

XX PR 30-NOV-1999; 99WO-US28313.

XX PR 01-DEC-1999; 99WO-US30095.

XX PR 20-DEC-1999; 99WO-US30911.

XX PR 05-JAN-2000; 2000WO-US00219.

XX PR 06-JAN-2000; 2000WO-US00376.

XX PR 11-FEB-2000; 2000WO-US03565.

XX PR 18-FEB-2000; 2000WO-US04341.

XX PR 22-FEB-2000; 2000WO-US04414.

XX PR 24-FEB-2000; 2000WO-US04914.

XX PR 02-MAR-2000; 2000WO-US05004.

XX PR 15-MAR-2000; 2000WO-US05841.

XX PR 20-MAR-2000; 2000WO-US06884.

XX XX (GETH) GENENTECH INC.

XX PI Ashkenazi AJ, Baker KP, Botstein D, Desnoyers L, Eaton DL;

PI Ferrara N, Fong S, Gerber H, Gerritsen ME, Goddard A, Godowski PJ;

PI Grimaldi CJ, Gurney AL, Kijavini IJ, Napier MA, Pan J, Paoni NF;

PI Roy MA, Stewart TA, Tumas D, Watanabe CK, Williams PM, Wood WI;

PI Zhang Z;

XX WPI; 2001-032150/04.

XX DR P-FSDB; AAB65264.

XX XX PRO polynucleotides used to produce polypeptides used to target

PT bioactive molecules such as toxins, radiolabels or antibodies, to

PT specific cells, to cause targeted cell death -

XX Claim 2; Fig 257; 935pp; English.

XX The present invention describes human secreted and transmembrane PRO
CC proteins. The PRO proteins have cytotostatic activity. The PRO proteins
CC can be used for targeted delivery of bioactive molecules, such as
CC toxins, radiolabels or antibodies, that cause cell death. PRO nucleotide
CC sequences, and their fragments, can be used as hybridisation probes, in
CC chromosomal and gene mapping, and in the generation of anti-sense RNA
CC and DNA. They may also be used to produce transgenic animals which are
CC used to develop and screen therapeutically useful reagents. The PRO
CC nucleotide and protein sequence can be used for tissue typing and in
CC treating cancer. Anti-PRO antibodies can be used in diagnostic assays.
CC AAF44270 to AAF44470 represent PCR primers and hybridisation probes used
CC in the isolation of human PRO sequences. AAF44087 to AAF44269 and
CC AAB5154 to AAB5300 represent human PRO polynucleotide and protein
CC sequences given in the exemplification of the present invention.
XX
SQ Sequence 422 BP; 84 A; 134 C; 104 G; 100 T; 0 other;

Query Match 100.0%; Score 234; DB 22; Length 422;
Best Local Similarity 100.0%; Pred. No. 2.5e-65;
Matches 234; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGGGGCTGGCGTGGCCCTTGTCTCTCTGTGACCTCTTGGCAGCTCACATGGAACA 50
DB 58 ATGGGGCTGGCGTGGCCCTTGTCTCTCTGTGACCTCTTGGCAGCTCACATGGAACA 117
QY 61 GGGCGGGTATGACTTTGCAACTGAAGCTGAAGAGTCTTTCTGACAAATTCCTCTAT 120
DB 118 GGGCGGGTATGACTTTGCAACTGAAGCTGAAGAGTCTTTCTGACAAATTCCTCTAT 177
QY 121 GAGTCCAGCTTCCTGGAATGCTTGAAGAGTCTGCTCTCTCTCTCTCTCTCTAT 180
DB 178 GAGTCCAGCTTCCTGGAATGCTTGAAGAGTCTGCTCTCTCTCTCTCTCTAT 237
QY 181 ACCAGCGTCACCTCCACCATGCAAGATCTCAACACCATGTTGTCTGCAACACA 234
DB 238 ACCAGCGTCACCTCCACCATGCAAGATCTCAACACCATGTTGTCTGCAACACA 291

RESULT 5
ID AA298124 standard; cDNA; 431 BP.
XX AC AA298124;
XX
DT 11-MAY-2000 (first entry)
XX
DE Human signal peptide containing protein HSP-16 cDNA SEQ ID NO:150.
XX
KW Human; signal peptide-containing protein; HSP; diagnosis; cancer;
KW inflammation; cardiovascular disease; anticancer; anti-inflammatory;
KW antimicrobial; neurotropic; neuroprotective; cardiovascular; hepatotropic;
KW antisthmatic; gene therapy; cell proliferation; neurological disorder;
KW reproductive disorder; developmental disorder; arteriosclerosis;
KW cirrhosis; psoriasis; acquired immune deficiency syndrome; anaemia;
KW asthma; Crohn's disease; infection; Alzheimer's disease; schizophrenia;
KW Parkinson's disease; Huntington's disease; ovulatory defect;
KW muscular dystrophy; ss.
XX
OS Homo sapiens.
XX
PN WO200000610-A2.
XX
PD 06-JAN-2000.
XX
PF 25-JUN-1999; 99WO-US14484.
XX
PR 26-JUN-1998; 98US-0090762.
PR 31-JUL-1998; 98US-0094983.
PR 01-OCT-1998; 98US-0102686.
PR 11-DEC-1998; 98US-0112129.
XX
PA (INCY-) INCYTE PHARM INC.

XX
PI Lal P, Tang YT, Gorgone CA, Corley NC, Guegler KJ, Baughn MR;
PI Akerblom IE, Au-Young J, Yue H, Patterson C, Reddy R, Hillman JL;
PI Bandman O;
XX
XX WPI; 2000-160673/14.
XX P-PSDB; AAY87239.
XX
XX New human signal peptide-containing proteins useful in treatment,
XX prevention and diagnosis of e.g. cancer, inflammation and
XX cardiovascular disease
XX
XX Claim 9; Page 261; 327pp; English.
XX
XX AA298109 to AA298242 encode AAY87224 to AAY87357 which represent the
XX human signal peptide-containing proteins HSP-1 to HSP-134. HSPs have
XX anticancer, anti-inflammatory, antimicrobial, neurotropic, hepatotropic,
XX neuroprotective, cardiovascular and antiasthmatic activities, and can
XX be used in gene therapy. HSPs can be used to treat or prevent disorders
XX associated with decreased activity or function of HSP. Antagonists of
XX HSP are used to treat or prevent disorders associated with increased
XX activity or function of HSP. Such diseases include cell proliferation
XX (including cancer), inflammation, cardiovascular, neurological,
XX reproductive or developmental disorders, (e.g. arteriosclerosis,
XX cirrhosis, psoriasis, acquired immune deficiency syndrome, anaemia,
XX asthma, Crohn's disease, microbial or other infections, congestive or
XX ischaemic heart disease, Alzheimer's, Parkinson's or Huntington's
XX diseases, schizophrenia, ovulatory defects, muscular dystrophy). HSP
XX nucleic acids can be used for the recombinant production of HSP, for
XX detecting HSP in standard hybridisation and amplification assays (for
XX diagnosis and monitoring), in gene therapy, as antisense,
XX triplex-forming or ribozyme therapeutics, for detecting related sequences
XX or genetic variations, and for chromosomal mapping. HSP are also used to
XX raise specific antibodies (Ab) and to screen for agonists and
XX antagonists (potential therapeutic agents). Ab are used to diagnose, or
XX monitor, HSP-related diseases (in usual immunoassays), as therapeutic
XX antagonists, in competitive drug screens, and for purification of HSP
XX from natural sources.
XX
SQ Sequence 431 BP; 93 A; 135 C; 101 G; 102 T; 0 other;

Query Match 100.0%; Score 234; DB 21; Length 431;
Best Local Similarity 100.0%; Pred. No. 2.6e-65;
Matches 234; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGGGGTCTGGGTGGCCCTTGTCTCTCTTGAACCTCTTGGCAGCTCACATGGAACA 50
DB 51 ATGGGGTCTGGGTGGCCCTTGTCTCTCTTGAACCTCTTGGCAGCTCACATGGAACA 110
QY 61 GGGCGGGTATGACTTTGCAACTGAAGTGAAGAGTCTTTCTGACAAATTCCTCTAT 120
DB 111 GGGCGGGTATGACTTTGCAACTGAAGTGAAGAGTCTTTCTGACAAATTCCTCTAT 170
QY 121 GAGTCCAGCTTCCTGGAATGCTTGAAGAGTCTGCTCTCTCTCTCTCTCTAT 180
DB 171 GAGTCCAGCTTCCTGGAATGCTTGAAGAGTCTGCTCTCTCTCTCTCTAT 230
QY 181 ACCAGCGTCACCTCCACCATGCAAGATCTCAACACCATGTTGTCTGCAACACA 234
DB 231 ACCAGCGTCACCTCCACCATGCAAGATCTCAACACCATGTTGTCTGCAACACA 284

RESULT 6
ID AAV84366
XX
XX AAV84366 standard; cDNA to mRNA; 439 BP.
XX AC AAV84366;
XX
DT 30-MAR-1999 (first entry)
XX
XX Human stomach carcinoma cDNA clone HP10408.
XX DE Transmembrane protein; HP10408; human; stomach cancer; ds.
XX KW

```
XX OS Homo sapiens.
XX AC
XX FT Key Location/Qualifiers
XX CDS 75..311
FT /*tag= a
FT /note= "cDNA comprising the coding region (minus
FT the stop codon) is claimed (Claim 3)"
XX
XX PN WO9855508-A2.
XX PD 10-DEC-1998.
XX PF 03-JUN-1998; 98WO-JP02445.
XX PR 03-JUN-1997; 97JP-0144948.
XX PA (PROT-) PROTEGENE INC.
XX (SAGA ) SAGAMI CHEM RES CENTRE.
XX PI Kato S, Sekine S, Yamaguchi T;
XX WPI; 1999-045730/04.
XX DR P-PSDB; AAW88498.
XX
XX New human proteins containing transmembrane domains and their
XX encoding sequences - useful in the preparation of antibodies and
XX large-scale protein production, gene diagnosis, and gene therapy
XX
XX Claim 4; Page 135; 178pp; Eng114sh.
XX
XX This is the nucleotide sequence of cDNA clone HPL0408, which
XX includes a coding region (also claimed) for a novel human
XX transmembrane protein (see AAW88498). The clone was isolated from a
XX stomach cancer cDNA library using a signal sequence detection
XX method, and by protein synthesis by in vitro translation. The
XX encoded protein has a putative signal sequence and a putative
XX internal transmembrane domain. The invention provides nucleotide
XX sequences (see AAW84359-76) coding for 18 transmembrane proteins
XX (see AAW8491-508), vectors containing such polynucleotides, and
XX eukaryotic cells containing the vectors. The proteins can be
XX used as antigens or as compositions in the preparation of
XX antibodies against the proteins. The polynucleotides can be used
XX as probes for gene diagnosis, and as gene sources for gene therapy
XX and large-scale production of proteins encoded by the cDNA. The
XX host cells are used for the detection of ligands corresponding to
XX the expressed proteins, and the screening of low mol.wt. medicines.
XX
XX SQ Sequence 439 BP; 89 A; 137 C; 109 G; 104 T; 0 other;

Query Match 100.0%; Score 234; DB 20; Length 439;
Best Local Similarity 100.0%; Pred. No. 2.6e-65;
Matches 234; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATGGGCTCTGGCTGCCCTTCTCTCTCTGACCTTGGAGGAGTCTTTTCTGACAAATTCCTCTAT 120
Db 75 ATGGGCTCTGGGCTGCCCTTCTCTCTCTGACCTTGGAGGAGTCTTTTCTGACAAATTCCTCTAT 134
Qy 61 GGGCGGGGTATGACCTTGGCAACTGAAGCTGAAGGAGTCTTTTCTGACAAATTCCTCTAT 120
Db 135 GGGCGGGGTATGACCTTGGCAACTGAAGCTGAAGGAGTCTTTTCTGACAAATTCCTCTAT 194
Qy 121 GAGTCCAGCTTCTTGGAAATGCTTGAAGCTCTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 180
Db 195 GAGTCCAGCTTCTTGGAAATGCTTGAAGCTCTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 254
Qy 181 ACCAGGCTCACCTCCACATGCAAGATCTCAACACCATGTTGTCTGCAACACA 234
Db 255 ACCAGGCTCACCTCCACATGCAAGATCTCAACACCATGTTGTCTGCAACACA 308

RESULT 7
ABK81818
```

```
ID ABK81818 standard; DNA; 624 BP.
XX
XX AC ABK81818;
XX
XX DT 13-AUG-2002 (first entry)
XX
XX DE DNA representing lung specific gene #4.
XX
XX KW Lung specific gene; gene therapy; vaccine; lung cancer;
XX cancer staging; cancer monitoring; cancer diagnosis;
XX imaging lung cancer; metastases; gene; ss.
XX
XX OS Homo sapiens.
XX
XX PN WO200218576-A2.
XX
XX PD 07-MAR-2002.
XX
XX PF 27-AUG-2001; 2001WO-US26684.
XX
XX PR 28-AUG-2000; 2000US-228378P.
XX
XX PA (DIAD-) DIADEXUS INC.
XX
XX PI Chen S, Macina RA, Sun Y, Recipon H;
XX
XX DR WPI; 2002-434904/46.
XX
XX New lung specific genes and their encoded proteins, useful in gene
XX therapy or as a vaccine for treating lung cancer, as well as for
XX measuring metastases of lung cancer, or staging, monitoring, diagnosing
XX or imaging lung cancer -
XX
XX PS Claim 1; Page 161; 206pp; English.
XX
XX The invention describes a new lung specific gene and its variants. The
XX lung specific gene proteins and genes are useful in gene therapy or as a
XX vaccine for treating lung cancer. Lung specific genes are also useful for
XX staging, monitoring, diagnosing or imaging lung cancer, as well as for
XX measuring metastases of lung cancer. This sequence represents a lung
XX specific gene described in the invention.
XX
XX SQ Sequence 624 BP; 129 A; 175 C; 182 G; 138 T; 0 other;

Query Match 75.2%; Score 176; DB 24; Length 624;
Best Local Similarity 100.0%; Pred. No. 1.4e-46;
Matches 176; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 59 CAGGGCGGGGTATGACCTTGGCAACTGAAGCTGAAGGAGTCTTTTCTGACAAATTCCTCT 118
Db 314 CAGGGCGGGGTATGACCTTGGCAACTGAAGCTGAAGGAGTCTTTTCTGACAAATTCCTCT 373
Qy 119 ATGAGTCCAGCTTCTCTGGAATGCTTGAAGCTCTGCTCTCTCTCTCTCTCTCTCTCTCTCT 178
Db 374 ATGAGTCCAGCTTCTCTGGAATGCTTGAAGCTCTGCTCTCTCTCTCTCTCTCTCTCTCTCT 433
Qy 179 GGACAGGCTCACCTCCACATGCAAGATCTCAACACCATGTTGTCTGCAACACA 234
Db 434 GGACAGGCTCACCTCCACATGCAAGATCTCAACACCATGTTGTCTGCAACACA 489

RESULT 8
AAS65519
ID AAS65519 standard; cDNA; 729 BP.
XX
XX AC AAS65519;
XX
XX DT 13-FEB-2002 (first entry)
XX
XX DE DNA encoding novel human diagnostic protein #1323.
XX
XX KW Human; chromosome mapping; gene mapping; gene therapy; forensic; ss.
XX food supplement; medical imaging; diagnostic; genetic disorder; ss.
```

XX Homo sapiens.
OS WO200175067-A2.
PN 11-OCT-2001.
XX 30-MAR-2001; 2001WO-US08631.
XX 31-MAR-2000; 2000US-0540217.
PR 23-AUG-2000; 2000US-0649167.
XX (HYSE-) HYSEQ INC.
PA Drmanac RT, Liu C, Tang YT;
XX WPI; 2001-639362/73.
DR P-PSDB; ABG01332.
XX New isolated polynucleotide and encoded polypeptides, useful in
PT diagnostics, forensics, gene mapping, identification of mutations
PT responsible for genetic disorders or other traits and to assess
PT biodiversity -
XX Claim 1; SEQ ID No 1323; 103pp; English.
PS The invention relates to isolated polynucleotide (I) and
XX polypeptide (II) sequences. (I) is useful as hybridisation probes,
CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome
CC and gene mapping, and in recombinant production of (II). The
CC polynucleotides are also used in diagnostics as expressed sequence tags
CC for identifying expressed genes. (I) is useful in gene therapy techniques
CC to restore normal activity of (II) or to treat disease states involving
CC (II). (II) is useful for generating antibodies against it, detecting or
CC quantitating a polypeptide in tissue, as molecular weight markers and as
CC a food supplement. (II) and its binding partners are useful in medical
CC imaging of sites expressing (II). (I) and (II) are useful for treating
CC disorders involving aberrant protein expression or biological activity.
CC The polypeptide and polynucleotide sequences have applications in
CC diagnostics, forensics, gene mapping, identification of mutations
CC responsible for genetic disorders or other traits to assess biodiversity
CC and to produce other types of data and products dependent on DNA and
CC amino acid sequences. AAS64197-AAS94564 represent novel human
CC diagnostic coding sequences of the invention.
CC Note: The sequence data for this patent did not appear in the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences.
XX Sequence 729 BP; 187 A; 169 C; 152 G; 146 T; 75 other;
SQ
Query Match 40.3%; Score 94.4; DB 23; Length 729;
Best Local Similarity 99.0%; Pred. No. 2.8e-20;
Matches 95; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 ATGGGCTGTGGCTGGCCCTTGTCTCTCTTGTACCTCTCTGGCAGCTCACATGAACA 50
DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
25 ATGGGCTGTGGCTGGCCCTTGTCTCTCTTGTACCTCTCTGGCAGCTCACATGAACA 84
QY 61 GGCCCGGTATGACTTGTGAACCTGAAGTGAAGG 96
DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
85 GGACCGGTATGACTTGTGAACCTGAAGTGAAGG 120
RESULT 9
ABAI9667/C
ID ABAI9667 standard; DNA; 1611 BP.
XX
AC ABAI9667;
XX
DT 23-JAN-2002 (first entry)
XX
DE Human nervous system related polynucleotide SEQ ID NO 11998.
XX

KW Human; nootropic; neuroprotective; cytostatic; dermatological; virucide;
KW immunosuppressive; antiinflammatory; anti-HIV; antibacterial; vulnery;
KW antiparkinsonian; antiskling; antianaemic; antiarthritic; cancer;
KW antirheumatic; hepatotropic; cerebroprotective; antiinflammatory;
KW antiallergic; antidiabetic; antilucer; anticonvulsant; antifungal;
KW antiparasitic; cardiant; immune disorder; cardiovascular disorder;
KW neurological disease; infection; nephrotropic; gene therapy; vaccine; ds.
XX
OS Homo sapiens.
PN WO200159063-A2.
XX 16-AUG-2001.
XX 17-JAN-2001; 2001WO-US01334.
XX 31-JAN-2000; 2000US-0179065.
PR 04-FEB-2000; 2000US-0180628.
PR 24-FEB-2000; 2000US-0184664.
PR 02-MAR-2000; 2000US-0186350.
PR 16-MAR-2000; 2000US-0189874.
PR 17-MAR-2000; 2000US-0190076.
PR 18-APR-2000; 2000US-0198123.
PR 19-MAY-2000; 2000US-0205315.
PR 07-JUN-2000; 2000US-0209467.
PR 28-JUN-2000; 2000US-0214886.
PR 30-JUN-2000; 2000US-0215135.
PR 07-JUL-2000; 2000US-0216647.
PR 07-JUL-2000; 2000US-0216880.
PR 11-JUL-2000; 2000US-0217487.
PR 14-JUL-2000; 2000US-0217496.
PR 26-JUL-2000; 2000US-0218290.
PR 26-JUL-2000; 2000US-0220963.
PR 14-AUG-2000; 2000US-0220964.
PR 14-AUG-2000; 2000US-0224518.
PR 14-AUG-2000; 2000US-0224519.
PR 14-AUG-2000; 2000US-0225213.
PR 14-AUG-2000; 2000US-0225214.
PR 14-AUG-2000; 2000US-0225266.
PR 14-AUG-2000; 2000US-0225267.
PR 14-AUG-2000; 2000US-0225268.
PR 14-AUG-2000; 2000US-0225270.
PR 14-AUG-2000; 2000US-0225447.
PR 14-AUG-2000; 2000US-0225757.
PR 14-AUG-2000; 2000US-0225758.
PR 18-AUG-2000; 2000US-0225759.
PR 18-AUG-2000; 2000US-0226279.
PR 22-AUG-2000; 2000US-0226681.
PR 22-AUG-2000; 2000US-0226868.
PR 30-AUG-2000; 2000US-0227009.
PR 01-SEP-2000; 2000US-0228924.
PR 01-SEP-2000; 2000US-0229343.
PR 01-SEP-2000; 2000US-0229344.
PR 01-SEP-2000; 2000US-0229345.
PR 05-SEP-2000; 2000US-0229509.
PR 05-SEP-2000; 2000US-0229513.
PR 06-SEP-2000; 2000US-0230437.
PR 06-SEP-2000; 2000US-0230438.
PR 08-SEP-2000; 2000US-0231242.
PR 08-SEP-2000; 2000US-0231243.
PR 08-SEP-2000; 2000US-0231244.
PR 08-SEP-2000; 2000US-0231413.
PR 08-SEP-2000; 2000US-0231414.
PR 08-SEP-2000; 2000US-0232080.
PR 08-SEP-2000; 2000US-0232081.
PR 12-SEP-2000; 2000US-0231968.
PR 14-SEP-2000; 2000US-0232397.
PR 14-SEP-2000; 2000US-0232398.
PR 14-SEP-2000; 2000US-0232399.
PR 14-SEP-2000; 2000US-0232400.
PR 14-SEP-2000; 2000US-0232401.

XX 31-JAN-2000; 2000US-0179065.
PR 04-FEB-2000; 2000US-0180628.
PR 24-FEB-2000; 2000US-0184664.
PR 02-MAR-2000; 2000US-0186350.
PR 16-MAR-2000; 2000US-0189874.
PR 17-MAR-2000; 2000US-0190076.
PR 18-APR-2000; 2000US-0198123.
PR 19-MAY-2000; 2000US-0205515.
PR 07-JUN-2000; 2000US-0209467.
PR 28-JUN-2000; 2000US-0214886.
PR 30-JUN-2000; 2000US-0215135.
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PR 07-JUL-2000; 2000US-0216880.
PR 11-JUL-2000; 2000US-0217487.
PR 11-JUL-2000; 2000US-0217496.
PR 14-JUL-2000; 2000US-0218290.
PR 26-JUL-2000; 2000US-0220963.
PR 26-JUL-2000; 2000US-0220964.
PR 14-AUG-2000; 2000US-0224518.
PR 14-AUG-2000; 2000US-0224519.
PR 14-AUG-2000; 2000US-0225213.
PR 14-AUG-2000; 2000US-0225214.
PR 14-AUG-2000; 2000US-0225266.
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PR 14-AUG-2000; 2000US-0225270.
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PR 14-AUG-2000; 2000US-0225757.
PR 14-AUG-2000; 2000US-0225758.
PR 14-AUG-2000; 2000US-0225759.
PR 18-AUG-2000; 2000US-0226279.
PR 22-AUG-2000; 2000US-0226681.
PR 22-AUG-2000; 2000US-0227182.
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PR 08-SEP-2000; 2000US-0231413.
PR 08-SEP-2000; 2000US-0231414.
PR 08-SEP-2000; 2000US-0232080.
PR 08-SEP-2000; 2000US-0232081.
PR 12-SEP-2000; 2000US-0231968.
PR 14-SEP-2000; 2000US-0232397.
PR 14-SEP-2000; 2000US-0232398.
PR 14-SEP-2000; 2000US-0232399.
PR 14-SEP-2000; 2000US-0234400.
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PR 21-SEP-2000; 2000US-0234274.
PR 25-SEP-2000; 2000US-0234997.
PR 25-SEP-2000; 2000US-0234998.
PR 26-SEP-2000; 2000US-0235484.
PR 27-SEP-2000; 2000US-0235834.
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PR 29-SEP-2000; 2000US-0236368.
PR 29-SEP-2000; 2000US-0236369.
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PR 02-OCT-2000; 2000US-0237039.
PR 02-OCT-2000; 2000US-0237040.
PR 13-OCT-2000; 2000US-0239935.
PR 13-OCT-2000; 2000US-0239937.
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PR 20-OCT-2000; 2000US-0241785.
PR 20-OCT-2000; 2000US-0241786.
PR 20-OCT-2000; 2000US-0241787.
PR 20-OCT-2000; 2000US-0241808.
PR 20-OCT-2000; 2000US-0241809.
PR 01-NOV-2000; 2000US-0244826.
PR 01-NOV-2000; 2000US-0244817.
PR 08-NOV-2000; 2000US-0246474.
PR 08-NOV-2000; 2000US-0246475.
PR 08-NOV-2000; 2000US-0246476.
PR 08-NOV-2000; 2000US-0246477.
PR 08-NOV-2000; 2000US-0246478.
PR 08-NOV-2000; 2000US-0246523.
PR 08-NOV-2000; 2000US-0246524.
PR 08-NOV-2000; 2000US-0246525.
PR 08-NOV-2000; 2000US-0246526.
PR 08-NOV-2000; 2000US-0246527.
PR 08-NOV-2000; 2000US-0246528.
PR 08-NOV-2000; 2000US-0246532.
PR 08-NOV-2000; 2000US-0246609.
PR 08-NOV-2000; 2000US-0246610.
PR 08-NOV-2000; 2000US-0246611.
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PR 17-NOV-2000; 2000US-0249244.
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PR 17-NOV-2000; 2000US-0249300.
PR 01-DEC-2000; 2000US-0250160.
PR 01-DEC-2000; 2000US-0250391.
PR 05-DEC-2000; 2000US-0251030.
PR 05-DEC-2000; 2000US-0251988.
PR 05-DEC-2000; 2000US-0256719.
PR 06-DEC-2000; 2000US-0251479.
PR 08-DEC-2000; 2000US-0251856.
PR 08-DEC-2000; 2000US-0251868.
PR 08-DEC-2000; 2000US-0251869.
PR 08-DEC-2000; 2000US-0251989.
PR 11-DEC-2000; 2000US-0251990.
PR 05-JAN 2001; 2000US-0254097.
XX 05-JAN 2001; 2001US-0259678.
XX (HUMA-) HUMAN GENOME SCI INC.
XX
XX Rosen CA, Barash SC, Ruben SM;
PI WPI; 2001-483426/52.
XX
XX Nucleic acids encoding human immune/hematopoietic antigen polypeptides,
XX useful for preventing, diagnosing and/or treating cancers and
PT

PT metastasis -
XX Disclosure: SEQ ID NO 41095; 3071pp + Sequence Listing; English.
XX
CC AAK54951 to AAK64702 encode the human immune/haematopoietic antigen (I)
CC amino acid sequences given in AAK82170 to AAK91921. (I) have cytostatic
CC activity, and can be used in gene therapy and vaccine production. (I)
CC proteins and polynucleotides may be used in the prevention, diagnosis and
CC treatment of diseases associated with inappropriate (I) expression. For
CC example, they may be used to treat disorders associated with decreased
CC expression by rectifying mutations or deletions in a patient's genome
CC that affect the activity of (I) by expressing inactive proteins or to
CC supplement the patients own production of (I). Additionally, (I)
CC polynucleotides may be used to produce the secreted (I), by inserting
CC the nucleic acids into a host cell and culturing the cell to express the
CC protein. (I) proteins and polynucleotides may be used to prevent,
CC diagnose and treat immune/haematopoietic-related diseases, especially
CC cancers and cancer metastases of haematopoietic-derived cells. AAK64703
CC to AAK87694 represent human immune/haematopoietic antigen genomic
CC sequences from the present invention. AAK54942 to AAK54950 and AAK82169
CC represent sequences used in the exemplification of the present invention.
XX
XX Sequence 1611 BP; 462 A; 353 C; 296 G; 500 T; 0 other;

Query Match 15.6%; Score 36.4; DB 22; Length 1611;
Best Local Similarity 56.8%; Pred. No. 0.19;
Matches 67; Conservative 0; Mismatches 51; Indels 0; Gaps 0;

QY 87 GCTGAGGAGCTTTTCTGACAAATTCCTCTATGAGTCCAGCTTCCTGGAAATGCTTGA 146
DB 603 GATGATGACTGCTACTGTGCATATATAATCCACTAAATCCAGCTACAGGAACCTCGTGG 544

QY 147 AAGAGCTCTCCCTCCCTCCCTCCCTCCCTCCCTCCCTCCCTCCCTCCCTCCCTCCCTCC 204
DB 543 AACTGTGGCCATGCAATTTTTTTTCTTTAAAGACCAAGTGTGATAGTAGGCCATGCA 486

RESULT 11
AAC63412
ID AAC63412 standard; cDNA; 1146 BP.
XX
AC AAC63412;
XX
DT 09-FEB-2001 (first entry)
XX
DE Human secreted protein coding sequence SEQ ID NO: 13.
XX
KW Cytostatic; immunosuppressive; nootropic; neuroprotective; antiviral;
KW antiallergic; hepatotropic; antidiabetic; antiinflammatory; antiulcer;
KW vulnerary; anticonvulsant; antibacterial; antifungal; antiparasitic;
KW cardiant; gene therapy; cancer; immune disorder; cardiovascular disorder;
KW neurological disease; infection; human; secreted protein; ss.
XX
OS Homo sapiens.
XX
PN WO200061779-A1.
XX
PD 19-OCT-2000.
XX
PF 06-APR-2000; 2000WO-US09068.
XX
PR 09-APR-1999; 99US-0128699.
XX
PR 20-JAN-2000; 2000US-0177050.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
PI Rosen CA, Ruben SM, Komatsoulis G;
XX
XX WPI; 2000-647424/62.
DR P-PSDB; AAB29804.
XX
XX Isolated nucleic acid molecule encoding a human secreted protein is
PT used in preventing, treating or ameliorating a medical condition -
PT

XX Claim 1; Page 392-393; 495pp; English.
XX
XX The invention relates to the isolation of genes AAC63410-C63458 encoding
CC 49 human secreted proteins AAB29802-B29850. The genes can be used to
CC generate fusion proteins by linking to the gene for the human
CC immunoglobulin G Fc portion (SEQID1) for increasing the stability of
CC the fusion protein as compared to the human protein only. The genes and
CC proteins are useful for preventing, ameliorating or treating medical
CC conditions, e.g. by protein or gene therapy. The genes are isolated
CC from a range of human tissues disclosed in the specification. The
CC nucleic acids, proteins, antibodies and (ant)agonists are useful in
CC the diagnosis, treatment and prevention of: (a) cancer, e.g. breast
CC and ovarian cancer, and other cancers of the adrenal gland, bone, bone
CC marrow, breast, gastrointestinal tract, liver, lung, or urogenital;
CC (b) immune disorders e.g. Addison's disease, allergies, autoimmune
CC disease, multiple sclerosis, rheumatoid arthritis and ulcerative
CC colitis; (c) cardiovascular disorders such as myocardial ischaemias; (d)
CC wound healing; (e) neurological diseases e.g. cerebral anoxia and
CC epilepsy; and (f) infectious diseases such as viral, bacterial, fungal
CC and parasitic infections.
XX
XX Sequence 1146 BP; 370 A; 215 C; 239 G; 322 T; 0 other;
XX
Query Match 14.9%; Score 34.8; DB 21; Length 1146;
Best Local Similarity 55.9%; Pred. No. 0.53;
Matches 66; Conservative 0; Mismatches 52; Indels 0; Gaps 0;

QY 87 GCTGAGGAGCTTTTCTGACAAATTCCTCTATGAGTCCAGCTTCCTGGAAATGCTTGA 146
DB 839 GATGATGACTGCTACTGTGCATATATAATCCACTAAATCCAGCTACAGGAACCTCGTGG 898

QY 147 AAGAGCTCTCCCTCCCTCCCTCCCTCCCTCCCTCCCTCCCTCCCTCCCTCCCTCCCTCC 204
DB 899 AACTGTGGCCATGCAATTTTTTTTCTTTAAAGACCAAGTGTGATAGTAGGCCATGCA 956

RESULT 12
AAC63727/C
ID AAC63727 standard; cDNA; 550 BP.
XX
AC AAC63727;
XX
DT 19-FEB-2001 (first entry)
XX
DE Cat flea hindgut and Malpighian tubule (HMT) cDNA, SEQ ID NO:222.
XX
KW Cat flea; hindgut and Malpighian tubule nucleic acid; HMT;
KW flea infestation; vaccine; antiparasitic; therapeutic target;
KW diagnosis; detection; ss.
XX
OS Ctenocephalides felis.
XX
PN WO200061621-A2.
XX
PD 19-OCT-2000.
XX
PF 07-APR-2000; 2000WO-US09437.
XX
PR 09-APR-1999; 99US-0128704.
XX
PA (HESK-) HESKA CORP.
XX
PI Brandt KS, Gaines PJ, Stinchcomb DT, Wisniewski N;
XX
XX WPI; 2000-656323/63.
XX
XX Flea Malpighian tubule and head and nerve cord tissue derived nucleic
PT acids useful for the prevention, diagnosis and treatment of flea
XX infestations -
XX
XX Claim 26; Page 319; 964pp; English.
XX

XX The invention relates to novel cat flea (*Ctenocephalides felis*) nucleic
CC acids which are expressed in hindgut (HNC) tissue. The invention also relates to the
CC or head and nerve cord (HNC) tissue. The invention also relates to the
CC encoded proteins. The invention additionally encompasses expression
CC constructs, recombinant viruses and recombinant cells comprising the
CC nucleic acids of the invention, a method of identifying inhibitors of
CC the proteins, and compositions comprising the inhibitors for
CC administration to an animal. The nucleic acids, and the proteins they
CC encode may be used in the prevention, treatment and diagnosis of diseases
CC associated with flea infestations. For example, the nucleic acids may be
CC used to produce an HMT or HNC protein according to standard recombinant
CC DNA methodology by inserting the nucleic acids into a host cell and
CC culturing the cell to express the protein. The HMT and HNC nucleic acids
CC may also be used as DNA probes in diagnostic assays (e.g., PCR) to detect
CC and quantitate the presence of cat flea or other homologous nucleic acid
CC sequences in samples. They may also be used to study the expression and
CC function of the proteins and their role in metabolism. The HMT and HNC
CC proteins may be used as antigens in the production of specific
CC antibodies, and in assays to identify modulators (agonists and
CC antagonists) of HMT and/or HNC protein expression and activity. The
CC anti-HMT/HNC protein antibodies and antagonists may also be used to
CC down-regulate protein expression and activity. The antibodies may also be
CC used as diagnostic agents for detecting the presence of flea polypeptides
CC in samples (e.g., by enzyme linked immunosorbent assay (ELISA)). The
CC present sequence represents a cat flea HMT cDNA of the invention.

XX Sequence 550 BP; 153 A; 107 C; 144 G; 138 T; 8 other;

Query Match 14.3%; Score 33.4; DB 21; Length 550;

Best Local Similarity 58.6%; Pred. No. 1.1;

Matches 58; Conservative 0; Mismatches 41; Indels 0; Gaps 0;

Qy 76 TTCAACTGAGCTGAGGAGTCTTTCTGACAAATTCCTCTATGATCCAGTCCGCTCCG 135

Db 407 TTTCACAGATGTCATCTGGCTTTGACAGACAGCGCGACATGTCTCCAGTGCATT 348

Qy 136 GAATTCCTGTAAGAGCTCTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 174

Db 347 GCATCTGTAGCATCGTTCAGCCCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 309

XX

RESULT 13

AA544656/c

ID AA544656 standard; DNA; 4885 BP.

XX

AA544656;

XX

18-DEC-2001 (first entry)

XX

Human full-length polynucleotide sequence #81.

XX

Mammal; human; rhesus monkey; baker's yeast; fission yeast; Norway rat;

Kw mouse; Chinese hamster; African clawed frog; fruit fly; dog; leukaemia;

Kw cancer; lymphoma; neuroblastoma; autoimmune disorder; cell proliferation;

Kw nervous system disorder; inflammatory disorder; cell differentiation; GS;

Kw angiogenesis; stem cell growth factor; activin; inhibitor; cartilage; burn;

Kw genetic disorder; bone regeneration; tendon; ligament; tissue repair;

Kw cytostatic; antirheumatic; antiarthritic; vasotrophic; antiparkinsonian;

Kw antibacterial; immunosuppressive; vasotrophic; antiparkinsonian;

Kw neuroprotective; osteopathic; antidiabetic; antiasthmatic; anti-allergic;

Kw immunostimulant; analgesic; gene therapy.

XX

Homo sapiens.

OS

XX

HO200164834-A2.

XX

07-SEP-2001.

XX

26-FEB-2001; 2001WO-US04926.

XX

28-FEB-2000; 2000US-0515126.

XX

PR

PR 18-MAY-2000; 2000US-0577409.
PR 17-JUN-2000; 2000US-0597707.
PR 14-JUL-2000; 2000US-0616807.
PR 19-SEP-2000; 2000US-0664641.
XX (HYSE-) HYSEQ INC.
XX
XX Tang YT, Liu C, Zhou P, Asundi V, Zhang J, Zhao QA, Ren F;
XX Xue AJ, Yang Y, Wehrman T, Wang J, Ma Y, Wang D, Chen R, Xu C;
XX Dmanac R;
XX
XX WPI; 2001-589862/66.
XX P-PSDB; AAU27756.
XX
XX Novel polypeptides and nucleic acids obtained from cDNA libraries
XX prepared from various human tissues, for diagnosis, treatment of
XX cancer, neurological, inflammatory disorders and for use in arrays for
XX detection.
XX
XX Claim 1; SEQ ID No 81; 153pp; English.
XX
XX Sequences AA544576-AA544919 represent full-length polynucleotides and
XX contig polynucleotides encoding polypeptides of the invention. The DNA
XX and protein sequences are useful for the treatment, diagnosis and
XX prevention of various types of disorder in a mammalian subject such as a
XX human, dog, monkey, mouse, hamster or rat. The disorders include cancers
XX such as leukaemia, lymphoma and neuroblastoma, autoimmune disorders such
XX as multiple sclerosis, connective tissue disease, rheumatoid arthritis,
XX diabetes mellitus, allergic rhinitis, asthma and eczema, nervous system
XX disorders such as Parkinson's disease, Alzheimer's disease, Huntington's
XX chorea, amyotrophic lateral sclerosis, spinal muscular atrophy and
XX Wernicke disease, inflammatory disorders such as nephritis, Crohn's
XX disease, ischaemia-reperfusion injury, shock, sepsis and inflammatory
XX bowel disease. The sequences exhibit activity relating to angiogenesis,
XX cell proliferation, cell differentiation, stem cell growth factor,
XX activin or inhibin. Therefore, they can be used to manipulate stem cells
XX in culture to give rise to neuroepithelial cells that can be used to
XX augment or replace cells damaged by illness, accidental damage or genetic
XX disorders. The sequences may also be used for regeneration of bone,
XX cartilage, tendons and ligaments and in tissue repair and burn healing.
XX Note: Some sequences for this patent did not form part of the printed
XX specification, but were obtained in electronic format directly from WIPO
XX at ftp.wipo.int/pub/published_pct_sequences.
XX
XX Sequence 4885 BP; 1482 A; 920 C; 1159 G; 1324 T; 0 other;

Query Match 13.9%; Score 32.6; DB 22; Length 4885;

Best Local Similarity 51.7%; Pred. No. 5;

Matches 74; Conservative 0; Mismatches 69; Indels 0; Gaps 0;

Qy 59 CAGGGCGGGTATGACTTTGCACTGAGGCTGAGGAGGAGTCTTTTTCGACAAATTCCTCT 118

Db 1268 CTGACACCTGCGCTGAGTTCACCTTGAGTCTGAGGCGGTCTTTCTCTCTCTCTCTCT 1209

Qy 119 ATGAGTCTGAGTCTCTGGAATTCGTTGAAAAGCTCTGCTCTCTCTCTCTCTCTCTCT 178

Db 1208 CGAGATGCTGCT 1149

Qy 179 GGACACCGCTGCACCTCCACCAT 201

Db 1148 TTGGGGCGGCTGGAGTCTCTTCAT 1126

XX

RESULT 14

AAK70447

ID AAK70447 standard; DNA; 27082 BP.

XX

AAK70447;

XX

06-NOV-2001 (first entry)

XX

Human immune/haematopoietic antigen genomic sequence SEQ ID NO:25259.

XX

XX

KW	Human; immune; haematopoietic; immune/haematopoietic antigen; cancer;	25-SEP-2000; 2000US-0234997.	PR
KW	cytostatic; gene therapy; vaccine; metastasis; ds.	25-SEP-2000; 2000US-0234998.	PR
XX	Homo sapiens.	26-SEP-2000; 2000US-0234984.	PR
XX	WO200157182-A2.	27-SEP-2000; 2000US-0235834.	PR
XX	09-AUG-2001.	27-SEP-2000; 2000US-0235836.	PR
XX	17-JAN-2001; 2001WO-US01354.	29-SEP-2000; 2000US-0236327.	PR
XX	31-JAN-2000; 2000US-0179065.	29-SEP-2000; 2000US-0236367.	PR
XX	04-FEB-2000; 2000US-0180628.	29-SEP-2000; 2000US-0236368.	PR
XX	24-FEB-2000; 2000US-0184664.	29-SEP-2000; 2000US-0236369.	PR
XX	02-MAR-2000; 2000US-0186350.	29-SEP-2000; 2000US-0236370.	PR
XX	16-MAR-2000; 2000US-0189874.	29-SEP-2000; 2000US-0236370.	PR
XX	17-MAR-2000; 2000US-0190076.	02-OCT-2000; 2000US-0236802.	PR
XX	18-APR-2000; 2000US-0198123.	02-OCT-2000; 2000US-0237037.	PR
XX	19-MAY-2000; 2000US-0205515.	02-OCT-2000; 2000US-0237038.	PR
XX	07-JUN-2000; 2000US-0209467.	02-OCT-2000; 2000US-0237039.	PR
XX	28-JUN-2000; 2000US-0214886.	02-OCT-2000; 2000US-0237040.	PR
XX	30-JUN-2000; 2000US-0215135.	13-OCT-2000; 2000US-0239335.	PR
XX	07-JUL-2000; 2000US-0216647.	13-OCT-2000; 2000US-0239337.	PR
XX	07-JUL-2000; 2000US-0216880.	20-OCT-2000; 2000US-0240960.	PR
XX	11-JUL-2000; 2000US-0217487.	20-OCT-2000; 2000US-0241221.	PR
XX	11-JUL-2000; 2000US-0217496.	20-OCT-2000; 2000US-0241785.	PR
XX	14-JUL-2000; 2000US-0218290.	20-OCT-2000; 2000US-0241786.	PR
XX	26-JUL-2000; 2000US-0220963.	20-OCT-2000; 2000US-0241787.	PR
XX	26-JUL-2000; 2000US-0220964.	20-OCT-2000; 2000US-0241808.	PR
XX	14-AUG-2000; 2000US-0224518.	20-OCT-2000; 2000US-0241809.	PR
XX	14-AUG-2000; 2000US-0224519.	20-OCT-2000; 2000US-0241826.	PR
XX	14-AUG-2000; 2000US-0225213.	01-NOV-2000; 2000US-0244517.	PR
XX	14-AUG-2000; 2000US-0225214.	08-NOV-2000; 2000US-0246474.	PR
XX	14-AUG-2000; 2000US-0225267.	08-NOV-2000; 2000US-0246475.	PR
XX	14-AUG-2000; 2000US-0225268.	08-NOV-2000; 2000US-0246476.	PR
XX	14-AUG-2000; 2000US-0225270.	08-NOV-2000; 2000US-0246477.	PR
XX	14-AUG-2000; 2000US-0225447.	08-NOV-2000; 2000US-0246478.	PR
XX	14-AUG-2000; 2000US-0225757.	08-NOV-2000; 2000US-0246523.	PR
XX	14-AUG-2000; 2000US-0225758.	08-NOV-2000; 2000US-0246524.	PR
XX	14-AUG-2000; 2000US-0225759.	08-NOV-2000; 2000US-0246525.	PR
XX	18-AUG-2000; 2000US-0226279.	08-NOV-2000; 2000US-0246526.	PR
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XX	22-AUG-2000; 2000US-0227182.	08-NOV-2000; 2000US-0246532.	PR
XX	23-AUG-2000; 2000US-0227009.	08-NOV-2000; 2000US-0246609.	PR
XX	30-AUG-2000; 2000US-0228024.	08-NOV-2000; 2000US-0246610.	PR
XX	01-SEP-2000; 2000US-0229287.	08-NOV-2000; 2000US-0246611.	PR
XX	01-SEP-2000; 2000US-0229287.	17-NOV-2000; 2000US-0249210.	PR
XX	01-SEP-2000; 2000US-0229343.	17-NOV-2000; 2000US-0249211.	PR
XX	01-SEP-2000; 2000US-0229344.	17-NOV-2000; 2000US-0249212.	PR
XX	01-SEP-2000; 2000US-0229345.	17-NOV-2000; 2000US-0249213.	PR
XX	05-SEP-2000; 2000US-0229509.	17-NOV-2000; 2000US-0249214.	PR
XX	05-SEP-2000; 2000US-0229513.	17-NOV-2000; 2000US-0249215.	PR
XX	06-SEP-2000; 2000US-0230437.	17-NOV-2000; 2000US-0249216.	PR
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XX	06-SEP-2000; 2000US-0230438.	17-NOV-2000; 2000US-0249218.	PR
XX	08-SEP-2000; 2000US-0231242.	17-NOV-2000; 2000US-0249244.	PR
XX	08-SEP-2000; 2000US-0231243.	17-NOV-2000; 2000US-0249245.	PR
XX	08-SEP-2000; 2000US-0231244.	17-NOV-2000; 2000US-0249264.	PR
XX	08-SEP-2000; 2000US-0231413.	17-NOV-2000; 2000US-0249265.	PR
XX	08-SEP-2000; 2000US-0231414.	17-NOV-2000; 2000US-0249297.	PR
XX	08-SEP-2000; 2000US-0232080.	17-NOV-2000; 2000US-0249299.	PR
XX	08-SEP-2000; 2000US-0232081.	17-NOV-2000; 2000US-0249300.	PR
XX	12-SEP-2000; 2000US-0231968.	01-DEC-2000; 2000US-0250160.	PR
XX	14-SEP-2000; 2000US-0232397.	01-DEC-2000; 2000US-0250391.	PR
XX	14-SEP-2000; 2000US-0232398.	05-DEC-2000; 2000US-0251030.	PR
XX	14-SEP-2000; 2000US-0232399.	05-DEC-2000; 2000US-0251988.	PR
XX	14-SEP-2000; 2000US-0232400.	05-DEC-2000; 2000US-0256719.	PR
XX	14-SEP-2000; 2000US-0232401.	06-DEC-2000; 2000US-0251479.	PR
XX	14-SEP-2000; 2000US-0232401.	08-DEC-2000; 2000US-0251856.	PR
XX	14-SEP-2000; 2000US-0233063.	08-DEC-2000; 2000US-0251868.	PR
XX	14-SEP-2000; 2000US-0233064.	08-DEC-2000; 2000US-0251869.	PR
XX	14-SEP-2000; 2000US-0233065.	08-DEC-2000; 2000US-0251989.	PR
XX	21-SEP-2000; 2000US-0234223.	08-DEC-2000; 2000US-0251990.	PR
XX	21-SEP-2000; 2000US-0234274.	11-DEC-2000; 2000US-0254097.	PR

PR	13-OCT-2000;	2000US-0239937.
PR	20-OCT-2000;	2000US-0240960.
PR	20-OCT-2000;	2000US-0241221.
PR	20-OCT-2000;	2000US-0241785.
PR	20-OCT-2000;	2000US-0241786.
PR	20-OCT-2000;	2000US-0241787.
PR	20-OCT-2000;	2000US-0241808.
PR	20-OCT-2000;	2000US-0241809.
PR	20-OCT-2000;	2000US-0241826.
PR	01-NOV-2000;	2000US-0244617.
PR	08-NOV-2000;	2000US-0246474.
PR	08-NOV-2000;	2000US-0246475.
PR	08-NOV-2000;	2000US-0246476.
PR	08-NOV-2000;	2000US-0246477.
PR	08-NOV-2000;	2000US-0246478.
PR	08-NOV-2000;	2000US-0246524.
PR	08-NOV-2000;	2000US-0246524.
PR	08-NOV-2000;	2000US-0246524.
PR	08-NOV-2000;	2000US-0246526.
PR	08-NOV-2000;	2000US-0246526.
PR	08-NOV-2000;	2000US-0246528.
PR	08-NOV-2000;	2000US-0246532.
PR	08-NOV-2000;	2000US-0246609.
PR	08-NOV-2000;	2000US-0246610.
PR	08-NOV-2000;	2000US-0246611.
PR	17-NOV-2000;	2000US-0249213.
PR	17-NOV-2000;	2000US-0249217.
PR	17-NOV-2000;	2000US-0249208.
PR	17-NOV-2000;	2000US-0249208.
PR	17-NOV-2000;	2000US-0249210.
PR	17-NOV-2000;	2000US-0249211.
PR	17-NOV-2000;	2000US-0249212.
PR	17-NOV-2000;	2000US-0249213.
PR	17-NOV-2000;	2000US-0249214.
PR	17-NOV-2000;	2000US-0249215.
PR	17-NOV-2000;	2000US-0249216.
PR	17-NOV-2000;	2000US-0249217.
PR	17-NOV-2000;	2000US-0249218.
PR	17-NOV-2000;	2000US-0249244.
PR	17-NOV-2000;	2000US-0249245.
PR	17-NOV-2000;	2000US-0249245.
PR	17-NOV-2000;	2000US-0249264.
PR	17-NOV-2000;	2000US-0249265.
PR	17-NOV-2000;	2000US-0249297.
PR	17-NOV-2000;	2000US-0249299.
PR	17-NOV-2000;	2000US-0249300.
PR	17-NOV-2000;	2000US-0249300.
PR	01-DEC-2000;	2000US-0250160.
PR	01-DEC-2000;	2000US-0250391.
PR	05-DEC-2000;	2000US-0251030.
PR	05-DEC-2000;	2000US-0251988.
PR	05-DEC-2000;	2000US-0256719.
PR	06-DEC-2000;	2000US-0251479.
PR	08-DEC-2000;	2000US-0251856.
PR	08-DEC-2000;	2000US-0251868.
PR	08-DEC-2000;	2000US-0251869.
PR	08-DEC-2000;	2000US-0251989.
PR	08-DEC-2000;	2000US-0251990.
PR	11-DEC-2000;	2000US-0254097.
PR	05-JAN-2001;	2001US-02535678.
XX	(HUMA-) HUMAN GENOME SCI INC	
PA		

```

CC including cancer. The present sequence is a genomic sequence encoding a
CC protein of the invention.
XX
SQ Sequence 13216 BP; 3041 A; 3400 C; 3243 G; 3532 T; 0 other;
      Query Match      13.7%; Score 32; DB 22; Length 13216;
      Best Local Similarity 54.3%; Pred. No. 12;
      Matches 65; Conservative 0; Mismatches 55; Indels 0; Gaps 0;
QY 76 TTGCAACTGAAGCTCAAGGAGTCTTTTCTGCAGAAATTCCTCTATGAGTCCAGCTTCCTG 135
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DB 9407 TAGCCCTGACCTCTTGGAGTGTCTTTCGACTATTCCTTCGAGGTGCCCATGGAG 9466
QY 136 GAAATGTTGAAAGCTCTGCCTCTCTCCATCTCCCTTCAGGACACAGCTACCCCTC 195
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 9467 CAAATTCATTGGCATCTTTACCTTCCTCCCTCCCAAAACCAATTTGGAGGCTGGTTAGCCCC 9526

Search completed: May 1, 2003, 03:08:30
Job time : 173.776 secs

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; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 180 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-09-092-296-3

Query Match 100.0%; Score 180; DB 9; Length 180;
Best Local Similarity 100.0%; Pred. No. 5.9e-54; Indels 0; Gaps 0;
Matches 180; Conservative 0; Mismatches 0;
QY 1 CAGGAGCGCAGTGGCCACTATGGGCTCTGGGCTGCCCTTGTCTCTCTTGAACCTCTCT 60
Db 1 CAGGAGCGCAGTGGCCACTATGGGCTCTGGGCTGCCCTTGTCTCTCTTGAACCTCTCT 60
QY 61 TGGCAGCTCACATGGAACAGCGCGGGTATGACTTTGCAACTGAAGCTGAAGGAGTCTTT 120
Db 61 TGGCAGCTCACATGGAACAGCGCGGGTATGACTTTGCAACTGAAGCTGAAGGAGTCTTT 120
QY 121 TCTGACAAATTCCTCTATGAGTCCAGCTTCTGGAATTCCTGAAAGCTCTGCCTCTCT 180
Db 121 TCTGACAAATTCCTCTATGAGTCCAGCTTCTGGAATTCCTGAAAGCTCTGCCTCTCT 180

RESULT 2

US-09-092-296-5
; Sequence 5, Application US/09092296
; Publication No. US200201881141
; GENERAL INFORMATION:
; APPLICANT: BILLING-MEDEL, PATRICIA
; APPLICANT: COHEN, MAURICE
; APPLICANT: COLPITTS, TRACEY L.
; APPLICANT: FRIEDMAN, PAULA N.
; APPLICANT: KLASS, MICHAEL R.
; APPLICANT: RUSSELL, JOHN C.
; APPLICANT: STROUPE, STEPHEN D.
; TITLE OF INVENTION: REAGENTS AND METHODS USEFUL
; FOR DETECTING DISEASES OF THE LUNG
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Abbott Laboratories
; STREET: 100 Abbott Park Road
; CITY: Abbott Park
; STATE: IL
; COUNTRY: USA
; ZIP: 60064-3500
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/092,296
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/048,810
; FILING DATE: 05-JUN-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Becker, Cheryl L.
; REGISTRATION NUMBER: 35,441
; REFERENCE/DOCKET NUMBER: 6104.US.01
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 847/935-1729
; TELEFAX: 847/938-2623
; TELEX:
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 389 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear

US-09-092-296-5

Query Match 100.0%; Score 180; DB 9; Length 389;
Best Local Similarity 100.0%; Pred. No. 7.7e-54; Indels 0; Gaps 0;
Matches 180; Conservative 0; Mismatches 0;
QY 1 CAGGAGCGCAGTGGCCACTATGGGCTCTGGGCTGCCCTTGTCTCTCTTGAACCTCTCT 60
Db 1 CAGGAGCGCAGTGGCCACTATGGGCTCTGGGCTGCCCTTGTCTCTCTTGAACCTCTCT 60
QY 61 TGGCAGCTCACATGGAACAGCGCGGGTATGACTTTGCAACTGAAGCTGAAGGAGTCTTT 120
Db 61 TGGCAGCTCACATGGAACAGCGCGGGTATGACTTTGCAACTGAAGCTGAAGGAGTCTTT 120
QY 121 TCTGACAAATTCCTCTATGAGTCCAGCTTCTGGAATTCCTGAAAGCTCTGCCTCTCT 180
Db 121 TCTGACAAATTCCTCTATGAGTCCAGCTTCTGGAATTCCTGAAAGCTCTGCCTCTCT 180

RESULT 3

US-09-092-296-6
; Sequence 6, Application US/09092296
; Publication No. US200201881141
; GENERAL INFORMATION:
; APPLICANT: BILLING-MEDEL, PATRICIA
; APPLICANT: COHEN, MAURICE
; APPLICANT: COLPITTS, TRACEY L.
; APPLICANT: FRIEDMAN, PAULA N.
; APPLICANT: KLASS, MICHAEL R.
; APPLICANT: RUSSELL, JOHN C.
; APPLICANT: STROUPE, STEPHEN D.
; TITLE OF INVENTION: REAGENTS AND METHODS USEFUL
; FOR DETECTING DISEASES OF THE LUNG
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Abbott Laboratories
; STREET: 100 Abbott Park Road
; CITY: Abbott Park
; STATE: IL
; COUNTRY: USA
; ZIP: 60064-3500
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/092,296
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/048,810
; FILING DATE: 05-JUN-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Becker, Cheryl L.
; REGISTRATION NUMBER: 35,441
; REFERENCE/DOCKET NUMBER: 6104.US.01
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 847/935-1729
; TELEFAX: 847/938-2623
; TELEX:
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 413 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-09-092-296-6

Query Match 99.1%; Score 178.4; DB 9; Length 413;
Best Local Similarity 99.4%; Pred. No. 2.9e-53;
Matches 179; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY	1	CAGGAGCGCAGTGGCCACATATGGGTCGTGGCTGCCCTTGTCTCTCTTGA	60
Db	28	CAGGAGCGAGTGGCCACATATGGGTCGTGGCTGCCCTTGTCTCTTGA	87
QY	61	TGGCAGCTCACATGGAACAGGCGCGGTATGACTTTGGCACTGAAGGAGCTTTT	120
Db	88	TGGCAGCTCACATGGAACAGGCGCGGTATGACTTTGCACTGAAGGAGCTTTT	147
QY	121	TCTGCAAGTTCCTCTCTATGAGTCCAGCTTCTGGAAATGCTTGAAAGCTCTGC	180
Db	148	TCTGCAAAATTCCTCTATGAGTCCAGCTTCTGGAAATGCTTGAAAGCTCTGC	207

RESULT A

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US-09-992-598-362
; Sequence 362, Application US/09992598
; Patent No. US20020160384A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Collin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2730P1C20
; CURRENT APPLICATION NUMBER: US/09/992,598
; CURRENT FILING DATE: 2001-11-14
; PRIOR APPLICATION NUMBER: 60/049787
; PRIOR FILING DATE: 1997-06-16
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/065186
; PRIOR FILING DATE: 1997-11-12
; PRIOR APPLICATION NUMBER: 60/065311
; PRIOR FILING DATE: 1997-11-13
; PRIOR APPLICATION NUMBER: 60/066770
; PRIOR FILING DATE: 1997-11-24
; PRIOR APPLICATION NUMBER: 60/075945
; PRIOR FILING DATE: 1998-02-25
; PRIOR APPLICATION NUMBER: 60/078910
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/083322
; PRIOR FILING DATE: 1998-04-28
; PRIOR APPLICATION NUMBER: 60/084600
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; PRIOR APPLICATION NUMBER: 60/087106
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; PRIOR APPLICATION NUMBER: 60/087609
; PRIOR FILING DATE: 1998-06-02
; PRIOR APPLICATION NUMBER: 60/087759
; PRIOR FILING DATE: 1998-06-02

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;; PRIOR FILING DATE: 1998-06-19
;; PRIOR APPLICATION NUMBER: 60/089948
;; PRIOR FILING DATE: 1998-06-19
;; PRIOR APPLICATION NUMBER: 60/089952
;; PRIOR FILING DATE: 1998-06-19
;; PRIOR APPLICATION NUMBER: 60/090246
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;; PRIOR FILING DATE: 1998-07-02
;; PRIOR APPLICATION NUMBER: 60/091544
;; PRIOR FILING DATE: 1998-07-01
;; PRIOR APPLICATION NUMBER: 60/091519
;; PRIOR FILING DATE: 1998-07-02
;; PRIOR APPLICATION NUMBER: 60/091626
;; PRIOR FILING DATE: 1998-07-02
;; PRIOR APPLICATION NUMBER: 60/091633
;; PRIOR FILING DATE: 1998-07-02
;; PRIOR APPLICATION NUMBER: 60/091978
;; PRIOR FILING DATE: 1998-07-07
;; PRIOR APPLICATION NUMBER: 60/091982
;; PRIOR FILING DATE: 1998-07-07
;; PRIOR APPLICATION NUMBER: 60/092182
;; PRIOR FILING DATE: 1998-07-09

Query Match 99.1%; Score 178.4; DB 9; Length 422;
Best Local Similarity 99.4%; Pred. No. 2.9e-53;
Matches 179; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CAGGAGCGAGTGGCCACTATGGGGTCTGGGCTGCCCTTTGTCTCTCTTGGACCTCTCT 60
|||||
DB 39 CAGGAGCGAGTGGCCACTATGGGGTCTGGGCTGCCCTTTGTCTCTCTTGGACCTCTCT 98
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QY 61 TGGCAGCTCACATGGAACAGGCGCGGGTATGACTTTGCAACTGAAGAGTCTTT 120
|||||
DB 99 TGGCAGCTCACATGGAACAGGCGCGGGTATGACTTTGCAACTGAAGAGTCTTT 158
|||||
QY 121 TCTGACAAGTTCCTCTATGAGTCCAGCTTCTGGAATTTGTTGAAAAGCTTCTGCTCTCT 180
|||||
DB 159 TCTGACAAATTCCTCTATGATCCAGCTTCTGGAATTTGTTGAAAAGCTTCTGCTCTCT 218
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RESULT 5
US-09-989-293A-362
; Sequence 362, Application US/09989293A
; Patent No. US2002017164A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tamas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2730P1C66
; CURRENT APPLICATION NUMBER: US/09/989,293A
; CURRENT FILING DATE: 2001-11-20
; PRIOR APPLICATION NUMBER: 60/049787
; PRIOR FILING DATE: 1997-06-16
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/065186
; PRIOR FILING DATE: 1997-11-12
; PRIOR APPLICATION NUMBER: 60/065311
; PRIOR FILING DATE: 1997-11-13
; PRIOR APPLICATION NUMBER: 60/066770
; PRIOR FILING DATE: 1997-11-24
; PRIOR APPLICATION NUMBER: 60/075945
; PRIOR FILING DATE: 1998-02-25
; PRIOR APPLICATION NUMBER: 60/078910
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/083322
; PRIOR FILING DATE: 1998-04-28
; PRIOR APPLICATION NUMBER: 60/084600
; PRIOR FILING DATE: 1998-05-07
; PRIOR APPLICATION NUMBER: 60/087106
; PRIOR FILING DATE: 1998-05-28
; PRIOR APPLICATION NUMBER: 60/087607
; PRIOR FILING DATE: 1998-06-02
; PRIOR APPLICATION NUMBER: 60/087609
; PRIOR FILING DATE: 1998-06-02
; PRIOR APPLICATION NUMBER: 60/087759


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Matches 179; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 CAGAGCGCAGTGGCCACTATGGGCTCTGGGCTGCCCTTGTCTCTCTCTGACCCCTCT 60
DB 39 CAGAGCGCAGTGGCCACTATGGGCTCTGGGCTGCCCTTGTCTCTCTCTGACCCCTCT 98
QY 61 TGGCAGCTCACATGGAACAGCGCCGGGTATGACTTTCGAAGCTGAAGGAGTCTTT 120
DB 99 TGGCAGCTCACATGGAACAGCGCCGGGTATGACTTTCGAAGCTGAAGGAGTCTTT 158
QY 121 TCTGACAAATTCCTCTATGAGTCCAGCTTCTGGAATTCCTGAAAGCTCTGCCCTCT 180
DB 159 TCTGACAAATTCCTCTATGAGTCCAGCTTCTGGAATTCCTGAAAGCTCTGCCCTCT 218

RESULT 6
US-10-063-547-65
; Sequence 65, Application US/10063547
; Publication No. US20020102638A1
; GENERAL INFORMATION:
; APPLICANT: Eaton, Dan L.
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Kijavini, Ivar J.
; APPLICANT: Nepler, Mary A.
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumes, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P2730P1C61
; CURRENT APPLICATION NUMBER: US/09/989,735
; CURRENT FILING DATE: 2001-11-19
; PRIOR APPLICATION NUMBER: 60/049787
; PRIOR FILING DATE: 1997-06-16
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/065186
; PRIOR FILING DATE: 1997-11-12
; PRIOR APPLICATION NUMBER: 60/065311
; PRIOR FILING DATE: 1997-11-13
; PRIOR APPLICATION NUMBER: 60/066770
; PRIOR FILING DATE: 1997-11-24
; PRIOR APPLICATION NUMBER: 60/075945
; PRIOR FILING DATE: 1998-02-25
; PRIOR APPLICATION NUMBER: 60/078910
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/083322
; PRIOR FILING DATE: 1998-04-28
; PRIOR APPLICATION NUMBER: 60/084600
; PRIOR FILING DATE: 1998-05-07
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; PRIOR FILING DATE: 1998-06-04
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; PRIOR FILING DATE: 1998-06-04
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; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/088202
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/088212
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/088217
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/088655

Query Match 99.1%; Score 178.4; DB 9; Length 422;
Best Local Similarity 99.4%; Pred. No. 2.9e-53;
Matches 179; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 CAGAGCGCAGTGGCCACTATGGGCTCTGGGCTGCCCTTGTCTCTCTCTGACCCCTCT 60
DB 39 CAGAGCGCAGTGGCCACTATGGGCTCTGGGCTGCCCTTGTCTCTCTCTGACCCCTCT 98
QY 61 TGGCAGCTCACATGGAACAGCGCCGGGTATGACTTTCGAAGCTGAAGGAGTCTTT 120
DB 99 TGGCAGCTCACATGGAACAGCGCCGGGTATGACTTTCGAAGCTGAAGGAGTCTTT 158
QY 121 TCTGACAAATTCCTCTATGAGTCCAGCTTCTGGAATTCCTGAAAGCTCTGCCCTCT 180
DB 159 TCTGACAAATTCCTCTATGAGTCCAGCTTCTGGAATTCCTGAAAGCTCTGCCCTCT 218

RESULT 7
US-09-989-735-362
; Sequence 362, Application US/09989735
; Publication No. US20020103299A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnovers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
```


APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Kljavin, Ivar J.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Peoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2730P1C19
CURRENT APPLICATION NUMBER: US/09/990,444
PRIOR FILING DATE: 2001-11-14
PRIOR APPLICATION NUMBER: 60/049787
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; PRIOR APPLICATION NUMBER: 60/092182
; PRIOR FILING DATE: 1998-07-09

Query Match 99.1%; Score 178.4; DB 9; Length 422;
Best Local Similarity 99.4%; Pred. No. 2.9e-53;
Matches 179; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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QY 61 TGGCAGCTCACATGGAACAGCGCGGGTATGACCTTTCACACTGAAGCTGAAGGAGTCTTT 120
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 99 TGGCAGCTCACATGGAACAGCGCGGGTATGACCTTTCACACTGAAGCTGAAGGAGTCTTT 158
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 121 TCTGACAGTTCCTCTATGAGTCAGCTTCTCGGAATGCTTGAAGAGCTGTCCTCTCT 180
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 159 TCTGACAAATTCCTCTATGAGTCAGCTTCTCGGAATGCTTGAAGAGCTGTCCTCTCT 218
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

RESULT 9
US-09-989-730-362
; Sequence 362, Application US/09989730
; Publication No. US20020197674A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnovers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman

; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gertlisen, Mary E.
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; APPLICANT: Godowski, Paul J.
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; APPLICANT: Napier, Mary A.
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; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2730P1C69
; CURRENT APPLICATION NUMBER: US/09/989,730
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: PRIOR FILING DATE: 1998-07-09

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Query Match 99.18; Score 178.4; DB 9; Length 422;

BEST LOCAL SIMILARITY 99.4%; FREQ. NO. 2.9E-33;
Matches 179; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CAGGAGCGCAGTGGCCACTATGGGGTCTGGGCTGCCCTTGTCCTCCTCTTGACCCCTCCT 60

Db 39 CAGGAGCGCAGTGGCCACTATGGGGTCTGGGCTGCCCTTGCTCTCCTTGACCCCTCCT 98

QY 61 TGGCAGCTCACATGGAACAGGGCCGGGTATGACTTTGCAACTGAAGCTGAAGGAGTCTTT 120

Db 99 TGGCAGCTCACATGGAAACAGGGCCGGTATGACTTTGCAACTGAAGCTGAAGGAGTCTTT 158

QY 121 TCTGACAAAGTTCCCTCCTATGAGTCCAGCTTCCTGGAATTGCTTGAAAAGCTCTGCCTCCT 180

Db 159 TCTGACAAATTCTCCTATGAGTCCAGCTTCTGGAATTGCTTGAAAAGCTCTGCCTCCT 218

RESULT 10

US-09-990-436-362

US-09-590-430-302
; sequence 362, Application US/09990436

; Publication No. US20020198148A1

GENERAL INFORMATION:

APPLICANT: Ashkenazi, Avi J.

APPLICANT: Baker, Kevin P.

APPLICANT: Botstein, David

; APPLICANT: Desnoyers, Luc

APPLICANT: Eaton, Dan L.

; APPLICANT: Ferrara, Napoleone

APPLICANT: Fong, Sherman
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerritsen, Mary E.
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APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2730P1C14
CURRENT APPLICATION NUMBER: US/09/990,436
CURRENT FILING DATE: 2001-11-14
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; PRIOR APPLICATION NUMBER: 60/092182
; PRIOR FILING DATE: 1998-07-09

Query Match 99.18; Score 178.4; DB 9; Length 422;
Best Local Similarity 99.48; Pred. No. 2.9e-53;
Matches 179; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Db 39 CAGGAGCGCAGTGGCCACTATGGGGTCTGGGCTGCCCGCTTGCTCTCTTGTGACCTGCT 98
QY 61 TGGCAGCTCACATGGAACAGCGCGGCTATGACTTTGCACTGAAGCTGAAGGAGCTCTT 120
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Db 99 TGGCAGCTCACATGGAACAGCGCGGCTATGACTTTGCACTGAAGCTGAAGGAGCTCTT 158
QY 121 TGTGCAAGTTCTCTATGAGTCCAGCTTCTGGAATGCTTGAAGCTCTGCTGCT 180
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Db 159 TGTGCAAAATCTCTATGAGTCCAGCTTCTGGAATGCTTGAAGCTCTGCTGCT 218

RESULT 11

US-09-991-181-362
; Sequence 362, Application US/09991181
; Publication No. US20020197615A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnovers, Luc
; APPLICANT: Eaton, Dan L.

;
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerlisen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin I.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2730PIC53
; CURRENT APPLICATION NUMBER: US/09/991.181
; CURRENT FILING DATE: 2001-11-16
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; PRIOR APPLICATION NUMBER: 60/088212

APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Fong, Sherman
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Kijavlin, Ivar J.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2730P1C11
CURRENT APPLICATION NUMBER: US/09/993,687
CURRENT FILING DATE: 2002-11-14
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PRIOR FILING DATE: 1997-06-16
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APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Fong, Sherman
APPLICANT: Gerber, Hanspeter
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APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2730P1C38
CURRENT APPLICATION NUMBER: US/09/997,653
CURRENT FILING DATE: 2001-11-15
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; PRIOR FILING DATE: 1998-06-24
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; PRIOR FILING DATE: 1998-07-09

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Query Match          99.1%; Score 178.4; DB 9; Length 422;
Best Local Similarity 99.4%; Pred. No. 2.9e-53;
Matches 179; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CAGGAGCGCAGTGGCCACTATGGGCTGCGGCTGCCCTTGTCTCTCTTGTGACCCCTCT 60
Db 39 CAGGAGCGCAGTGGCCACTATGGGCTGCGGCTGCCCTTGTCTCTCTTGTGACCCCTCT 98

QY 61 TGGCAGCTCACATGGAACAGGCGCGGATGACTTTGCAACTGAAGCTGAAGGAGTCTTT 120
Db 99 TGGCAGCTCACATGGAACAGGCGCGGATGACTTTGCAACTGAAGCTGAAGGAGTCTTT 158

QY 121 TCTGCAAGTCTCTCTATGAGTCCAGCTTCTCGAATTGCTTGAAGCTCTGCTCCT 180
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RESULT 15
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; Sequence 241, Application US/10174590
; Publication No. US2003008352A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.

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; APPLICANT: Chen, Jian
; APPLICANT: Desnoyers, Luc
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Smith, Victoria
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3430R1642
; CURRENT APPLICATION NUMBER: US/10/174,590
; PRIOR APPLICATION DATE: 2002-06-18
; PRIOR APPLICATION REMOVED - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 241
; LENGTH: 422
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-174-590-241

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Best Local Similarity 99.4%; Pred. No. 2.9e-53;
Matches 179; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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QY 61 TGGCAGCTCACATGGAACAGGCGCGGATGACTTTGCAACTGAAGCTGAAGGAGTCTTT 120
Db 99 TGGCAGCTCACATGGAACAGGCGCGGATGACTTTGCAACTGAAGCTGAAGGAGTCTTT 158

QY 121 TCTGCAAGTCTCTCTATGAGTCCAGCTTCTCGAATTGCTTGAAGCTCTGCTCCT 180
Db 159 TCTGCAAAATTCCTCTATGAGTCCAGCTTCTCGAATTGCTTGAAGCTCTGCTCCT 218

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Job time : 50.3673 secs

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; FILING DATE: 14-APR-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/154,915
; FILING DATE: 18-NOV-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/991,997
; FILING DATE: 17-DEC-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Vincent, Matthew P.
; REGISTRATION NUMBER: 36,709
; REFERENCE/DOCKET NUMBER: MIV-071.05
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 832-1299
; TELEFAX: (617) 832-7000
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 580 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 91..480
; PCT-US95-04636-7
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; TITLE OF INVENTION: Cell-Cycle Regulatory Proteins, and Uses
; NUMBER OF SEQUENCES: 10
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: ASCII(text)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/04636
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/346,147
; FILING DATE: 29-NOV-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/306,511
; FILING DATE: 14-SEP-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/248,812
; FILING DATE: 25-MAY-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/227,371
; FILING DATE: 14-APR-1994
;
; TITLE OF INVENTION: Glyceroldehyde-3-phosphate
; DEHYDROGENASE AND NUCLEAR RESTORATION OF CYTOPLASMIC MAL
; NUMBER OF SEQUENCES: 3
; CORRESPONDENCE ADDRESS:
; ADDRESS: SWABEY OGILVY RENAULT
; STREET: 1981 McGill College Ave. - Suite 1600
; CITY: Montreal
; STATE: QC
; COUNTRY: Canada
; ZIP: H3A 2Y3
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/219,194
; FILING DATE: 23-Dec-1998
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/020,553
; FILING DATE: 26-JUN-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Cote, France
; REGISTRATION NUMBER: 4166
; REFERENCE/DOCKET NUMBER: 1770-152*PCT* FC
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 514 845-7126
; TELEFAX: 514-288-8389
; TELEX: <Unknown>
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1091 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-219-194-2
Query Match 15.9%; Score 30.4; DB 4; Length 1091;
Best Local Similarity 57.3%; Pred. No. 0.3;
Matches 55; Conservative 0; Mismatches 41; Indels 0; Gaps 0;

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```

; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 580 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 91..480
; PCT-US95-04636-7
;
; TITLE OF INVENTION: Glyceroldehyde-3-phosphate
; DEHYDROGENASE AND NUCLEAR RESTORATION OF CYTOPLASMIC MAL
; NUMBER OF SEQUENCES: 3
; CORRESPONDENCE ADDRESS:
; ADDRESS: SWABEY OGILVY RENAULT
; STREET: 1981 McGill College Ave. - Suite 1600
; CITY: Montreal
; STATE: QC
; COUNTRY: Canada
; ZIP: H3A 2Y3
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/219,194
; FILING DATE: 23-Dec-1998
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/020,553
; FILING DATE: 26-JUN-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Cote, France
; REGISTRATION NUMBER: 4166
; REFERENCE/DOCKET NUMBER: 1770-152*PCT* FC
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 514 845-7126
; TELEFAX: 514-288-8389
; TELEX: <Unknown>
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1091 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-219-194-2
Query Match 15.9%; Score 30.4; DB 4; Length 1091;
Best Local Similarity 57.3%; Pred. No. 0.3;
Matches 55; Conservative 0; Mismatches 41; Indels 0; Gaps 0;

```


;
;
SEQUENCE CHARACTERISTICS:

GenCore version 5.1.5
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: May 1, 2003, 03:08:45 ; Search time 901.429 Seconds
(without alignments)
3233.964 Million cell updates/sec

Title: US-09-092-296-3

Perfect score: 180

Sequence: 1 CAGGAGCGCAGTGGCCACTA.....CTTGAAAGCTCGCTCCT 180

Scoring table: IDENTITY_NUC

Gap 10.0 , Gapext 1.0

Searched: 16154066 seqs, 8097743376 residues

Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

EST:*

- 1: em_estba:*
- 2: em_esthum:*
- 3: em_estin:*
- 4: em_estmd:*
- 5: em_estov:*
- 6: em_estpl:*
- 7: em_estro:*
- 8: em_hic:*
- 9: gb_est1:*
- 10: gb_est2:*
- 11: gb_hic:*
- 12: gb_est3:*
- 13: gb_est4:*
- 14: gb_est5:*
- 15: em_estfun:*
- 16: em_estom:*
- 17: gb_gss:*
- 18: em_gss_hum:*
- 19: em_gss_inv:*
- 20: em_gss_pln:*
- 21: em_gss_vrt:*
- 22: em_gss_fun:*
- 23: em_gss_man:*
- 24: em_gss_mus:*
- 25: em_gss_other:*
- 26: em_gss_pro:*
- 27: em_gss_rod:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
c 1	180	100.0	449	10	AW293443	AW293443 UI-H-BI2-
2	178.4	99.1	456	12	BG506690	BG506690 601861290
3	176.8	98.2	830	13	BI759796	BI759796 603045679
c 4	166.4	92.4	422	12	BF002050	BF002050 7998c11.x
5	119.6	66.4	895	13	BI820029	BI820029 603037210
6	106.6	59.2	865	13	BI820110	BI820110 603037110

c	7	100.4	55.8	404	9	A1857998	wj69b01.x
		85.8	47.7	361	12	BF521842	UI-R-C2p-
	9	83	46.1	521	10	BB533837	BB533837
		83	46.1	522	10	BB664284	BB664284
c	11	74.2	41.2	552	17	AQ18761	HS_5511_B
c	12	55.6	30.9	328	9	A1136523	UI-R-C2p-
c	13	44.4	24.7	506	17	A2241329	RPCI-23-7
c	14	44.4	24.7	633	17	AZ079350	RPCI-23-4
c	15	36.2	20.1	261	10	BB411111	BB411111
c	16	33.4	18.6	568	17	AQ290553	nxb0037C
c	17	33.2	18.4	533	13	BM317927	FL1_13_CO
c	18	33.2	18.4	709	10	BE355728	DGL_116_G
c	19	32.4	18.0	434	13	BI318611	IP73b11.Y
c	20	32.4	18.0	523	10	AW128453	fe16b05.Y
c	21	32.4	18.0	537	10	AW078074	fe24b05.Y
c	22	32.4	18.0	562	13	BI683276	fe24b05.Y
c	23	32.4	18.0	582	13	BI706799	fg10e03.Y
c	24	32.4	18.0	2252	17	BH770934	LMGT4066
c	25	31.8	17.7	408	10	AW405843	UI-HF-BLO
c	26	31.8	17.7	1143	12	BE871161	601448727
c	27	31.6	17.6	343	10	BB446166	BB446166
c	28	31.6	17.6	468	14	BQ743962	WHE4110.B
c	29	31.6	17.6	550	12	BF779666	3232-2.hi
c	30	31.6	17.6	919	14	BQ228365	AGENCOURT
c	31	31.4	17.4	339	14	F08745	HSC1DB011.n
c	32	31.4	17.4	623	10	BB616110	BB616110
c	33	31.2	17.3	669	17	AG037872	Pan trogl
c	34	31.2	17.3	777	13	BI911281	603062883
c	35	31.2	17.3	1031	14	BQ960402	AGENCOURT
c	36	31	17.2	376	13	BM401493	JH2B05F.S
c	37	31	17.2	389	13	BM401452	JH1B11F.S
c	38	31	17.2	396	10	AV525985	AV525985
c	39	31	17.2	431	13	BM401638	JL1G12F.S
c	40	31	17.2	440	13	BM401560	JH3G08F.S
c	41	31	17.2	472	13	BM401478	JH1G05F.S
c	42	31	17.2	516	13	BM401409	GH038F.Sn
c	43	31	17.2	538	10	BB769028	BB769028
c	44	31	17.2	545	14	T41524	10105.Lambd
c	45	31	17.2	548	13	BM401534	JH3A12F.S

ALIGNMENTS

RESULT 1
AW293443/c
LOCUS AW293443 449 bp mRNA linear EST 16-JAN-2000
DEFINITION UI-H-BI2-ahm-c-08-0-UI.s1 NCI_CGAP_Sub4 Homo sapiens cDNA clone
IMAGE:2727182 3', mRNA sequence.
ACCESSION AW293443
VERSION AW293443.1 GI:6700079
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 449)
AUTHORS NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
The sequence contained an oligo-dT track that was present in the
oligonucleotide that was used to prime the synthesis of first
strand cDNA and therefore this may represent a bonafide poly A
tail. cDNA Library Preparation: M.B. Soares Lab Clone Distribution:
NCI-CGAP clone distribution/INL at:
I.M.A.G.E. Consortium/INL at:
www-bio.llnl.gov/bbrp/image/image.html
Seq primer: M13 Forward
POLFA-res. Location/Qualifiers

source

l. 449

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/organism="Homo sapiens"  
/db_xref="taxon:9606"  
/clone_image="IMAGE:2727182"  
/clone_lib="NCI_CGAP_Sub4"  
/lab_host="DHIOB (Life Technologies)"  
/notes=Vector: p7r73-Pac (Pharmacia) with a modified  
polylinker; Site_1: Not I; Site_2: Eco RI; The  
NCI_CGAP_Sub4 library is a subtracted library derived from  
the NCI_CGAP_Sub2 library which is a subtracted library  
derived from the NCI_CGAP_Sub1 library, which is a  
subtracted library derived from B1. B1 constitutes a  
mixture of 21 normalized or subtracted NCI_CGAP  
libraries: NCI_CGAP_C04, NCI_CGAP_Pr22, NCI_CGAP_Pr28,  
NCI_CGAP_C010, NCI_CGAP_C016, NCI_CGAP_Kid5,  
NCI_CGAP_Kid2, NCI_CGAP_Kid3, NCI_CGAP_Kid11,  
NCI_CGAP_Lym2, NCI_CGAP_Pr2, NCI_CGAP_C08, NCI_CGAP_CLL11,  
NCI_CGAP_Lym2, NCI_CGAP_Pr2, NCI_CGAP_C08, NCI_CGAP_CLL11,  
NCI_CGAP_Ly22, NCI_CGAP_Pr3, NCI_CGAP_Ly5  
NCI_CGAP_Ly24, NCI_CGAP_Ly13, NCI_CGAP_C04, NCI_CGAP_C06,  
NCI_CGAP_Pr25, these 21 libraries were pooled and a  
single-stranded DNA preparation of the resulting mixture  
was used as a tracer in a subtractive hybridization with  
a driver whose composition is detailed below:  
NCI_CGAP_Kid3 pool 1 : LAM 3324-3337, 3682-3683,  
3758-3803 { IMAGE CloneIDs 1323376-1323911.  
1456008-1456775, 1500552-1502855} NCI_CGAP_Kid5 pool 1 :  
LAM 3338-3342, 3722-3725, 3776-3778 { IMAGE CloneIDs  
1323912-1325831, 1471368-1472903, 1492104-1493235}  
NCI_CGAP_Ly5 pool 1 : LAM 3578-3582, 3851-3854 { IMAGE  
CloneIDs 1414920-1417991, 1520904-1522439} NCI_CGAP_C04  
pool 1 : LAM 3164-3167, 3716-3720, 3733-3735 { IMAGE  
CloneIDs 1257096-1258631, 1469064-1470983, 1475592-1476743}  
NCI_CGAP_Pr22 pool 1 : LAM 2457-2459, 2758-2759,  
3082-3088 { IMAGE CloneIDs 985608-986759, 101192-1101959,  
1217928-1220615} NCI_CGAP_C010 pool 1 : LAM 2644-2653,  
2871-2872 { IMAGE CloneIDs 1057416-1061255, 1144584-1145351}  
Subtraction was performed as previously described  
[Bonadio, Lennon & Soares (1996): Normalization and  
Subtraction: Two Approaches To Facilitate Gene Discovery.  
Genome Research 6, 791-806.]  
TAG_LIB=NCI_CGAP_C04  
TAG_TISSUE=COLON  
TAG_SEQ=CGTCGC"
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BASE COUNT	104 a	108 c	134 q	103 t
140_SEQ-CITCO				

BASE CO
ORIGIN

	Query Match	100.0%;	Score 180;	DB 10;	Length 449;
	Best Local Similarity	100.0%;	Pred. No. 3.7e-43;		
	Matches 180;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
QY	1	CAGGAGCGGACGTGGCCACTATGGGCTGCGGCTGCCCTTGCCTCTCTTGACCCCTCCT	60		
Db	406	CAGGAGCGGACGTGGCCACTATGGGCTGCGGCTGCCCTTGCCTCTTGACCCCTCCT	347		
QY	61	TGGCAGCTCACATGATGACAGGGCCGGGTATGACTTTGGCACTGAACTGAAGCTGAAGAGCTCTTT	120		
Db	346	TGGCAGCTCACATGATGACAGGGCCGGGTATGACTTTGGCACTGAACTGAAGAGCTCTTT	287		
QY	121	TCTGACAACTTCCTCTCTATGAGTCCAGCTTCCTCGAAATGCTTGAAGAGCTCGCCTCCT	180		
Db	286	TCCTGACAACTTCCTCTCTATGAGTCCAGCTTCCTCGAAATGCTTGAAGAGCTCGCCTCCT	227		

2. **DELETED**

RESULT_2	RG506690	456 bp	mRNA	linear	EST 27-MAR-2001			
LOCUS	601861290F1	NIH_MGC_77	Homo sapiens	cdna clone	IMAGE:4070759 5',			
DEFINITION	mRNA sequence.							
ACCESSION	RG506690							
VERSION	RG506690.1	GI:13468207						
KEYWORDS	EST.							
SOURCE	human.							
ORGANISM	Homo sapiens							

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Seq primer: -40UP from Gibco.
Location/Qualifiers
1. 422
   /organism="Homo sapiens"
   /db_xref="taxon:9606"
   /clone="IMAGE:3314516"
   /clone_lib="NCI_CGAP_Col6"
   /tissue_type="colon tumor, RER+"
   /lab_host="DH102"

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/tissue_type="colon
tumor, renal"
/lab_host="DH10B"
/lab_host="DH10B"
/not_e="Organ: colon: Vector: pMT33N-Pac (Pharmacia) with a

```

```

/Note=Organ; colon; Vector: pT73D-Pac (Pharmacia) with a
plasmid polylinker; Site_1: Not I; Site_2: Eco RI;
Planned DNA from the normalized library NCI_CGAP_Colo was
prepared, and ss circles were made in vitro. Following HAP
purification, this DNA was used as tracer in a subtractive
hybridization reaction. The driver was PCR-amplified cDNAs
from a pool of 5,000 clones made from the same library
(cloneIDs 1057416-1061255, and 1144584-1145351).
Subtraction by Bento Soares and M. Fatima Ronaldo. *
102 a 99 c 130 g 88 t 3 others
ch 92.4%; Score 166.4; DB 12; Length 422;
Similarity 99.4%; Pred. No. 4.1e-39;
167; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
AGGAGCGCAGTGGCCACTATGGGTCTGGCGCTGCCCTTGCTCTCTTGACCTCT 60

```

AGGAGGCGAGTGGCCACCTATGGGGCTGGGCTGCCCTTGTCCTCTTGACCCTCCT 337

GGCAGCTCACATGGAAACAGGCGCGGTATGACTTTGCAACTGAAGCTGAAGAGTCTTTT 120

GGCAGCTCACATGGAAACAGGCGCGGTATGACTTTGCAACTGAAGCTGAAGAGTCTTTT 277

BTGACAGATTCCTCTATGAGTCACAGTTCCTGGAATTCGCTGAAA 168
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 BTGACAAATTCCTCTATGAGTCACAGTTCCTGGAATTCGCTGAAA 229
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

EST.
human.
Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 895)
NTH <http://mgc.nci.nih.gov/>.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1995)
Contact: Robert Strausberg, Ph.D.
Email: cgabbs@email.nih.gov
Tissue Procurement: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
Plate: L14M11444 Row: C Column: 04

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nucp://image.llnl.gov
Plate: LIAW11444 row: c column: 04
High quality sequence start: 5
High quality sequence stop: 422.
Location/Qualifiers
1..895
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:5178171"
/clone_lib="NIH_MGC_115"
/lab_host="DH10B"

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/note="Organ: pooled brain, lung, testis; Vector: pCMV-SPORT6; Site.1: NotI; Site.2: EcoRV (destroyed); RNA source anonymous pool of 6 male brains, age range 23-27; 1 male lung, age 27; and 1 male testis, age 69. Library is oligo-dT primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.8 Kb, insert size range 1-3 Kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 021. Note: this is a NIH_MGC Library."

BASE COUNT 349 a 229 c 202 g 115 t
ORIGIN

Query Match 66.48; Score 119.6; DB 13; Length 895;
Best Local Similarity 96.88; Pred. No. 5.3e-25;
Matches 122; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 55 CCTCTTGGCAGCTCACATGGAACAGGCGGGTATGACTTTGCAACTGAAGCTGAAGGA 114
||| |
Db 6 CCTCTTGGCAGCTCACATGGAACAGGCGGGTATGACTTTGCAACTGAAGCTGAAGGA 65

QY 115 GTCTTTTCGACAAAGTTCTCTCTATGAGTCCAGCTTCTCGAATTCGTTGAAAAGCTCTG 174
|||||
Db 66 GTCTTTTCGACAAATTCCTCTATGAGTCCAGCTTCTCGAATTCGTTGAAAAGCTCTG 125

QY 175 CCTCT 180
|||||
Db 126 CCTCT 131

RESULT 6
BI820110
LOCUS BI820110 865 bp mRNA linear EST 04-OCT-2001
DEFINITION 603037110F1 NIH_MGC_115 Homo sapiens cDNA clone IMAGE:5178170 5',
mRNA sequence.

ACCESSION BI820110
VERSION BI820110.1 GI:15931660
KEYWORDS EST.
SOURCE human.

ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 865)
NIH-MGC http://mgc.nci.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.

Email: cgapbs-remail.nih.gov
Tissue Procurement: Life Technologies, Inc.
cDNA Library Arrayed by: Washington University Genome Sequencing Center
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
Plate: LLAM1444 row: c column: 03
High quality sequence stop: 417.
Location/Qualifiers
1..865

FEATURES
source

/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:5178170"
/clone_lib="NIH_MGC_115"
/lab_host="DH108"
/note="Organ: pooled brain, lung, testis; Vector: pCMV-SPORT6; Site.1: NotI; Site.2: EcoRV (destroyed); RNA source anonymous pool of 6 male brains, age range 23-27; 1 male lung, age 27; and 1 male testis, age 69. Library is oligo-dT primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.8 Kb, insert size range 1-3 Kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code

BASE COUNT 330 a 219 c 198 g 117 t
ORIGIN

Query Match 59.28; Score 106.6; DB 13; Length 865;
Best Local Similarity 95.28; Pred. No. 3.9e-21;
Matches 120; Conservative 0; Mismatches 5; Indels 1; Gaps 1;

QY 55 CCTCTTGGCAGCTCACATGGAACAGGCGGGTATGACTTTGCAACTGAAGCTGAAGGA 114
||| |
Db 6 CCTCTTGGCAGCTCACATGGAACAGGCGGGTATGACTTTGCAACTGAAGCTGAAGGA 65

QY 115 GTCTTTTCGACAAAGTTCTCTCTATGAGTCCAGCTTCTCGAATTCGTTGAAAAGCTCTG 174
|||||
Db 66 GTCTTTTCGACAAATTCCTCTATGAGTCCAGCTTCTCGAATTCGTTGAAAAGCTCTG 124

QY 175 CCTCT 180
|||||
Db 125 CCTCT 130

RESULT 7
AI857998/c
LOCUS AI857998 404 bp mRNA linear EST 21-DEC-1999
DEFINITION wj69b01.x1 NCI_CGAP_Lu19 Homo sapiens cDNA clone IMAGE:2408041 3',
mRNA sequence.

ACCESSION AI857998
VERSION AI857998.1 GI:5511614
KEYWORDS EST.
SOURCE human.

ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 404)
NCI-CGAP http://www.ncbi.nlm.nih.gov/hcicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.

Email: cgapbs-remail.nih.gov
Tissue Procurement: Christopher Miskaluk, M.D., Ph.D., Michael R. Emmert-Buck, M.D., Ph.D.
cDNA Library Preparation: M. Bento Soares, Ph.D.
cDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: www.bio.llnl.gov/bbrp/image/image.html

Insert Length: 629 Std Error: 0.00
Seq primer: -40UP from Gibco
High quality sequence stop: 395.
Location/Qualifiers
1..404
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:2408041"
/clone_lib="NCI_CGAP_Lu19"
/tissue_type="squamous cell carcinoma, poorly differentiated (4 pooled tumors, including primary and metastatic)"
/dev_stage="adult"
/lab_host="DH108 (phage-resistant)"
/note="Organ: lung; Vector: pT73D-Pac (Pharmacia) with a modified polylinker; 1st strand cDNA was prepared from pooled lung tumor tissue, and was then primed with a Not I - oligo(dT) primer. Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT73 vector. Library went through one round of normalization. Library constructed by Bento Soares and M. Fatima Bonaldo."

FEATURES
source

97 a 105 c 117 g 84 t 1 others
BASE COUNT
ORIGIN

Query Match 55.8%; Score 100.4; DB 9; Length 404;
 Best Local Similarity 98.1%; Pred. No. 1.9e-19;
 Matches 101; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 78 CAGGCCGGGTATGACTTGGCAACTGAAGCTGAAGAGTCTTTTCTGACAAAGTTCCTCT 137
 |||||
 Db 311 CAGGCCGGGTATGACTTGGCAACTGAAGCTGAAGAGTCTTTTCTGACAAATTCCTCT 252
 |||||

QY 138 ATGAGTCCAGCTTCTCTGGAATGCTTGAAGAAGCTCGCCTCT 180
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 Db 251 ATGAGTCCAGCTTCTCTGGAATGCTTGAAGAAGCTTCCTCT 209
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RESULT 8
 BF521842 361 bp mRNA linear EST 11-DEC-2000
 LOCUS UI-R-C2p-ng-e-02-0-UI.r1 UI-R-C2p Rattus norvegicus cDNA clone
 DEFINITION UI-R-C2p-ng-e-02-0-UI 5', mRNA sequence.
 ACCESSION BF521842
 VERSION BF521842.1 GI:11629809
 KEYWORDS EST.
 SOURCE Norway rat.
 ORGANISM Rattus norvegicus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Murinae;
 Rattus.
 1 (bases 1 to 361)
 REFERENCE Bonaldo,M.F., Lennon,G. and Soares,M.B.
 AUTHORS Normalization and subtraction: two approaches to facilitate gene
 TITLE discovery
 JOURNAL Genome Res. 6 (9), 791-806 (1996)
 MEDLINE 97044477
 COMMENT Contact: Soares, MB
 Program for Rat Gene Discovery and Mapping
 University of Iowa
 451 Eckstein Medical Research Building Iowa City, IA 52242, USA
 Tel: 319 335 8250
 Fax: 319 335 9565
 Email: mcares@blue.weeg.uiowa.edu
 cDNA library preparation: M.B. Soares Lab clone distribution:
 clones will be available through Research Genetics (www.resgen.com)
 This clone is also available through the I.M.A.G.E. Consortium at
 LNL (info@image.llnl.gov). IMAGE ID= 1792770
 Seq primer: M13 Forward
 Location/Qualifiers
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 /strain="Sprague-Dawley"
 /db_xref="taxon:10116"
 /clone="UI-R-C2p-ng-e-02-0-UI"
 /clone_lib="UI-R-C2p"
 /dev_stage="adult"
 /lab_host="DH10B (Life Technologies)"
 /note="Vector: pT73D-pac (Pharmacia) with a modified
 polylinker; Site.1: Not I; Site.2: Eco RI; The UI-R-C2p
 library is a subtracted library derived from the UI-R-C1
 library, which is a subtracted library derived from the
 UI-R-C0 library. The UI-R-C0 library consisted of a
 mixture of individually tagged normalized libraries
 constructed from rat placenta, adult lung, brain, liver,
 kidney, heart, spleen, ovary, muscle, 8, 12 and 18-day
 embryo. The tag is a string of 3-5 nucleotides present
 between the Not I site and the oligo-ct track which allows
 identification of the library of origin of a clone within
 the mixture. The subtracted library (UI-R-C2p) was
 constructed as follows: PCR amplified cDNA inserts from
 UI-R-C1 clones from which 3' ESTs had been derived was
 used as a driver in a hybridization with the UI-R-C1
 library in the form of single-stranded circles. The
 remaining single-stranded circles (subtracted library) was
 purified by hydroxyapatite column chromatography,
 converted to double-stranded circles and electroporated

into DH10B bacteria (Life Technologies) to generate the
 UI-R-C2p library. This procedure has been previously
 described (Bonaldo, Lennon and Soares, genome Research 6:
 791-806, 1996)"

BASE COUNT 79 a 121 c 91 g 70 t

Query Match 47.7%; Score 85.8; DB 12; Length 361;
 Best Local Similarity 67.8%; Pred. No. 4.1e-15;
 Matches 120; Conservative 0; Mismatches 57; Indels 0; Gaps 0;

QY 4 GAGCCAGTGGCCACTATGGGTCTGGGCTGCCCTTGTCTCTGTGACCTCTGG 63
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 Db 6 GGGTGAAGCGGCCACCATGGAGCCTTCGATGTCTCTCTCTCTCTCTCTCTG 65
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QY 64 CAGCTCACATGGAACAGGCGCGGTATGACTTTTGCACCTGAAGCTGAGTCTTTCT 123
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 Db 66 CAGCTCACTGAAGGCCCAACAAGGTGACTTTGCAAGTAAACTGACCGGCACTCA 125
 |||||

QY 124 GACAAGTTCCTCTATGAGTCCAGTTCCTCGAATTCCTTGAAGTCTGCTCTCT 180
 |||||
 Db 126 GGCCAAGACCTCCCAAGACTCGGCTTCTTGACATGCTCCAAAAGATCTGCTCTCT 182
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RESULT 9
 BB533837 521 bp mRNA linear EST 26-OCT-2001
 LOCUS BB533837 RIKEN full-length enriched, 0 day neonate lung Mus
 DEFINITION musculus cDNA clone E030032D13 3', mRNA sequence.
 ACCESSION BB533837
 VERSION BB533837.2 GI:16446306
 KEYWORDS EST.
 SOURCE house mouse.
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 521)

REFERENCE Arakawa,T., Carninci,P., Fukuda,S., Furuno,M., Hanagaki,T., Hara,A.,
 Hiramoto,K., Hori,F., Ishii,Y., Ito,M., Kawai,J., Konno,H., Kouda
 M., Koya,S., Matsuyama,T., Miyazaki,A., Nomura,K., Ohno,M.,
 Okazaki,Y., Okido,T., Saito,R., Sakai,C., Sakai,K., Sano,H., Sasaki
 D., Shibata,K., Shingawa,A., Shiraki,T., Sogabe,Y., Suzuki,H.,
 Tagami,M., Tagawa,A., Takahashi,F., Takeda,Y., Tanaka,T., Toya,T.,
 Muramatsu,M. and Hayashizaki,Y.
 RIKEN Mouse ESTs (Arakawa,T., et al. 2001)
 JOURNAL Unpublished (2001)
 COMMENT On Jul 29, 2000 this sequence version replaced gi:9585766.
 Contact: Yoshihide Hayashizaki
 Laboratory for Genome Exploration Research Group, RIKEN Genomic
 Sciences Center (GSC), Yokohama Institute
 The Institute of Physical and Chemical Research (RIKEN)
 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
 Tel: 81-45-503-9222
 Fax: 81-45-503-9216
 Email: genome-res@sc.riken.go.jp,
 URL:http://genome.sci.riken.go.jp/
 Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh
 M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
 Normalization and subtraction of cap-trapper-selected cDNAs to
 prepare full-length cDNA libraries for rapid discovery of new
 genes. Genome Res. 10 (10), 1617-1630 (2000)
 wagi,K., Fujiwara,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E.,
 Wataniki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura
 S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and
 Hayashizaki,Y.
 RIKEN integrated sequence analysis (RISA) system--384-format
 sequencing pipeline with 384 multicapillary sequencer. Genome Res.
 10 (11), 1757-1771 (2000)
 Konno,H., Fukunishi,Y., Shibata,K., Itoh,M., Carninci,P., Sugahara
 Y., and Hayashizaki,Y.
 Computer-based methods for the mouse full-length cDNA
 encyclopedia: real-time sequence clustering for construction of a
 nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)

Kondo,S., Shinagawa,A., Saito,T., Kiyosawa,H., Yamanaka,I., Aizawa,K., Fukuda,S., Hara,A., Itoh,M., Kawai,J., Shibata,K. and Hayashizaki,Y.
Computational Analysis of Full-Length Mouse cDNAs Compared with Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)
Please visit our web site (<http://genome.gsc.riken.go.jp/>) for further details.
cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.

FEATURES
source
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/organism="Mus musculus"
/db_xref="taxon:10090"
/clone="E030032D13"
/clone_lib="RIKEN full-length enriched, 0 day neonate lung"
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/lab_host="DH10B"
/note="Site_1: Sali; Site_2: BamHI; cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. 1st strand cDNA was primed with a primer [5'
GAGGAGAGCGCGCCGACCTGAGTCTTTTCTTTTCTTTT 3'], cDNA was prepared by using trehalose thermo-activated reverse transcriptase and subsequently enriched for full-length by cap-trapper. Second strand cDNA was prepared with the primer adapter of sequence [5'
GAGAGAGATCTCGAGTTAAATTAATTAATTCGCCCCGCC 3']. cDNA was cleaved with BamHI and XhoI. Vector: a modified pBluescript KS(+) after bulk excision from Lambda FLC I."
BASE COUNT 119 a 163 c 125 g 114 t
ORIGIN

Query Match 46.1%; Score 83; DB 10; Length 521;
Best Local Similarity 70.4%; Pred. No. 3.4e-14;
Matches 126; Conservative 0; Mismatches 50; Indels 3; Gaps 1;
QY 2 AGGAGCGAGTGGCCATGATGGGTCTGGGCTGCCCTTCTCTCTCTTGACCCCTT 61
DB 156 AGAGTGGGTAGCCACCATTGGATCTTTGATGGCTCTCTCTCTCTGGCCCTC 215
QY 62 GGCAGCTCAGTGAACAGCGCGGGTATGACTTTGCAACTGAAGCTGAAGAGTCTTT 121
DB 216 AGCAGCTCAGCAGC---CAGGCGCCAAAGGTGACTTTGCGAGTAAAGCTGACCGAGACTTT 272
QY 122 CTGACAAGTTCTCTCTATGAGTCCAGCTTCTCGGAATTCGTTGAAAGCTCTGCCTCT 180
DB 273 CAGGACAAGACCTCCGCACTCCAGTCTGTCGACATGCTCCAAAGATCTGCCTCT 331

RESULT 10
BB664284 522 bp mRNA linear EST 26-OCT-2001
LOCUS BB664284 RIKEN full-length enriched, 0 day neonate lung Mus
DEFINITION musculus cDNA clone E030032D13 5', mRNA sequence.
ACCESSION BB664284.1 GI:16498038
VERSION EST.
KEYWORDS house mouse.
SOURCE Mus musculus
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1. (bases 1 to 522)
AUTHORS Arakawa,T., Carninci,P., Fukuda,S., Furuno,M., Hanagaki,T., Hara,A., Hiramoto,K., Hori,F., Ishii,Y., Ito,M., Kawai,J., Konno,H., Kouda,M., Koya,S., Matsuyama,T., Miyazaki,A., Nomura,K., Ohno,M.,

TITLE
JOURNAL
COMMENT

Okazaki,Y., Okido,T., Saito,R., Sakai,C., Sakai,K., Sano,H., Sasaki,D., Shibata,K., Shinagawa,A., Shiraki,T., Sogabe,Y., Suzuki,H., Tagami,M., Tagawa,A., Takahashi,F., Takeda,Y., Tanaka,T., Toya,T., Muramatsu,M. and Hayashizaki,Y.
RIKEN Mouse ESTs (Arakawa,T., et al. 2001)
Unpublished (2001)
Contact: Yoshinori Hayashizaki
Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
Tel: 81-45-503-9222
Fax: 81-45-503-9216
Email: genome-res@gsc.riken.go.jp,
URL:<http://genome.gsc.riken.go.jp/>
Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. Genome Res. 10 (10), 1617-1630 (2000)
wagi,K., Fujiwara,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsura,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kita,A. and Hayashizaki,Y.
RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000)
Konno,H., Fukunishi,Y., Shibata,K., Itoh,M., Carninci,P., Sugahara,Y. and Hayashizaki,Y.
Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)
Kondo,S., Shinagawa,A., Saito,T., Kiyosawa,H., Yamanaka,I., Aizawa,K., Fukuda,S., Hara,A., Itoh,M., Kawai,J., Shibata,K. and Hayashizaki,Y.
Computational Analysis of Full-Length Mouse cDNAs Compared with Human Genome Sequences. Mamm. Genome. 12, 673-677 (2001)
Please visit our web site (<http://genome.gsc.riken.go.jp/>) for further details.
e mouse tissues.
Location/Qualifiers
1. .522
/organism="Mus musculus"
/db_xref="taxon:10090"
/clone="E030032D13"
/clone_lib="RIKEN full-length enriched, 0 day neonate lung"
/tissue_type="lung"
/dev_stage="0 day neonate"
/lab_host="DH10B"
/note="Site_1: Sali; Site_2: BamHI; cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. 1st strand cDNA was primed with a primer [5'
GAGGAGAGCGCGCCGACCTGAGTCTTTTCTTTTCTTTT 3'], cDNA was prepared by using trehalose thermo-activated reverse transcriptase and subsequently enriched for full-length by cap-trapper. Second strand cDNA was prepared with the primer adapter of sequence [5'
GAGAGAGATCTCGAGTTAAATTAATTAATTCGCCCCGCC 3']. cDNA was cleaved with BamHI and XhoI. Vector: a modified pBluescript KS(+) after bulk excision from Lambda FLC I."

BASE COUNT 132 a 151 c 125 g 114 t
ORIGIN
Query Match 46.1%; Score 83; DB 10; Length 522;
Best Local Similarity 70.4%; Pred. No. 3.4e-14;
Matches 126; Conservative 0; Mismatches 50; Indels 3; Gaps 1;
QY 2 AGGAGCGAGTGGCCATGATGGGTCTGGGCTGCCCTTCTCTCTTGACCCCTT 61


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Matches 79; Conservative 0; Mismatches 39; Indels 0; Gaps 0;

QY 63 GCAGCTCACATGGAACAGGCGCGGTATGACTTGCACACTCAAGCTGAAGGACTCTTTTC 122
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QY 123 TGACAAGTTCCTCTATGAGTCCAGCTTCCTCGAATTCCTTGAAGAAGCTCTCCCTCT 180
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Db 267 AGGCCAAGAGCTCCCAAGACTCCGGCTTCTGTGACATGCTCCAAAAGATCTGCTCTCT 210
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

RESULT 13
AZ241329/c
LOCUS
DEFINITION
  RPCI-23-75C13.TJ RPCI-23 Mus musculus genomic clone RPCI-23-75C13,
  DNA sequence.
ACCESSION
  AZ241329
VERSION
  1
KEYWORDS
  GSS.
SOURCE
  house mouse.
ORGANISM
  Mus musculus
  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE
  1 (bases 1 to 506)
  Zhao,S., Nierman,W., Feldblyum,T., Malek,J., Shatsman,S., Akinret
  ,B., Levins,M., McGann,S., Tsegaye,G., Geer,K., Krol,M., de Jong,P.
  and Fraser,C.M.
  Mouse BAC End Sequences from Library RPCI-23
  Unpublished (1999)
  Other_GSSs: RPCI-23-75C13.TJ
  Contact: Shaying Zhao
  Department of Eukaryotic Genomics
  The Institute for Genomic Research
  9712 Medical Center Dr., Rockville, MD 20850, USA
  Tel: 301 838 0200
  Fax: 301 838 0208
  Email: szhao@tigr.org
  Clones are derived from the mouse BAC library RPCI-23. For BAC
  library availability, please contact Pieter de Jong
  (pieterdejong.med.buffalo.edu). Clones may be purchased from
  BACPAC Resources (http://bacpac.med.buffalo.edu/orderingframe.htm)
  or from Resea ch Genetics (info@resgen.com). BAC end page:
  http://www.tigr.org/tdb/bac_ends/mouse/bac_end_intro.html
  plate: 75 row: C column: 13
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  Class: BAC ends.
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    /clone="RPCI-23-75C13"
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    /sex="Female"
    /lab_host="DH10B"
    /note="Organ: Kidney/Brain; Vector: pBACe3.6; Site_1:
    EcoRI; Site_2: EcoRI; Female C57BL/6J mouse kidney and/or
    brain genomic DNA was isolated and partially digested
    with a combination of EcoRI and EcoRI MethyIase. Size
    selected DNA was cloned into the pBACe3.6 vector at the
    EcoRI sites. The ligation products were transformed into
    DH10B electrocompetent cells (BRL Life Technologies)."
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    Best Local Similarity 67.0%; Pred.No.0.011;
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QY 78 CAGGCGCGGTATGACTTGCACACTGAAGCTGAAGAGTCTTTCTGACAAAGTCTCTCT 137
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Db 403 CAGGCCAAAGGTGACTTTGCAGGTAAGCTGACCGAGACTTTTCAGGACAAGACTCCC 344
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

RESULT 14
AZ079350/c
LOCUS
DEFINITION
  RPCI-23-438H19.TV RPCI-23 Mus musculus genomic clone RPCI-23-438H19
  , DNA sequence.
ACCESSION
  AZ079350
VERSION
  1
KEYWORDS
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SOURCE
  house mouse.
ORGANISM
  Mus musculus
  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE
  1 (bases 1 to 633)
  Zhao,S., Nierman,W., Feldblyum,T., Malek,J., Shatsman,S., Akinret
  ,B., Levins,M., McGann,S., Tsegaye,G., Geer,K., Krol,M., de Jong,P.
  and Fraser,C.M.
  Mouse BAC End Sequences from Library RPCI-23
  Unpublished (1999)
  Other_GSSs: RPCI-23-438H19.TJ
  Contact: Shaying Zhao
  Department of Eukaryotic Genomics
  The Institute for Genomic Research
  9712 Medical Center Dr., Rockville, MD 20850, USA
  Tel: 301 838 0200
  Fax: 301 838 0208
  Email: szhao@tigr.org
  Clones are derived from the mouse BAC library RPCI-23. For BAC
  library availability, please contact Pieter de Jong
  (pieterdejong.med.buffalo.edu). Clones may be purchased from
  BACPAC Resources (http://bacpac.med.buffalo.edu/orderingframe.htm)
  or from Resea ch Genetics (info@resgen.com). BAC end page:
  http://www.tigr.org/tdb/bac_ends/mouse/bac_end_intro.html
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    /lab_host="DH10B"
    /note="Organ: Kidney/Brain; Vector: pBACe3.6; Site_1:
    EcoRI; Site_2: EcoRI; Female C57BL/6J mouse kidney and/or
    brain genomic DNA was isolated and partially digested
    with a combination of EcoRI and EcoRI MethyIase. Size
    selected DNA was cloned into the pBACe3.6 vector at the
    EcoRI sites. The ligation products were transformed into
    DH10B electrocompetent cells (BRL Life Technologies)."
  BASE COUNT
  138 a 191 c 161 g 143 t
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    Query Match 24.7%; Score 44.4; DB 17; Length 633;
    Best Local Similarity 67.0%; Pred.No.0.012;
    Matches 63; Conservative 0; Mismatches 31; Indels 0; Gaps 0;

QY 78 CAGGCGCGGTATGACTTGCACACTGAAGCTGAAGAGTCTTTCTGACAAAGTCTCTCT 137
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Db 403 CAGGCCAAAGGTGACTTTGCAGGTAAGCTGACCGAGACTTTTCAGGACAAGACTCCC 344
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QY 138 ATGAGTCCAGCTTCCTCGAATTCGTTGAAAAGCT 171
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RESULT 15

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GenCore version 5.1.5
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OM nucleic - nucleic search, using sw model

Run on: May 1, 2003, 02:55:40 ; Search time 123.673 Seconds
(without alignments)
3277.661 Million cell updates/sec

Title: US-09-092-296-3
Perfect score: 180
Sequence: 1 CAGAGCGCAGTGGCCACTA.....CTTGAAAGCTGTGCTCTCT 180

Scoring table: IDENTITY_NUC
Gapop 10.0 , Capext 1.0

Searched: 2185239 seqs, 1125999159 residues

Total number of hits satisfying chosen parameters: 4370478

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Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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4:	/SID22/gcgdata/geneseq/geneseq-emb1/NA1983.DAT.*
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7:	/SID22/gcgdata/geneseq/geneseq-emb1/NA1986.DAT.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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3	178.4	99.1	422	22	AAZ65087
4	178.4	99.1	422	22	AAZ65087
5	178.4	99.1	422	22	AAZ65087
6	178.4	99.1	422	22	AAZ65087
7	178.4	99.1	422	22	AAZ65087
8	178.4	99.1	422	22	AAZ65087
9	178.4	99.1	422	22	AAZ65087
10	178.4	99.1	422	22	AAZ65087
11	178.4	99.1	422	22	AAZ65087
12	178.4	99.1	422	22	AAZ65087
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19	178.4	99.1	422	22	AAZ65087
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22	178.4	99.1	422	22	AAZ65087
23	178.4	99.1	422	22	AAZ65087
24	178.4	99.1	422	22	AAZ65087

10	32.2	17.9	27082	22	AAZ65087	Human immune/haema
11	32	17.8	1128	19	AAZ65087	Mouse coxsackievir
12	31.6	17.6	550	22	AAZ65087	Cat flea hindgut a
13	31.2	17.3	16596	22	AAZ65087	Human immune/haema
14	31.2	17.3	16596	22	AAZ65087	DNA encoding human
15	30.8	17.1	11749	22	AAZ65087	Human musculoskele
16	30.8	17.1	11749	22	AAZ65087	DNA encoding human
17	30.8	17.1	11749	22	AAZ65087	Human reproductive
18	30.8	17.1	11749	22	AAZ65087	Human immune/haema
19	30.8	17.1	11749	22	AAZ65087	Human musculoskele
20	30.8	17.1	11749	22	AAZ65087	DNA encoding human
21	30.8	17.1	11749	22	AAZ65087	Human musculoskele
22	30.4	16.9	580	16	AAZ65087	Cell-cycle regulat
23	30.4	16.9	580	20	AAZ65087	Mouse INK-4 protei
24	30.4	16.9	580	21	AAZ65087	Murine cell cycle
25	30.4	16.9	580	24	AAZ65087	Mouse CDNA encodin
26	30.4	16.9	580	24	AAZ65087	Mouse coxsackievir
27	30	16.7	665	21	AAZ65087	Arabidopsis thalia
28	30	16.7	820	24	AAZ65087	Arabidopsis thalia
29	30	16.7	831	21	AAZ65087	Arabidopsis thalia
30	30	16.7	833	21	AAZ65087	Arabidopsis thalia
31	30	16.7	843	21	AAZ65087	Arabidopsis thalia
32	30	16.7	845	21	AAZ65087	Arabidopsis thalia
33	30	16.7	879	21	AAZ65087	Arabidopsis thalia
34	29.8	16.6	291	20	AAZ65087	EST clone AK34. H
35	29.8	16.6	1695	22	AAZ65087	Human CDNA encodin
36	29.8	16.6	1788	22	AAZ65087	Human CDNA encodin
37	29.6	16.4	10388	22	AAZ65087	Human excretory re
38	29.6	16.4	10388	22	AAZ65087	Human kidney relat
39	29.6	16.4	11294	23	AAZ65087	Drosophila melanog
40	29.4	16.3	1251	24	AAZ65087	Eastern cottonmout
41	29.4	16.3	7275	23	AAZ65087	Drosophila melanog
42	29.4	16.3	12235	23	AAZ65087	Drosophila melanog
43	29.2	16.2	1359	23	AAZ65087	DNA encoding novel
44	29	16.1	977	23	AAZ65087	Genomic sequence #
45	29	16.1	4417	21	AAZ65087	Murine TANGO 197 c

ALIGNMENTS

RESULT 1	
AAZ65087	
ID	AAZ65087 standard; CDNA; 422 BP.
XX	AAZ65087;
AC	AAZ65087;
XX	
DT	05-APR-2000 (first entry)
XX	
DE	Membrane-bound protein PRO1098 encoding CDNA.
XX	
DE	Membrane-bound polypeptide; PRO polypeptide; LDL receptor; TIE ligand;
KW	pharmaceutical; receptor immunoadhesin; gene mapping; ss.
KW	
XX	
CS	Homo sapiens.
XX	
PN	WO9963088-A2.
XX	
PD	09-DEC-1999.
XX	
PF	02-JUN-1999; 99WO-0512252.
XX	
PR	02-JUN-1998; 98US-0087607.
PR	02-JUN-1998; 98US-0087609.
PR	02-JUN-1998; 98US-0087759.
PR	03-JUN-1998; 98US-0087827.
PR	04-JUN-1998; 98US-0088021.
PR	04-JUN-1998; 98US-0088025.
PR	04-JUN-1998; 98US-0088028.
PR	04-JUN-1998; 98US-0088029.
PR	04-JUN-1998; 98US-0088030.
PR	04-JUN-1998; 98US-0088033.
PR	04-JUN-1998; 98US-0088326.

PR 05-JUN-1998; 98US-0088167.
PR 05-JUN-1998; 98US-0088202.
PR 05-JUN-1998; 98US-0088212.
PR 05-JUN-1998; 98US-0088217.
PR 09-JUN-1998; 98US-0088655.
PR 10-JUN-1998; 98US-0088722.
PR 10-JUN-1998; 98US-0088730.
PR 10-JUN-1998; 98US-0088734.
PR 10-JUN-1998; 98US-0088738.
PR 10-JUN-1998; 98US-0088740.
PR 10-JUN-1998; 98US-0088741.
PR 10-JUN-1998; 98US-0088742.
PR 10-JUN-1998; 98US-0088810.
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PR 10-JUN-1998; 98US-0088824.
PR 10-JUN-1998; 98US-0088825.
PR 10-JUN-1998; 98US-0088826.
PR 11-JUN-1998; 98US-0088858.
PR 11-JUN-1998; 98US-0088861.
PR 11-JUN-1998; 98US-0088863.
PR 11-JUN-1998; 98US-0088876.
PR 12-JUN-1998; 98US-0089090.
PR 12-JUN-1998; 98US-0089105.
PR 16-JUN-1998; 98US-0089440.
PR 16-JUN-1998; 98US-0089512.
PR 16-JUN-1998; 98US-0089514.
PR 17-JUN-1998; 98US-0089532.
PR 17-JUN-1998; 98US-0089538.
PR 17-JUN-1998; 98US-0089598.
PR 17-JUN-1998; 98US-0089599.
PR 17-JUN-1998; 98US-0089600.
PR 17-JUN-1998; 98US-0089653.
PR 18-JUN-1998; 98US-0089801.
PR 18-JUN-1998; 98US-0089907.
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PR 19-JUN-1998; 98US-0089947.
PR 19-JUN-1998; 98US-0089952.
PR 19-JUN-1998; 98US-0089958.
PR 22-JUN-1998; 98US-0090246.
PR 22-JUN-1998; 98US-0090252.
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PR 23-JUN-1998; 98US-0090349.
PR 23-JUN-1998; 98US-0090355.
PR 24-JUN-1998; 98US-0090429.
PR 24-JUN-1998; 98US-0090431.
PR 24-JUN-1998; 98US-0090435.
PR 24-JUN-1998; 98US-0090444.
PR 24-JUN-1998; 98US-0090445.
PR 24-JUN-1998; 98US-0090451.
PR 24-JUN-1998; 98US-0090472.
PR 24-JUN-1998; 98US-0090535.
PR 24-JUN-1998; 98US-0090538.
PR 24-JUN-1998; 98US-0090540.
PR 24-JUN-1998; 98US-0090557.
PR 25-JUN-1998; 98US-0090676.
PR 25-JUN-1998; 98US-0090678.
PR 25-JUN-1998; 98US-0090688.
PR 25-JUN-1998; 98US-0090690.
PR 25-JUN-1998; 98US-0090691.
PR 25-JUN-1998; 98US-0090694.
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PR 26-JUN-1998; 98US-0090696.
PR 26-JUN-1998; 98US-0090862.
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PR 01-JUL-1998; 98US-0091358.
PR 01-JUL-1998; 98US-0091360.
PR 01-JUL-1998; 98US-0091544.
PR 02-JUL-1998; 98US-0091478.
PR 02-JUL-1998; 98US-0091486.
PR 02-JUL-1998; 98US-0091519.
PR 02-JUL-1998; 98US-0091626.
PR 02-JUL-1998; 98US-0091628.
PR 02-JUL-1998; 98US-0091633.
PR 02-JUL-1998; 98US-0091646.
PR 02-JUL-1998; 98US-0091673.
PR 07-JUL-1998; 98US-0091978.
PR 07-JUL-1998; 98US-0091982.
PR 09-JUL-1998; 98US-0092182.
PR 10-JUL-1998; 98US-0092472.
PR 20-JUL-1998; 98US-0093339.
PR 30-JUL-1998; 98US-0094651.
PR 04-AUG-1998; 98US-0095282.
PR 04-AUG-1998; 98US-0095285.
PR 04-AUG-1998; 98US-0095301.
PR 04-AUG-1998; 98US-0095302.
PR 04-AUG-1998; 98US-0095318.
PR 04-AUG-1998; 98US-0095321.
PR 04-AUG-1998; 98US-0095325.
PR 10-AUG-1998; 98US-0095916.
PR 10-AUG-1998; 98US-0095929.
PR 10-AUG-1998; 98US-0096012.
PR 11-AUG-1998; 98US-0096143.
PR 11-AUG-1998; 98US-0096146.
PR 12-AUG-1998; 98US-0096329.
PR 17-AUG-1998; 98US-0096757.
PR 17-AUG-1998; 98US-0096766.
PR 17-AUG-1998; 98US-0096768.
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PR 17-AUG-1998; 98US-0096897.
PR 18-AUG-1998; 98US-0096949.
PR 18-AUG-1998; 98US-0096950.
PR 18-AUG-1998; 98US-0096959.
PR 18-AUG-1998; 98US-0096960.
PR 18-AUG-1998; 98US-0097022.
PR 19-AUG-1998; 98US-0097141.
PR 20-AUG-1998; 98US-0097218.
PR 24-AUG-1998; 98US-0097661.
PR 26-AUG-1998; 98US-0097951.
PR 26-AUG-1998; 98US-0097952.
PR 26-AUG-1998; 98US-0097954.
PR 26-AUG-1998; 98US-0097955.
PR 26-AUG-1998; 98US-0097971.
PR 26-AUG-1998; 98US-0097974.
PR 26-AUG-1998; 98US-0097978.
PR 26-AUG-1998; 98US-0097979.
PR 26-AUG-1998; 98US-0097986.
PR 26-AUG-1998; 98US-0098014.
PR 31-AUG-1998; 98US-0098325.
PR 16-SEP-1998; 98US-0100634.
PR 12-JAN-1999; 99US-0115565.
XX
XX (GETH) GENENTECH INC.
XX Baker K, Chen J, Goddard A, Gurney AL, Smith V, Watanabe CK;
PI Wood WI, Yuan J;
XX
XX WPI; 2000-072883/06.
XX P-PSDB; AAX66741.
XX
XX Membrane-bound proteins and related nucleotide sequences -
XX Claim 2; Fig 257; 822pp; English.
XX The invention provides membrane-bound PRO polypeptides and
CC polynucleotides encoding them. The PRO sequences of the invention were
CC identified based on extracellular domain homology screening. The PRO
CC sequences have homology with proteins including LDL receptors, TIE
CC ligands and various enzymes. The membrane-bound proteins and receptor
CC molecules are useful as pharmaceutical and diagnostic agents. Receptor
CC immunoadhesins, for instance, can be used as therapeutic agents to block
CC receptor-ligand interactions. The membrane-bound proteins can also be

employed for screening of potential peptide or small molecule inhibitors of the relevant receptor/ligand interaction. The PRO encoding sequences are useful as hybridization probes, in chromosome and gene mapping and in the generation of antisense RNA and DNA. PRO nucleic acid sequences will also be useful for the preparation of PRO polypeptides, especially by recombinant techniques.

XX
SQ
Sequence 422 BP; 84 A; 134 C; 104 G; 100 T; 0 other;

Query Match	99.1%	Score 178.4;	DB 21;	Length 422;
Best Local Similarity	99.4%	Pred. NO. 1.9e-49;		

QY	1	CAGGAGCGGAGTGGCCACTATGGGCTTGGGCTGCCCTTGTCTCTCTTGAACCTCCT	60
Db	39	CAGGAGCGGAGTGGCCACTATGGGCTTGGGCTGCCCTTGTCTCTCTTGAACCTCCT	98
QY	61	TGGCAGCTCACATGGAAACAGCGCGGGTATGACTTGGCACTGAAGCTGAAGAGTCTTT	120
Db	99	TGGCAGCTCACATGGAAACAGCGCGGGTATGACTTGGCACTGAAGCTGAAGAGTCTTT	158
QY	121	TCTGACAAGTTCCTCTATGAGTCCAGCTTCTCGGAATTCGTTGAAAAGCTTCGCCTCCT	180
Db	159	TCTGACAAATTCCTCTATGAGTCCAGCTTCTCGGAATTCGTTGAAAAGCTTCGCCTCCT	218

RESULT 2

AAS46045
ID AAS46045 standard; cDNA; 422 BP.

AA
AC

XX
DT 18-DEC-2001 / f4 vct cont...

XX
DE Human DNA encoding PRO polypeptide sequence #121.

PRO polypeptide; mammal; tumour; cancer; human; cattle; horse; sheep; ss;
KW dog; cat; pig; goat; rabbit; tumour necrosis factor alpha; TNF-alpha;
KW blood; chondrocyte cell; cell proliferation; cell differentiation; colon;
KW adrenal; lung; breast; prostate; rectum; cervix; liver; genetic disorder;
KW PCR primer.

Homo sapiens

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DN
W0200150040 32

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XX	28-FEB-2001	2001WO-US060520
PR	01-MAR-2000	2000WO-US054601
PR	02-MAR-2000	2000WO-US05841
PR	03-MAR-2000	2000US-187020P
PR	06-MAR-2000	2000US-186688P
PR	14-MAR-2000	2000US-189320P
PR	14-MAR-2000	2000US-189628P
PR	15-MAR-2000	2000US-195368P
PR	21-MAR-2000	2000WO-US06384
PR	21-MAR-2000	2000US-193028P
PR	21-MAR-2000	2000US-191007P
PR	21-MAR-2000	2000US-191048P
PR	21-MAR-2000	2000US-191314P
PR	28-MAR-2000	2000US-192655P
PR	29-MAR-2000	2000US-193032P
PR	29-MAR-2000	2000US-193053P
PR	30-MAR-2000	2000WO-US060439
PR	04-APR-2000	2000US-194449P
PR	04-APR-2000	2000US-194647P
PR	11-APR-2000	2000US-195075P
PR	11-APR-2000	2000US-196000P
PR	11-APR-2000	2000US-196187P
PR	11-APR-2000	2000US-196690P
PR	11-APR-2000	2000US-196620P
PR	18-APR-2000	2000US-198212P

DT 15-MAY-2001 (first entry)
 XX Human PRO1098 cDNA.
 DE Human; PRO protein; mapping; ss.
 KW Homo sapiens.
 XX W0200116318-A2.
 XX 08-MAR-2001.
 XX 24-AUG-2000; 2000WO-US23328.
 XX 01-SEP-1999; 99WO-US20111.
 PR 15-SEP-1999; 99WO-US21090.
 PR 07-DEC-1999; 99US-0169495.
 PR 09-DEC-1999; 99US-0170262.
 PR 11-JAN-2000; 2000US-0175481.
 PR 18-FEB-2000; 2000WO-US04341.
 PR 22-FEB-2000; 2000WO-US04342.
 PR 01-MAR-2000; 2000WO-US05601.
 PR 03-MAR-2000; 2000US-0187202.
 PR 25-APR-2000; 2000US-0199397.
 PR 22-MAY-2000; 2000WO-US14042.
 PR 05-JUN-2000; 2000US-0209832.
 XX (GETH) GENENTECH INC.
 XX Eaton DL, Filvaroff E, Gerritsen ME, Goddard A, Godowski PJ;
 PI Grimaldi CJ, Gurney AL, Watanabe CK, Wood WI;
 XX WPI; 2001-183260/18.
 DR P-PSDB: AAB87558.
 XX Eighty four nucleic acids encoding PRO polypeptides, useful in
 PT molecular biology, including use as hybridization probes, and in
 PT chromosome and gene mapping. -
 XX Claim 2; Fig 65; 278pp; English.
 XX The present sequence is the coding sequence for a human PRO polypeptide
 CC (secreted and transmembrane). The PRO protein, and PRO agonists, PRO
 CC antagonists or anti-PRO antibodies are useful for preparation of a
 CC medicament useful in the treatment of a condition which is responsive to
 CC the PRO protein, agonists, antagonists or anti-PRO antibodies. The PRO
 CC protein may also be employed as molecular weight markers for protein
 CC electrophoresis. The PRO coding sequence has applications in molecular
 CC biology, including use as hybridisation probes, and in chromosome and
 CC gene mapping.
 XX Sequence 422 BP; 84 A; 134 C; 104 G; 100 T; 0 other;
 SQ
 Query Match 99.1%; Score 178.4; DB 22; Length 422;
 Best Local Similarity 99.4%; Pred No. 1.9e-49;
 Matches 179; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 CAGGAGCGCAGTGGCCACTATGGGGTCTGGGCTGCCCTTGTCTCTTGGACCTCCT 60
 Db 39 CAGGAGCGCAGTGGCCACTATGGGGTCTGGGCTGCCCTTGTCTCTTGGACCTCCT 98
 QY 61 TGGCAGCTACATGGACAGGCGCGGTATGACTTTGCACTGAAGTGAAGGACTCTTT 120
 Db 99 TGGCAGCTACATGGACAGGCGCGGTATGACTTTGCACTGAAGTGAAGGACTCTTT 158
 QY 121 TCTGACAAATTCCTCTATGAGTCCAGCTTCTCGAATTCCTGGAATTCCTGCAATTCCT 180
 Db 159 TCTGACAAATTCCTCTATGAGTCCAGCTTCTCGAATTCCTGGAATTCCTGCAATTCCT 218
 RESULT 4
 AAF44233

ID AAF44233 standard; cDNA; 422 BP.
 XX AAF44233;
 XX 02-APR-2001 (first entry)
 DT Human PRO1098 (UNQ541) nucleotide sequence SEQ ID NO:362.
 DE Human; secreted and transmembrane protein; PRO; cytotstatic;
 KW cell death; cancer; chromosomal mapping; gene mapping; tissue typing;
 KW diagnostic assay; ss.
 XX Homo sapiens.
 OS W0200073454-A1.
 XX 07-DEC-2000.
 XX 30-MAR-2000; 2000WO-US08439.
 XX 02-JUN-1999; 99WO-US12252.
 PR 23-JUN-1999; 99US-0141037.
 PR 07-JUL-1999; 99US-0143048.
 PR 20-JUL-1999; 99US-0144758.
 PR 28-JUL-1999; 99US-0145698.
 PR 28-JUL-1999; 99US-0146222.
 PR 17-AUG-1999; 99US-0149396.
 PR 15-SEP-1999; 99WO-US21090.
 PR 08-OCT-1999; 99US-0158653.
 PR 30-NOV-1999; 99WO-US28313.
 PR 01-DEC-1999; 99WO-US28301.
 PR 16-DEC-1999; 99WO-US30095.
 PR 20-DEC-1999; 99WO-US30911.
 PR 05-JAN-2000; 2000WO-US00219.
 PR 06-JAN-2000; 2000WO-US00376.
 PR 11-FEB-2000; 2000WO-US03565.
 PR 18-FEB-2000; 2000WO-US04341.
 PR 22-FEB-2000; 2000WO-US04414.
 PR 24-FEB-2000; 2000WO-US04914.
 PR 24-FEB-2000; 2000WO-US05004.
 PR 02-MAR-2000; 2000WO-US05841.
 PR 15-MAR-2000; 2000WO-US06884.
 PR 20-MAR-2000; 2000WO-US07377.
 XX (GETH) GENENTECH INC.
 XX Ashkenazi AJ, Baker KP, Botstein D, Desnoyers L, Eaton DL;
 PI Ferrara N, Fong S, Gerber H, Gerritsen ME, Goddard A, Godowski PJ;
 PI Grimaldi CJ, Gurney AL, Kijavini IJ, Napier MA, Pan J, Paoni NF;
 PI Roy WA, Stewart TA, Tumas D, Watanabe CK, Williams PM, Wood WI;
 PI Zhang Z;
 XX WPI; 2001-032160/04.
 DR P-PSDB: AAB65264.
 XX PRO polynucleotides used to produce polypeptides used to target
 PT bioactive molecules such as toxins, radiolabels or antibodies, to
 PT specific cells, to cause targeted cell death -
 XX Claim 2; Fig 257; 935pp; English.
 XX The present invention describes human secreted and transmembrane PRO
 CC proteins. The PRO proteins have cytostatic activity. The PRO proteins
 CC can be used for targeted delivery of bioactive molecules, such as
 CC toxins, radiolabels or antibodies, that cause cell death. PRO nucleotide
 CC sequences, and their fragments, can be used as hybridisation probes. In
 CC chromosomal and gene mapping, and in the generation of anti-sense RNA
 CC and DNA. They may also be used to produce transgenic animals which are
 CC used to develop and screen therapeutically useful reagents. The PRO
 CC nucleotide and protein sequence can be used for tissue typing and in
 CC treating cancer. Anti-PRO antibodies can be used in diagnostic assays.
 CC AAF44270 to AAF44470 represent PCR primers and hybridisation probes used

PI Kato S, Sekine S, Yamaguchi T;
XX
DR WPI; 1999-045730/04.
DR P-PSDB: AAW88498.

xx New human proteins containing transmembrane domains and their
xx PT encoding sequences - useful in the preparation of antibodies and
xx PT large-scale protein production, gene diagnosis, and gene therapy
xx
xx
xx Claim 4: Page 135; 178pp: English.
xx PS

This is the nucleotide sequence of cDNA clone HP10408, which includes a coding region (also claimed) for a novel human transmembrane protein (see NAW88498). The clone was isolated from a stomach cancer cDNA library using a signal sequence detection method, and by protein synthesis by *in vitro* translation. The encoded protein has a putative signal sequence and a putative internal transmembrane domain. The invention provides nucleotide sequences (see NAW84359-76) coding for 18 transmembrane proteins (see NAW88491-508), vectors containing such polynucleotides, and eukaryotic cells containing the vectors. The proteins can be used as antigens or as compositions in the preparation of antibodies against the proteins. The polynucleotides can be used as probes for gene diagnosis, and as gene sources for gene therapy and large-scale production of proteins encoded by the cDNA. The host cells are used for the detection of ligands corresponding to the expressed proteins, and the screening of low molecular weight medicines.

SQ Sequence 439 BP; 89 A; 137 C; 109 G; 104 T; 0 other;

PT	Dmanac RT, Liu C, Tang YT;
XX	
XX	WPI: 2001-639362/73.
DR	P-FSDB: ABG01332.
DR	
XX	
XX	New isolated polynucleotide and encoded polypeptides, useful in
PT	diagnostics, forensics, gene mapping, identification of mutations
PT	responsible for genetic disorders or other traits and to assess
PT	biodiversity -
PT	
XX	Claim 1: SEQ ID No 1323; 103bp; English.
PS	

The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and amino acid sequences. AAS64197-AAS94564 represent novel human diatomic coding sequences of the invention.

Sequence 729 BP; 187 A; 169 C; 152 G; 146 T; 75 other;

CC proteins may be used as antigens in the production of specific
CC antibodies, and in assays to identify modulators (agonists and
CC antagonists) of HMT and/or HNC protein expression and activity. The
CC anti-HMT/HNC protein antibodies and antagonists may also be used to
CC downregulate protein expression and activity. The antibodies may also be
CC used as diagnostic agents for detecting the presence of flea polypeptides
CC in samples (e.g., by enzyme linked immunosorbent assay (ELISA)). The
CC present sequence represents a cat flea HMT cDNA of the invention.
XX
SQ Sequence 550 BP; 153 A; 107 C; 144 G; 138 T; 8 other;

Query Match 17.6%; Score 31.6; DB 21; Length 550;
Best Local Similarity 60.5%; Pred. No. 1.7;
Matches 32; Conservative 0; Mismatches 34; Indels 0; Gaps 0;

QY 95 TTGCACTGAAGCTGAAGAGTCTTTCTGACAGTTCCTCTATGAGTCACGCTTCTG 154
||||| | | | | | | | | | | | | | | | | |
Db 407 TTGTAACAGATGTCATCTGGGCTTTGCAGACGCGAGCAATGTGCCAGTGCCATT 348
||||| | | | | | | | | | | | | | | | | |

QY 155 GAATTGCTTGAAGCTCTGCTCCT 180
||||| | | | | | | | | | | | | | | | | |
Db 347 GCATCTGTAGCATCGTGCAGCTCCT 322
||||| | | | | | | | | | | | | | | | | |

RESULT 13

AAK83767
ID AAK83767 standard; DNA; 16596 bp.

AC AAK83767;

XX 07-NOV-2001 (first entry)

DT Human immune/haematopoietic antigen genomic sequence SEQ ID NO:38579.

DE Human; immune; haematopoietic; immune/haematopoietic antigen; cancer;
KW cytostatic; gene therapy; vaccine; metastasis; ds.

XX Homo sapiens.

PN WO200157182-A2.

XX 09-AUG-2001.

XX 17-JAN-2001; 2001WO-US01354.

XX 31-JAN-2000; 2000US-0179065.

PR 04-FEB-2000; 2000US-0180628.

PR 24-FEB-2000; 2000US-0184664.

PR 02-MAR-2000; 2000US-0186350.

PR 16-MAR-2000; 2000US-0189874.

PR 17-MAR-2000; 2000US-0190076.

PR 18-APR-2000; 2000US-0198123.

PR 19-MAY-2000; 2000US-0205515.

PR 07-JUN-2000; 2000US-0209467.

PR 28-JUN-2000; 2000US-0214886.

PR 30-JUN-2000; 2000US-0215135.

PR 07-JUL-2000; 2000US-0216647.

PR 07-JUL-2000; 2000US-0216880.

PR 11-JUL-2000; 2000US-0217487.

PR 11-JUL-2000; 2000US-0217496.

PR 14-JUL-2000; 2000US-0218290.

PR 26-JUL-2000; 2000US-0220963.

PR 26-JUL-2000; 2000US-0220964.

PR 14-AUG-2000; 2000US-0224518.

PR 14-AUG-2000; 2000US-0225213.

PR 14-AUG-2000; 2000US-0225214.

PR 14-AUG-2000; 2000US-0225266.

PR 14-AUG-2000; 2000US-0225267.

PR 14-AUG-2000; 2000US-0225268.

PR 14-AUG-2000; 2000US-0225270.

PR 14-AUG-2000; 2000US-0225447.

PR 14-AUG-2000; 2000US-0225757.

PR 14-AUG-2000; 2000US-0225758.
PR 14-AUG-2000; 2000US-0225759.
PR 18-AUG-2000; 2000US-0226279.
PR 22-AUG-2000; 2000US-0226681.
PR 22-AUG-2000; 2000US-0226868.
PR 22-AUG-2000; 2000US-0227182.
PR 23-AUG-2000; 2000US-0227009.
PR 30-AUG-2000; 2000US-0228924.
PR 01-SEP-2000; 2000US-0229287.
PR 01-SEP-2000; 2000US-0229343.
PR 01-SEP-2000; 2000US-0229345.
PR 05-SEP-2000; 2000US-0229509.
PR 05-SEP-2000; 2000US-0229513.
PR 06-SEP-2000; 2000US-0230437.
PR 06-SEP-2000; 2000US-0230438.
PR 08-SEP-2000; 2000US-0231242.
PR 08-SEP-2000; 2000US-0231243.
PR 08-SEP-2000; 2000US-0231244.
PR 08-SEP-2000; 2000US-0231413.
PR 08-SEP-2000; 2000US-0231414.
PR 08-SEP-2000; 2000US-0232080.
PR 08-SEP-2000; 2000US-0232081.
PR 12-SEP-2000; 2000US-0231968.
PR 14-SEP-2000; 2000US-0232397.
PR 14-SEP-2000; 2000US-0232398.
PR 14-SEP-2000; 2000US-0232399.
PR 14-SEP-2000; 2000US-0232400.
PR 14-SEP-2000; 2000US-0232401.
PR 14-SEP-2000; 2000US-0233063.
PR 14-SEP-2000; 2000US-0233064.
PR 14-SEP-2000; 2000US-0233065.
PR 21-SEP-2000; 2000US-0234223.
PR 21-SEP-2000; 2000US-0234274.
PR 25-SEP-2000; 2000US-0234997.
PR 25-SEP-2000; 2000US-0234998.
PR 26-SEP-2000; 2000US-0235484.
PR 27-SEP-2000; 2000US-0235834.
PR 27-SEP-2000; 2000US-0235836.
PR 29-SEP-2000; 2000US-0236327.
PR 29-SEP-2000; 2000US-0236367.
PR 29-SEP-2000; 2000US-0236368.
PR 29-SEP-2000; 2000US-0236369.
PR 29-SEP-2000; 2000US-0236370.
PR 02-OCT-2000; 2000US-0236802.
PR 02-OCT-2000; 2000US-0237037.
PR 02-OCT-2000; 2000US-0237038.
PR 02-OCT-2000; 2000US-0237039.
PR 02-OCT-2000; 2000US-0237040.
PR 13-OCT-2000; 2000US-0239935.
PR 13-OCT-2000; 2000US-0239937.
PR 20-OCT-2000; 2000US-0240960.
PR 20-OCT-2000; 2000US-0241221.
PR 20-OCT-2000; 2000US-0241785.
PR 20-OCT-2000; 2000US-0241786.
PR 20-OCT-2000; 2000US-0241787.
PR 20-OCT-2000; 2000US-0241808.
PR 20-OCT-2000; 2000US-0241809.
PR 20-OCT-2000; 2000US-0241826.
PR 01-NOV-2000; 2000US-0246417.
PR 08-NOV-2000; 2000US-0246474.
PR 08-NOV-2000; 2000US-0246475.
PR 08-NOV-2000; 2000US-0246476.
PR 08-NOV-2000; 2000US-0246477.
PR 08-NOV-2000; 2000US-0246478.
PR 08-NOV-2000; 2000US-0246523.
PR 08-NOV-2000; 2000US-0246524.
PR 08-NOV-2000; 2000US-0246525.
PR 08-NOV-2000; 2000US-0246526.
PR 08-NOV-2000; 2000US-0246527.
PR 08-NOV-2000; 2000US-0246528.
PR 08-NOV-2000; 2000US-0246532.
PR 08-NOV-2000; 2000US-0246539.
PR 08-NOV-2000; 2000US-0246609.

PR 08-NOV-2000; 2000US-0246610.
 PR 08-NOV-2000; 2000US-0246611.
 PR 08-NOV-2000; 2000US-0246613.
 PR 17-NOV-2000; 2000US-0249207.
 PR 17-NOV-2000; 2000US-0249208.
 PR 17-NOV-2000; 2000US-0249209.
 PR 17-NOV-2000; 2000US-0249210.
 PR 17-NOV-2000; 2000US-0249211.
 PR 17-NOV-2000; 2000US-0249212.
 PR 17-NOV-2000; 2000US-0249213.
 PR 17-NOV-2000; 2000US-0249214.
 PR 17-NOV-2000; 2000US-0249215.
 PR 17-NOV-2000; 2000US-0249216.
 PR 17-NOV-2000; 2000US-0249217.
 PR 17-NOV-2000; 2000US-0249218.
 PR 17-NOV-2000; 2000US-0249244.
 PR 17-NOV-2000; 2000US-0249245.
 PR 17-NOV-2000; 2000US-0249245.
 PR 17-NOV-2000; 2000US-0249264.
 PR 17-NOV-2000; 2000US-0249265.
 PR 17-NOV-2000; 2000US-0249297.
 PR 17-NOV-2000; 2000US-0249299.
 PR 17-NOV-2000; 2000US-0249300.
 PR 01-DEC-2000; 2000US-0250160.
 PR 01-DEC-2000; 2000US-0250391.
 PR 05-DEC-2000; 2000US-0251030.
 PR 05-DEC-2000; 2000US-0251988.
 PR 05-DEC-2000; 2000US-0256719.
 PR 06-DEC-2000; 2000US-0251479.
 PR 08-DEC-2000; 2000US-0251856.
 PR 08-DEC-2000; 2000US-0251868.
 PR 08-DEC-2000; 2000US-0251869.
 PR 08-DEC-2000; 2000US-0251989.
 PR 08-DEC-2000; 2000US-0251990.
 PR 11-DEC-2000; 2000US-0254097.
 PR 05-JAN-2001; 2001US-0259678.
 XX (HUMA-) HUMAN GENOME SCI INC.
 XX
 XX Rosen CA, Barash SC, Ruben SM;
 XX WPI; 2001-483426/52.
 DR
 XX
 PT Nucleic acids encoding human immune/hematopoietic antigen polypeptides,
 PT useful for preventing, diagnosing and/or treating cancers and
 PT metastasis -
 XX
 PS Disclosure; SEQ ID NO 38579; 3071pp + Sequence Listing; English.
 XX
 CC AAK54951 to AAK64702 encode the human immune/hematopoietic antigen (I)
 CC amino acid sequences given in AAK52170 to AAK591921. (I) have cytostatic
 CC activity, and can be used in gene therapy and vaccine production. (I)
 CC proteins and polynucleotides may be used in the prevention, diagnosis and
 CC treatment of diseases associated with inappropriate (I) expression. For
 CC example, they may be used to treat disorders associated with decreased
 CC expression by rectifying mutations or deletions in a patient's genome
 CC that affect the activity of (I) by expressing inactive proteins or to
 CC supplement the patients own production of (I). Additionally, (I)
 CC polynucleotides may be used to produce the secreted (I), by inserting
 CC the nucleic acids into a host cell and culturing the cell to express the
 CC protein. (I) proteins and polynucleotides may be used to prevent,
 CC diagnose and treat immune/hematopoietic-related diseases, especially
 CC cancers and cancer metastases of hematopoietic-derived cells. AAK64703
 CC to AAK87694 represent human immune/hematopoietic antigen genomic
 CC sequences from the present invention. AAK54942 to AAK54950 and AAK82169
 CC represent sequences used in the exemplification of the present invention.
 XX
 SQ Sequence 16596 BP; 3984 A; 4873 C; 4372 G; 3367 T; 0 other;
 Query Match 17.3%; Score 31.2; DB 22; Length 16596;
 Best Local Similarity 57.0%; Pred. No. 9.2;
 Matches 57; Conservative 0; Mismatches 43; Indels 0; Gaps 0;
 OY 16 CACTATGGGGTCTGGGTCGCCCTTGTCTCTCTTGACCCCTTGCACGCTCACATGG 75

DB 8094 CACCAGGCTGCCAGCGGCTCTCCGGCCCTTGTGAGCCCATGCCACCCACATGG 8153
 OY 76 AACAGGGCCGGGTATGACTTTGCAACTGAAGCTGAAGGAG 115
 DB 8154 AACATGGCTGGGGTGGACTGCAGGATGAGCTGGGGCAG 8193
 RESULT 14
 AAS33396/C
 ID AAS33396 standard; DNA; 16596 BP.
 XX
 AC AAS33396;
 XX
 DT 04-DEC-2001 (first entry)
 XX
 DE DNA encoding human secreted protein, Seq ID No 679.
 XX
 KW Immunomodulatory; human immunodeficiency virus; HIV; anaemia; angina;
 KW rheumatoid arthritis; antiarteriosclerotic; cardiant; vascular;
 KW cerebroprotective; thrombolytic; antimicrobial; ophthalmological;
 KW cytostatic; Alzheimer's disease; Parkinson's disease; human; cancer;
 KW multiple sclerosis; cancer; hyperproliferative disorder; infection;
 KW Gaucher's disease; neurological disease; cerebrovascular disorder;
 KW thrombosis; wound healing; ds.
 XX
 OS Homo sapiens.
 XX
 PN WO200155326-A2.
 XX
 PD 02-AUG-2001.
 XX
 PF 17-JAN-2001; 2001WO-US01347.
 XX
 PR 31-JAN-2000; 2000US-0179065.
 XX
 PA (HUMA-) HUMAN GENOME SCI INC.
 XX
 PI Rosen CA, Barash SC, Ruben SM;
 XX WPI; 2001-451931/48.
 DR
 PT New nucleic acids and polypeptides, useful for diagnosing, preventing
 PT or treating medical conditions -
 XX
 PS Disclosure; SEQ ID No 679; 753pp; English.
 XX
 CC The invention relates to novel isolated nucleic acid molecules (I)
 CC encoding human secreted proteins (II). (I) and (II) are used to prevent,
 CC treat or ameliorate a medical condition in e.g. humans, mice, rabbits,
 CC goats, horses, cats, dogs, chickens or sheep. (I) and (II) may be used in
 CC the prevention, treatment and diagnosis of diseases associated with
 CC inappropriate expression of secreted proteins. (I) and complementary
 CC sequences may also be used as DNA probes in diagnostic assays (e.g.
 CC polymerase chain reactions (PCR)) to detect and quantitate the presence
 CC of similar nucleic acid sequences in samples, and so which patients may
 CC be in need of restorative therapy. (II) may also be used as antigens in
 CC the production of antibodies and in assays to identify modulators
 CC (agonists and antagonists) of the expression and activity of the secreted
 CC proteins. The anti-(II) antibodies and antagonists may also be used to
 CC down regulate expression and activity of (II). The anti-(II) antibodies
 CC may also be used as diagnostic agents for detecting the presence of (II)
 CC in samples (e.g. by enzyme linked immunosorbent assay (ELISA)). The
 CC disorders include for example: immune/autoimmune diseases (e.g. HIV
 CC (human immunodeficiency virus) infections, anaemia, rheumatoid arthritis
 CC and multiple sclerosis), cancers and hyperproliferative disorders (e.g.
 CC melanomas, neoplasms of the breast or liver, Sezary syndrome and
 CC Gaucher's disease), neurological diseases (e.g. Alzheimer's disease,
 CC Parkinson's disease and Charcot-Marie-Tooth disease), cardio-/
 CC cerebrovascular disorders (e.g. cardiac arrest, tachycardia,
 CC angina and thrombosis), infections caused by bacteria, viruses and
 CC fungi and ocular disorders (e.g. corneal infections). (I) and (II),
 CC agonists, antagonists and antibodies can also be used to promote wound

CC healing, maintain organs before transplantation, and support cell culture
CC of primary tissues. AAS33043-AAS33486 represent human secreted protein
CC coding sequences, PCR primers, and related sequences of the invention.
CC Note: The sequence data for this patent did not appear in the printed
CC specification but was obtained in electronic format directly from WIPO
CC at: ftp.wipo.int/pub/published_pct_sequences.

XX
SQ Sequence 16596 BP: 3367 A; 4372 C; 4873 G; 3984 T; 0 other;

Query Match 17.3% Score 31.2; DB 22; Length 16596;
Best Local Similarity 57.0%; Pred No. 9.2;
Matches 57; Conservative 0; Mismatches 43; Indels. 0; Gaps 0;

QY 16 CACTATGGGGTGTGGGCGCCCTTCTCTCTTGACCTCTTGCGAGCGTCACTGG 75

Db 8503 CACGAGGCTGCCCGAGGGCTCTCCCGGCTTCTGAGCGCCATGCCACCATGG 8444

QY 76 AACAGGCGCGGTATGACTTGCNACTGAAGCTGAAGGAG 115

Db 8443 AACATGGCTGGGTGACTGCAGGATGAGCTGGGCGAG 8404

RESULT 15

AAI36066

ID AAL36066 standard; DNA; 11749 BP.

XX

AC AAL36066;

DT 08-JAN-2002 (first entry)

XX

DE Human musculoskeletal system related polynucleotide SEQ ID NO 2431.

XX

KW Cytostatic; immunosuppressive; nootropic; neuroprotective; antiviral;
KW antiallergic; hepatotropic; antidiabetic; antiinflammatory; antiulcer;
KW vulnary; anticonvulsant; antibacterial; antifungal; antiparasitic;
KW cardiant; gene therapy; cancer; immune disorder; cardiovascular disorder;
KW neurological disease; infection; human; secreted protein;
KW musculoskeletal system; ds.

XX Homo sapiens.

XX WO20015367-A1.

PN

PD 02-AUG-2001.

XX

XX 17-JAN-2001; 2001WO-US01338.

PF

XX 31-JAN-2000; 2000US-0179065.

PR 04-FEB-2000; 2000US-0180628.

PR 24-FEB-2000; 2000US-0184664.

PR 02-MAR-2000; 2000US-0186350.

PR 16-MAR-2000; 2000US-0189874.

PR 17-MAR-2000; 2000US-0190076.

PR 18-APR-2000; 2000US-0198123.

PR 19-MAY-2000; 2000US-0205515.

PR 07-JUN-2000; 2000US-0209487.

PR 28-JUN-2000; 2000US-0214886.

PR 30-JUN-2000; 2000US-0215135.

PR 07-JUL-2000; 2000US-0216647.

PR 07-JUL-2000; 2000US-0216880.

PR 11-JUL-2000; 2000US-0217487.

PR 11-JUL-2000; 2000US-0217496.

PR 14-JUL-2000; 2000US-0218290.

PR 26-JUL-2000; 2000US-0220963.

PR 26-JUL-2000; 2000US-0220964.

PR 14-AUG-2000; 2000US-0224518.

PR 14-AUG-2000; 2000US-0224519.

PR 14-AUG-2000; 2000US-0225213.

PR 14-AUG-2000; 2000US-0225214.

PR 14-AUG-2000; 2000US-0225266.

PR 14-AUG-2000; 2000US-0225267.

PR 14-AUG-2000; 2000US-0225268.

PR 14-AUG-2000; 2000US-0225270.

PR 14-AUG-2000; 2000US-0225447.
PR 14-AUG-2000; 2000US-0225757.
PR 14-AUG-2000; 2000US-0225758.
PR 14-AUG-2000; 2000US-0225759.
PR 18-AUG-2000; 2000US-0226279.
PR 22-AUG-2000; 2000US-0226681.
PR 22-AUG-2000; 2000US-0226688.
PR 22-AUG-2000; 2000US-0227182.
PR 23-AUG-2000; 2000US-0227009.
PR 30-AUG-2000; 2000US-0228924.
PR 01-SEP-2000; 2000US-0229287.
PR 01-SEP-2000; 2000US-0229343.
PR 01-SEP-2000; 2000US-0229344.
PR 01-SEP-2000; 2000US-0229345.
PR 03-SEP-2000; 2000US-0229509.
PR 05-SEP-2000; 2000US-0229513.
PR 06-SEP-2000; 2000US-0230437.
PR 06-SEP-2000; 2000US-0230438.
PR 08-SEP-2000; 2000US-0231242.
PR 08-SEP-2000; 2000US-0231243.
PR 08-SEP-2000; 2000US-0231244.
PR 08-SEP-2000; 2000US-0231413.
PR 08-SEP-2000; 2000US-0231414.
PR 08-SEP-2000; 2000US-0232080.
PR 08-SEP-2000; 2000US-0232081.
PR 12-SEP-2000; 2000US-0231968.
PR 14-SEP-2000; 2000US-0232397.
PR 14-SEP-2000; 2000US-0232398.
PR 14-SEP-2000; 2000US-0232399.
PR 14-SEP-2000; 2000US-0232400.
PR 14-SEP-2000; 2000US-0232401.
PR 14-SEP-2000; 2000US-0233063.
PR 14-SEP-2000; 2000US-0233064.
PR 14-SEP-2000; 2000US-0233065.
PR 21-SEP-2000; 2000US-0234223.
PR 21-SEP-2000; 2000US-0234274.
PR 25-SEP-2000; 2000US-0234997.
PR 25-SEP-2000; 2000US-0234998.
PR 26-SEP-2000; 2000US-0235484.
PR 27-SEP-2000; 2000US-0235834.
PR 27-SEP-2000; 2000US-0235836.
PR 29-SEP-2000; 2000US-0236327.
PR 29-SEP-2000; 2000US-0236367.
PR 29-SEP-2000; 2000US-0236368.
PR 29-SEP-2000; 2000US-0236369.
PR 29-SEP-2000; 2000US-0236370.
PR 02-OCT-2000; 2000US-0236802.
PR 02-OCT-2000; 2000US-0237037.
PR 02-OCT-2000; 2000US-0237038.
PR 02-OCT-2000; 2000US-0237039.
PR 02-OCT-2000; 2000US-0237040.
PR 13-OCT-2000; 2000US-0239935.
PR 13-OCT-2000; 2000US-0239937.
PR 20-OCT-2000; 2000US-0240960.
PR 20-OCT-2000; 2000US-0241221.
PR 20-OCT-2000; 2000US-0241785.
PR 20-OCT-2000; 2000US-0241786.
PR 20-OCT-2000; 2000US-0241787.
PR 20-OCT-2000; 2000US-0241808.
PR 20-OCT-2000; 2000US-0241809.
PR 20-OCT-2000; 2000US-0241826.
PR 01-NOV-2000; 2000US-0244617.
PR 08-NOV-2000; 2000US-0246474.
PR 08-NOV-2000; 2000US-0246475.
PR 08-NOV-2000; 2000US-0246476.
PR 08-NOV-2000; 2000US-0246477.
PR 08-NOV-2000; 2000US-0246478.
PR 08-NOV-2000; 2000US-0246523.
PR 08-NOV-2000; 2000US-0246524.
PR 08-NOV-2000; 2000US-0246525.
PR 08-NOV-2000; 2000US-0246526.
PR 08-NOV-2000; 2000US-0246527.
PR 08-NOV-2000; 2000US-0246528.

gencore version 5.1.5
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OM nucleic - nucleic search, using sw model

Run on: May 1, 2003, 02:59:25 ; Search time 588.571 Seconds
(without alignments)
8900.373 Million cell updates/sec

Title: US-09-092-296-3
Perfect score: 180
Sequence: 1 CAGAGCGCAGTGGCCACTA.....CTTGAAAAGCTGCTGCTCT 180

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl.*

- 1: gb_ba.*
- 2: gb_htg.*
- 3: gb_in.*
- 4: gb_om.*
- 5: gb_ov.*
- 6: gb_pat.*
- 7: gb_ph.*
- 8: gb_pl.*
- 9: gb_pr.*
- 10: gb_ro.*
- 11: gb_sts.*
- 12: gb_sy.*
- 13: gb_un.*
- 14: gb_vi.*
- 15: em_ba.*
- 16: em_fun.*
- 17: em_hum.*
- 18: em_in.*
- 19: em_mu.*
- 20: em_om.*
- 21: em_or.*
- 22: em_ov.*
- 23: em_pat.*
- 24: em_ph.*
- 25: em_pl.*
- 26: em_ro.*
- 27: em_sts.*
- 28: em_un.*
- 29: em_vi.*
- 30: em_htg_hum.*
- 31: em_htg_inv.*
- 32: em_htg_other.*
- 33: em_htg_mus.*
- 34: em_htg_pln.*
- 35: em_htg_rod.*
- 36: em_htg_mam.*
- 37: em_htg_vrt.*
- 38: em_sy.*
- 39: em_htgo_hum.*
- 40: em_htgo_mus.*
- 41: em_htgo_other.*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	180	100.0	484	9	AY102070	AY102070 Homo sapi
2	178.4	99.1	422	6	AX092334	AX092334 Sequence
3	178.4	99.1	422	6	AX376174	AX376174 Sequence
4	178.4	99.1	422	6	AX403475	AX403475 Sequence
5	101.4	56.3	624	6	AX472955	AX472955 Sequence
6	92.4	51.3	8474	9	AL662854	AL662854 Human DNA
7	90.8	50.4	47323	9	AC005937	AC005937 Homo sapi
8	90.8	50.4	104154	2	AL773541	AL773541 Homo sapi
9	90.8	50.4	156272	2	AL669830	AL669830 Human DNA
10	90.8	50.4	178688	2	AL713893	AL713893 Homo sapi
11	90.8	50.4	192650	9	AB023048	AB023048 Homo sapi
12	90.8	50.4	200000	9	AF000511	AF000511 Homo sapi
13	61	33.9	349980	6	AX344571	AX344571 Sequence
14	55.8	31.0	349980	6	AX344553	AX344553 Sequence
15	55.8	31.0	349980	6	AX344554	AX344554 Sequence
16	44.4	24.7	175345	2	AC022301	AC022301 Mus muscu
17	43.6	24.2	132977	2	RN510020	AC022301 Mus muscu
18	43.6	24.2	337832	2	AC099175	AC099175 Rattus no
19	36.2	20.1	185154	2	AC127110	AC127110 Rattus no
20	34.4	19.1	155406	2	AC105514	AC127110 Rattus no
21	34.2	19.0	188082	2	AC121784	AC105514 Rattus no
22	33.6	18.7	292172	2	AC125207	AC121784 Mus muscu
23	33.4	18.6	6855	9	AB051446	AC125207 Mus muscu
24	33.4	18.6	97580	9	HS591N18	AB051446 Homo sapi
25	33	18.3	250442	2	AC113213	AL031594 Human DNA
26	33	18.3	349116	1	AF005003	AC113213 Rattus no
27	32.8	18.2	145105	2	AC018432	AC003003 Mesorhizo
28	32.8	18.2	158481	9	AL158063	AC018432 Homo sapi
29	32.6	18.1	165618	9	AL442636	AL158063 Human DNA
30	32.6	18.1	177088	9	AC022203	AL442636 Human DNA
31	32.4	18.0	130742	2	AP005653	AC022203 Homo sapi
32	32.4	18.0	136733	2	AC127917	AP005653 Oryza sat
33	32.2	17.9	36676	9	HS1858B16	AC127917 Rattus no
34	32	17.8	178410	2	AC125148	AL096768 Human DNA
35	31.8	17.7	76854	2	AC130321	AC125148 Mus muscu
36	31.8	17.7	188121	2	AC093394	AC130321 Homo sapi
37	31.8	17.7	258446	2	AL691445	AC093394 Bos tauru
38	31.6	17.6	92756	2	AF322454	AL691445 Mus muscu
39	31.6	17.6	135171	2	AC120056	AF322454 Homo sapi
40	31.6	17.6	140678	9	AC079922	AC120056 Homo sapi
41	31.6	17.6	168421	2	AL808133	AC079922 Homo sapi
42	31.6	17.6	175773	2	AC113472	AL808133 Mus muscu
43	31.6	17.6	178531	2	AC067802	AC113472 Mus muscu
44	31.6	17.6	193450	2	AC111003	AC067802 Homo sapi
45	31.6	17.6	203269	2	AC080187	AC111003 Homo sapi
						AC080187 Homo sapi

ALIGNMENTS

RESULT 1
AY102070
LOCUS Homo sapiens surfactant associated protein G mRNA, partial
DEFINITION sequence.
ACCESSION AY102070
VERSION AY102070.1 GI:21464498
KEYWORDS human.
SOURCE Homo sapiens
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 484)
AUTHORS Walker, M.G. and Spiro, P.
TITLE Genes co-expressed with pulmonary surfactants

JOURNAL Unpublished
REFERENCE 2 (bases 1 to 484)
AUTHORS Walker,M.G. and Spiro,P.
TITLE Direct Submission
JOURNAL Submitted (07-MAY-2002) Incyte Genomics, 1475 Flamingo Way,
Sunnyvale, CA 94087-3405, USA
FEATURES
source 1..484
Location/Qualifiers
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="236582"
/c1..>484
gene
/genes="surfactant associated protein G"
/note="SFTPG"
BASE COUNT 124 a 149 c 110 g 101 t
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Best Local Similarity 100.0%; Pred. No. 3e-48; 0; Indels 0; Gaps 0;
Matches 180; Conservative 0; Mismatches 0;
QY 1 CAGGAGCGAGTGGCCACTATGGGGTCTGGGGTGGCCCTTGTCTCTCTCTGACCCCTCT 60
Db 36 CAGGAGCGAGTGGCCACTATGGGGTCTGGGGTGGCCCTTGTCTCTCTCTGACCCCTCT 95
QY 61 TGGCAGCTCACATGGAACAGGCGCGGGTATGACTTTGCAACTGAAGCTGAAGGAGTCTTT 120
Db 96 TGGCAGCTCACATGGAACAGGCGCGGGTATGACTTTGCAACTGAAGCTGAAGGAGTCTTT 155
QY 121 TCTGACAGTTCCTCTATGAGTCCAGCTTCCTGGAATTCCTGAAAGCTCTGCCCTCT 180
Db 156 TCTGACAGTTCCTCTATGAGTCCAGCTTCCTGGAATTCCTGAAAGCTCTGCCCTCT 215
RESULT 2
AX092334
LOCUS AX092334
DEFINITION Sequence 65 from Patent WO0116318.
ACCESSION AX092334
VERSION AX092334.1 GI:13444481
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Euthera; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 422)
AUTHORS Eaton,D.L., Filvaroff,E., Gerritsen,M.E., Goddard,A.,
Godowski,P.J., Grimaldi,C.J., Gurney,A.L., Watanabe,C.K. and
Wood,W.I.
TITLE Secreted and transmembrane polypeptides and nucleic acids encoding
the same
JOURNAL Patent: WO 0116318-A 55 08-MAR-2001;
Genentech, Inc. (US)
FEATURES
source 1..422
Location/Qualifiers
/organism="Homo sapiens"
/db_xref="taxon:9606"
BASE COUNT 84 a 134 c 104 g 100 t
ORIGIN
Query Match 99.1%; Score 178.4; DB 6; Length 422;
Best Local Similarity 99.4%; Pred. No. 1e-47;
Matches 179; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 CAGGAGCGAGTGGCCACTATGGGGTCTGGGGTGGCCCTTGTCTCTCTCTGACCCCTCT 60
Db 39 CAGGAGCGAGTGGCCACTATGGGGTCTGGGGTGGCCCTTGTCTCTCTCTGACCCCTCT 98
QY 61 TGGCAGCTCACATGGAACAGGCGCGGGTATGACTTTGCAACTGAAGCTGAAGGAGTCTTT 120
Db 99 TGGCAGCTCACATGGAACAGGCGCGGGTATGACTTTGCAACTGAAGCTGAAGGAGTCTTT 158
QY 121 TCTGACAGTTCCTCTATGAGTCCAGCTTCCTGGAATTCCTGAAAGCTCTGCCCTCT 180
Db 156 TCTGACAGTTCCTCTATGAGTCCAGCTTCCTGGAATTCCTGAAAGCTCTGCCCTCT 218
RESULT 3
AX376174
LOCUS AX376174
DEFINITION Sequence 241 from Patent WO0168848.
ACCESSION AX376174
VERSION AX376174.1 GI:19170479
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Euthera; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1
AUTHORS Baker,K.P., Chen,J., Desnoyers,L., Goddard,A., Godowski,P.J.,
Gurney,A.L., Pan,J., Smith,V., Watanabe,C.K., Wood,W.I. and
Zhang,Z.
TITLE Secreted and transmembrane polypeptides and nucleic acids encoding
the same
JOURNAL Patent: WO 0168848-A 241 20-SEP-2001;
Genentech, Inc. (US)
FEATURES
source 1..422
Location/Qualifiers
/organism="Homo sapiens"
/db_xref="taxon:9606"
BASE COUNT 84 a 134 c 104 g 100 t
ORIGIN
Query Match 99.1%; Score 178.4; DB 6; Length 422;
Best Local Similarity 99.4%; Pred. No. 1e-47;
Matches 179; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 CAGGAGCGAGTGGCCACTATGGGGTCTGGGGTGGCCCTTGTCTCTCTCTGACCCCTCT 60
Db 39 CAGGAGCGAGTGGCCACTATGGGGTCTGGGGTGGCCCTTGTCTCTCTCTGACCCCTCT 98
QY 61 TGGCAGCTCACATGGAACAGGCGCGGGTATGACTTTGCAACTGAAGCTGAAGGAGTCTTT 120
Db 99 TGGCAGCTCACATGGAACAGGCGCGGGTATGACTTTGCAACTGAAGCTGAAGGAGTCTTT 158
QY 121 TCTGACAGTTCCTCTATGAGTCCAGCTTCCTGGAATTCCTGAAAGCTCTGCCCTCT 180
Db 156 TCTGACAGTTCCTCTATGAGTCCAGCTTCCTGGAATTCCTGAAAGCTCTGCCCTCT 218
RESULT 4
AX403475
LOCUS AX403475
DEFINITION Sequence 362 from Patent WO0073454.
ACCESSION AX403475
VERSION AX403475.1 GI:21436973
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Euthera; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1
AUTHORS Ashkenazi,A.J., Baker,K.P., Botstein,D., Desnoyers,L., Eaton,D.,
Ferrara,N., Gerber,H., Gerritsen,M., Goddard,A., Godowski,P.,
Grimaldi,C.J., Gurney,A.L., Kijavini,I., Napier,M.A., Pan,J.,
Paoni,N.F., Roy,M., Stewart,T.A., Tamas,D., Watanabe,C.K.,
Williams,P., Wood,W.I. and Zhang,Z.
TITLE Secreted and transmembrane polypeptides and nucleic acids encoding
the same
JOURNAL Patent: WO 0073454-A 362 07-DEC-2000;
Genentech Inc. (US)
FEATURES
source 1..422
Location/Qualifiers
/organism="Homo sapiens"
/db_xref="taxon:9606"
BASE COUNT 84 a 134 c 104 g 100 t

Db 159 TCTGACAAATTCCTCTATGAGTCCAGCTTCCTGGAATTCCTGAAAGCTCTGCCCTCT 218
RESULT 3
AX376174
LOCUS AX376174
DEFINITION Sequence 241 from Patent WO0168848.
ACCESSION AX376174
VERSION AX376174.1 GI:19170479
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Euthera; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1
AUTHORS Baker,K.P., Chen,J., Desnoyers,L., Goddard,A., Godowski,P.J.,
Gurney,A.L., Pan,J., Smith,V., Watanabe,C.K., Wood,W.I. and
Zhang,Z.
TITLE Secreted and transmembrane polypeptides and nucleic acids encoding
the same
JOURNAL Patent: WO 0168848-A 241 20-SEP-2001;
Genentech, Inc. (US)
FEATURES
source 1..422
Location/Qualifiers
/organism="Homo sapiens"
/db_xref="taxon:9606"
BASE COUNT 84 a 134 c 104 g 100 t
ORIGIN
Query Match 99.1%; Score 178.4; DB 6; Length 422;
Best Local Similarity 99.4%; Pred. No. 1e-47;
Matches 179; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 CAGGAGCGAGTGGCCACTATGGGGTCTGGGGTGGCCCTTGTCTCTCTCTGACCCCTCT 60
Db 39 CAGGAGCGAGTGGCCACTATGGGGTCTGGGGTGGCCCTTGTCTCTCTCTGACCCCTCT 98
QY 61 TGGCAGCTCACATGGAACAGGCGCGGGTATGACTTTGCAACTGAAGCTGAAGGAGTCTTT 120
Db 99 TGGCAGCTCACATGGAACAGGCGCGGGTATGACTTTGCAACTGAAGCTGAAGGAGTCTTT 158
QY 121 TCTGACAAATTCCTCTATGAGTCCAGCTTCCTGGAATTCCTGAAAGCTCTGCCCTCT 180
Db 159 TCTGACAAATTCCTCTATGAGTCCAGCTTCCTGGAATTCCTGAAAGCTCTGCCCTCT 218
RESULT 4
AX403475
LOCUS AX403475
DEFINITION Sequence 362 from Patent WO0073454.
ACCESSION AX403475
VERSION AX403475.1 GI:21436973
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Euthera; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1
AUTHORS Ashkenazi,A.J., Baker,K.P., Botstein,D., Desnoyers,L., Eaton,D.,
Ferrara,N., Gerber,H., Gerritsen,M., Goddard,A., Godowski,P.,
Grimaldi,C.J., Gurney,A.L., Kijavini,I., Napier,M.A., Pan,J.,
Paoni,N.F., Roy,M., Stewart,T.A., Tamas,D., Watanabe,C.K.,
Williams,P., Wood,W.I. and Zhang,Z.
TITLE Secreted and transmembrane polypeptides and nucleic acids encoding
the same
JOURNAL Patent: WO 0073454-A 362 07-DEC-2000;
Genentech Inc. (US)
FEATURES
source 1..422
Location/Qualifiers
/organism="Homo sapiens"
/db_xref="taxon:9606"
BASE COUNT 84 a 134 c 104 g 100 t

DRUGLISM
 homo sapiens
 Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
 1
 Tracey, A.
 Direct Submission
 Submitted (23-Apr-2002) Wellcome Trust Sanger Institute, Hinxton,
 Cambridgeshire, CB10 1SA, UK. E-mail enquiries:
 humpquies@sanger.ac.uk
 Clone requests: clonerequest@sanger.ac.uk

JOURNAL

Submitted (05-NOV-1998) Human Genome Center, University of Washington, Box 352145, Seattle, WA 98105, USA

REMARK

University of Washington Human Genome Center
Box 352145 Seattle, WA 98195
Contact: Daniel E. Geraghty (geraghty@fhrc.org)
Overlapping Sequences:
5': UWGC:370m23.013 (Genbank Accession: AC005530)
3': UWGC:y67c112 (Genbank Accession: AC004211)

COMMENT

Sequence Quality Assessment:
This entry has been annotated with sequence quality estimates computed by the Phrap assembly program. All manually edited bases have been reduced to quality zero. Quality levels above 40 are expected to have less than 1 error in 10,000 bp.
Base-by-base quality values are not generally visible from the GenBank flat file format but are available as part of this entry's ASN.1 file.

Double stranded (DS) coverage: 75.5%
DS or two chemistry coverage: 98.9%
Single stranded regions: 3

Sequence Validation:
This sequence has been validated by Multiple Complete Digest Mapping. Comparison of the experimentally derived map digest fragments with sequence-predicted fragments is given below. Small fragments below a variable cutoff (approximately 400-600bp) are not mapped and hence do not appear in the table. There are no significant remaining discrepancies between the experimental and predicted values. Uniquely ordered fragment groups are separated by dashed lines.

BgIII		HindIII		NsiI	
Map	Seq	Map	Seq	Map	Seq
1069.11	1050.00	889.55	866.00	30541.40	30653.00
20320.67	20855.00	1050.18	1015.00	3279.08	3231.00
2171.50	2147.00	7268.78	7196.00		
2560.20	2531.00	10085.80	9992.00		
4335.42	4269.00	11212.78	11131.00		
2698.62	2628.00				
1927.50	1887.00				
3130.46	3090.00				
2166.69	2129.00				
2044.67	2005.00				

FEATURES

source	Location/Qualifiers
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	/db_xref="taxon:9606"
	/chromosome="6"
	/map="6p21"
	/sub_clone="UWGC:370M23.002"
	/clone_lib="Research Genetics BAC Library"
repeat_region	3647..3932
repeat_region	/rpt_family="Alu"
repeat_region	complement(4999..5277)
repeat_region	/rpt_family="Alu"
repeat_region	6285..6572
repeat_region	/rpt_family="Alu"
repeat_region	complement(6972..7050)
repeat_region	/rpt_family="MLT1"
repeat_region	7286..7584
repeat_region	/rpt_family="Alu"
repeat_region	complement(8164..8609)
repeat_region	/rpt_family="Alu"

repeat_region	complement(21287..21895)
repeat_region	/rpt_family="Alu"
repeat_region	22715..22957
repeat_region	/rpt_family="Alu"
repeat_region	25510..25802
repeat_region	/rpt_family="Alu"
repeat_region	27835..28010
repeat_region	/rpt_family="MER20"
repeat_region	31295..31594
repeat_region	/rpt_family="Alu"
repeat_region	33515..33767
repeat_region	/rpt_family="Alu"
repeat_region	34223..34290
repeat_region	/rpt_family="MIR"
repeat_region	37372..37648
repeat_region	/rpt_family="Alu"
repeat_region	38526..38700
repeat_region	/rpt_family="MER3"
repeat_region	39583..40010
repeat_region	/rpt_family="Alu"
repeat_region	40046..40156
repeat_region	/rpt_family="Alu"
repeat_region	43194..43372
repeat_region	/rpt_family="MER5"
variation	43325
variation	/note="clonal variation with 3' overlapping clone"
variation	44149
variation	/note="clonal variation with 3' overlapping clone"
variation	4451
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variation	44537
variation	/note="clonal variation with 3' overlapping clone"
variation	44814
variation	/note="clonal variation with 3' overlapping clone"
variation	44965
variation	/note="clonal variation with 3' overlapping clone"
variation	45760
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variation	45900
variation	/note="clonal variation with 3' overlapping clone"
variation	46851
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variation	47032
variation	/note="clonal variation with 3' overlapping clone"
variation	47240..47256
variation	/note="clonal variation with 3' overlapping clone - insertion of 17bp repeat"

BASE COUNT 11556 a 11489 c 12284 g 11994 t
ORIGIN

Query Match	50.4%;	Score 90.8;	DB 9;	Length 47323;
Best Local Similarity	97.9%;	Pred. No. 9,2e-19;		
Matches 92;	Conservative 0;	Mismatches 2;	Indels 0;	Gaps 0;
QY 78	CAGGCGCGGTATGACCTTGCACCTGAAGGAGCTTTTCTGACAAAGTTCCTCT 137			
DB 35465	CAGGCGCGGTATGACCTTGCACCTGAAGGAGCTTTTCTGACAAATTCCTCT 35524			
QY 138	ATGAGTCCAGCTTCTGGAATTCCTGAAAAGCT 171			
DB 35525	ATGAGTCCAGCTTCTGGAATTCCTGAAAAGGT 35558			

RESULT 8
AL773541
LOCUS Homo sapiens chromosome 6 clone XDbac-11J22, *** SEQUENCING IN DEFINITION
PROGRESS ***, in ordered pieces.
ACCESSION AL773541
VERSION AL773541.4 GI:22204637
KEYWORDS HTG; HTGS_PHRASE2; HTGS_ACTIVEFIN; HTGS_DRAFT; HTGS_FULLTOP.

SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 104154)
 AUTHORS Almeida, J.
 TITLE Direct Submission
 JOURNAL Submitted (31-JUL-2002) Wellcome Trust Sanger Institute, Hinxton,
 Cambridgeshire, CB10 1SA, UK. E-mail enquiries:
 humquerry@sanger.ac.uk
 COMMENT On Aug 11, 2002 this sequence version replaced gi:21621737.
 ----- Genome Center
 Center: Wellcome Trust Sanger Institute
 Center code: SC
 Web site: <http://www.sanger.ac.uk>
 Contact: humquerry@sanger.ac.uk
 ----- Project Information
 Center project name: BOB11J22
 ----- Summary Statistics
 Assembly program: XGAP4; version 4.5
 Chemistry: Dye-terminator; 100% of reads
 Consensus quality: 104135 bases at least Q40
 Consensus quality: 104142 bases at least Q30
 Consensus quality: 104145 bases at least Q20
 Insert size: 104154; sum-of-contigs
 Quality coverage: 110727; 1.1% error; agarose-fp
 Quality coverage: 19,52x in Q20 bases; sum-of-contigs Quality
 coverage: 18,64x in Q20 bases; agarose-fp

 * NOTE: This is a 'working draft' sequence.
 * This sequence will be replaced
 * by the finished sequence as soon as it is available and
 * the accession number will be preserved.

FEATURES
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 1..104154
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /chromosome="6"
 /clone="XXbac-11J22"
 /clone_lib="DNA-arts-BAC.1-OB.L.1"
 misc_feature 1..104154
 /note="assembly fragment:00090"
 BASE COUNT 26560 a 25418 c 26093 g 26083 t
 ORIGIN
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 QY 78 CAGGCCGGGTATGACTTTGCAACTGAAGCTGAAGAGTCTTTTCTGACAAAGTTCTCTCT 137
 Db 67846 CAGGCCGGGTATGACTTTGCAACTGAAGCTGAAGAGTCTTTTCTGACAAATTCCTCT 67905
 |||||
 QY 138 ATGAGTCCAGCTTCCTGGAATTCCTGAAAAGCT 171
 Db 67906 ATGAGTCCAGCTTCCTGGAATTCCTGAAAAGCT 67939
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 RESULT 9
 AL669830/c
 LOCUS Human DNA sequence from clone XXbac-118E17 on chromosome 6,
 DEFINITION complete sequence.
 ACCESSION AL669830
 VERSION AL669830.9 GI:20135762
 KEYWORDS HTG.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1
 AUTHORS Johnson, C.
 TITLE Direct Submission

JOURNAL Submitted (23-APR-2002) Wellcome Trust Sanger Institute, Hinxton,
 Cambridgeshire, CB10 1SA, UK. E-mail enquiries:
 humquerry@sanger.ac.uk
 COMMENT On Apr 10, 2002 this sequence version replaced gi:20067510.
 During sequence assembly data is compared from overlapping clones.
 Where differences are found these are annotated as variations
 together with a note of the overlapping clone name. Note that the
 variation annotation may not be found in the sequence submission
 corresponding to the overlapping clone, as we submit sequences with
 only a small overlap as described above.
 This sequence was finished as follows unless otherwise noted: all
 regions were either double-stranded or sequenced with an alternate
 chemistry or covered by high quality data (i.e., phred quality >= 30);
 an attempt was made to resolve all sequencing problems, such
 as compressions and repeats; all regions were covered by at least
 one plasmid subclone or more than one M13 subclone; and the
 assembly was confirmed by restriction digest. The following
 abbreviations are used to associate primary accession numbers given
 in the feature table with their source databases: Em', EMBL; Sw',
 SWISSPROT; Tr', TREMBL; Wp', WORMPEP; Information on the WORMPEP
 database can be found at
http://www.sanger.ac.uk/projects/C_elegans/wormpep
 from a CHORI-501 human bac - P6F cell line library VECTOR:
 pTARBAC2.1
 This sequence was generated from part of bacterial clone contigs
 constructed by the MHC Haplotype Consortium and collaborators.
 Further information can be found at
<http://www.sanger.ac.uk/HGP/Chr6/MHC>.

FEATURES
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 1..156272
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /chromosome="6"
 /clone="XXbac-118E17"
 /clone_lib="CHORI-501"
 BASE COUNT 41135 a 37989 c 36907 g 40241 t
 ORIGIN
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 Query Match 50.4%; Score 90.8; DB 9; Length 156272;
 Best Local Similarity 97.9%; Pred. No. 9.7e-19;
 Matches 92; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
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 QY 78 CAGGCCGGGTATGACTTTGCAACTGAAGCTGAAGAGTCTTTTCTGACAAAGTTCTCTCT 137
 Db 25558 CAGGCCGGGTATGACTTTGCAACTGAAGCTGAAGAGTCTTTTCTGACAAATTCCTCT 25499
 |||||
 QY 138 ATGAGTCCAGCTTCCTGGAATTCCTGAAAAGCT 171
 Db 25498 ATGAGTCCAGCTTCCTGGAATTCCTGAAAAGCT 25465
 |||||
 RESULT 10
 AL713893
 LOCUS Homo sapiens chromosome 6 clone XXbac-307M4, *** SEQUENCING IN
 DEFINITION PROGRESS ***, 6 unordered pieces.
 ACCESSION AL713893
 VERSION AL713893.5 GI:19847952
 KEYWORDS HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_FULLTOP.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1
 AUTHORS Sims, S.
 TITLE Direct Submission
 JOURNAL Submitted (26-MAR-2002) Wellcome Trust Sanger Institute, Hinxton,
 Cambridgeshire, CB10 1SA, UK. E-mail enquiries:
 humquerry@sanger.ac.uk
 COMMENT On Mar 29, 2002 this sequence version replaced gi:19772907.
 ----- Genome Center
 Center: Wellcome Trust Sanger Institute
 Center code: SC

Web site: <http://www.sanger.ac.uk>
 Contact: humquery@sanger.ac.uk
 ----- Project Information
 Center project name: bpg307M4
 ----- Summary Statistics

Assembly program: XGAP4; version 4.5
 Chemistry: Dye-terminator Big Dye; 100% of reads
 Consensus quality: 177277 bases at least Q40
 Consensus quality: 177708 bases at least Q30
 Consensus quality: 177956 bases at least Q20
 Insert size: 178188; sum-of-contigs
 Insert size: 192613; 0.9% error; agarose-fp
 Quality coverage: 8.57x in Q20 bases; sum-of-contigs Quality
 Coverage: 8.00x in Q20 bases; agarose-fp

 * NOTE: This is a 'working draft' sequence. It currently
 * consists of 6 contigs. The true order of the pieces
 * is not known and their order in this sequence record is
 * arbitrary. Gaps between the contigs are represented as
 * runs of N, but the exact sizes of the gaps are unknown.
 * This record will be updated with the finished sequence.
 * as soon as it is available and the accession number will
 * be preserved.

1 37410: contig of 37410 bp in length
 * 37411 37510: gap of 100 bp
 * 37511 82372: contig of 44862 bp in length
 * 82373 82472: gap of 100 bp
 * 82473 142457: contig of 59985 bp in length
 * 142458 142557: gap of 100 bp
 * 142558 152859: contig of 10302 bp in length
 * 152860 152959: gap of 100 bp
 * 152960 172054: contig of 19095 bp in length
 * 172055 172154: gap of 100 bp
 * 172155 178688: contig of 6534 bp in length.

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 Matches 92; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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RESULT 11

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 DEFINITION clone:53L9, complete sequence.

ACCESSION AB023048
 VERSION AB023048.1 GI:5672603

KEYWORDS HYG.

SOURCE Homo sapiens cell_line:978SK DNA, clone:53L9.

ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE

AUTHORS Shihina,T., Tamiya,G., Oka,A., Takishima,N., Yamagata,T.,
 Kikkawa,E., Iwata,K., Tomizawa,M., Okuaki,N., Kuwano,Y.,
 Watanabe,K., Fukuzumi,Y., Itakura,S., Sugawara,C., Ono,A.,
 Yamazaki,M., Tashiro,H., Ando,A., Ikemura,T., Soeda,E., Kimura,M.,
 Bahram,S. and Inoko,H.
 TITLE Molecular dynamics of MHC genesis unraveled by sequence analysis of
 the 1,796,938-bp HLA class I region
 JOURNAL Proc. Natl. Acad. Sci. U.S.A. 96 (23), 13282-13287 (1999)
 MEDLINE 20027539
 REFERENCE 2 (bases 1 to 192650)
 AUTHORS Shihina,T. and Takishima,N.
 TITLE Direct Submission
 JOURNAL Submitted (29-JAN-1999) Takashi Shihina, Tokai University School of
 Medicine, Department of Molecular Life Science 2; Bohseidai,
 Isehara, Kanagawa 259-1193, Japan
 (E-mail:tsihina@is.icc.u-tokai.ac.jp, Tel:81-463-93-1121,
 Fax:81-463-94-8884)

FEATURES

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RESULT 12

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 LOCUS Homo sapiens genomic DNA, chromosome 6p21.3, HLA Class I region,
 DEFINITION section 10/20.

ACCESSION AP000511 BA000025

VERSION AP000511.1 GI:5926698

KEYWORDS

SOURCE Homo sapiens DNA.

ORGANISM

Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE

AUTHORS Shihina,S., Tamiya,G., Oka,A. and Inoko,H.
 TITLE Homo sapiens 2,229,817bp genomic DNA of 6p21.3 HLA class I region

JOURNAL REFERENCE AUTHORS TITLE JOURNAL	Published Only in Database (1999) 2 (bases 1 to 20000) Hirakawa,M., Yamaguchi,H., Inai,K. and Shimada,J. Direct Submission Submitted (21-SEP-1999) Mika Hirakawa, Japan Science and Technology Corporation (JST), Advanced Databases Department; 5-3, Yonbancho, Chiyoda-ku, Tokyo 102-0081, Japan (E-mail:mika@tokyo.jst.go.jp, URL:http://www-alls.tokyo.jst.go.jp/, Tel:81-3-5214-8491, Fax:81-3-5214-8470) This sequence is conducted by Tokai University as a JST sequencing Team. Principal Investigator: Hidetoshi Inoko Ph.D Phone:81-463-93-1121, Fax:81-463-94-8884, The sequence is submitted by Human Genome Sequencing in ALIS project of JST Japan Science and Technology Corporation (JST) 5-3, Yonbancho, Chiyoda-ku, Tokyo, 102-0081 Japan For further infomation about this sequences, please visit our sequence archive Web site (http://www-alls.tokyo.jst.go.jp/HGS/top.html) or send email to webmaster@www-alls.tokyo.jst.go.jp. Location/Qualifiers 1. 200000 /organism="Homo sapiens" /db_xref="taxon:9606" /chromosome="6" /map="6p21.3" 108774..108864 /standard_name="D6S2088" /note="SHGC-12985:The location is between each flanking site of PCR primers." /db_xref="GBD:735268" 115648..115906 /standard_name="D6S1898" /note="WI-9418:The location is between each flanking site of PCR primers." /db_xref="GBD:678272" complement(115665..115896) /note="Cda0vhl0;The location is between each flanking site of PCR primers." /db_xref="GBD:443382" join(127993..128284,128708..128786,128938..128985,129637..129767,129949..130081,130328..130411,130596..130664,130826..130937,131154..131242,131334..131430,132032..132163,132556..132660,132922..133061,133692..133813) /genes="TFIIH" 127993..128284 /genes="TFIIH" /number=14 complement(join(128112..128284,128708..128786,128938..128985,129637..129767,129949..130081,130328..130411,130596..130664,130826..130937,131154..131242,131334..131430,132032..132163,132556..132660,132922..133058)) /genes="TFIIH" complement(join(128112..128284,128708..128786,128938..128985,129637..129767,129949..130081,130328..130411,130596..130664,130826..130937,131154..131242,131334..131430,132032..132163,132556..132660,132922..133058)) /genes="TFIIH" /codon_start=1 /product="Transcription factor II H" /protein_id="BAB63317.1" /db_xref="GI:15277224"	exon	VKRFWRQKHSS" 128708..128786 /gene="TFIIH" /number=13 128938..128985 /gene="TFIIH" /number=12 129637..129767 /gene="TFIIH" /number=11 129949..130081 /gene="TFIIH" /number=10 130328..130411 /gene="TFIIH" /number=9 130596..130664 /gene="TFIIH" /number=8 130826..130937 /gene="TFIIH" /number=7 131154..131242 /gene="TFIIH" /number=6 131334..131430 /gene="TFIIH" /number=5 132032..132163 /gene="TFIIH" /number=4 132556..132660 /gene="TFIIH" /number=3 132922..133061 /gene="TFIIH" /number=2 133692..133813 /gene="TFIIH" /number=1 join(141936..142934,143053..143202,143783..144017,14493..144711,144949..145076,145225..145469,146576..146686,147419..147584,148667..148818,148927..149022,149548..149794,149902..150089,150614..150712,150972..151119,152662..152890,153082..153184,153278..153703) /gene="DDR" 141936..142934 /gene="DDR" /number=17 142030..142159 /gene="DDR" /standard_name="D6S2203" /note="SHGC-16870:The location is between each flanking site of PCR primers." /db_xref="GBD:741215" complement(142085..142322) /note="RH18132:The location is between each flanking site of PCR primers." /db_xref="GBD:4573021" complement(142479..142740) /standard_name="D6S1851" /note="SHGC-10808:The location is between each flanking site of PCR primers." /db_xref="GBD:675281"
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Db 110306 CAGGCGCGGTATGCTTGCACCTGAAGCTGAAGGAGTCTTTCTGCACAAATTCCTCT 110365
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RESULT 13
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ACCESSION AX344571
VERSION AX344571.1 GI:18492457
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SOURCE synthetic construct.
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1
AUTHORS Olek,A., Piepenbrock,C. and Berlin,K.
TITLE Diagnosis of known genetic parameters within the mhc
JOURNAL Patent: WO 0200932-A 22 03-JAN-2002;
Epigenomics AG (DE)
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RESULT 14
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LOCUS Sequence 4 from Patent WO0200932.
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ACCESSION AX344553
VERSION AX344553.1 GI:18492439
KEYWORDS .
SOURCE synthetic construct.
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1
AUTHORS Olek,A., Piepenbrock,C. and Berlin,K.
TITLE Diagnosis of known genetic parameters within the mhc
JOURNAL Patent: WO 0200932-A 4 03-JAN-2002;
Epigenomics AG (DE)
FEATURES Location/Qualifiers
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BASE COUNT 86882 a 5859 c 85073 g 172166 t
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GenCore version 5.1.5
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OM nucleic - nucleic search, using sw model

Run on: May 1, 2003, 04:34:36 ; Search time 61.534 Seconds
(without alignments)
4397.425 Million cell updates/sec

Title: US-09-092-296-2

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Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 746064 seqs, 590810554 residues

Total number of hits satisfying chosen parameters: 1492128

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published_Applications_NA.*

1: /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq.*
2: /cgn2_6/ptodata/1/pubpna/FCI_NEW_PUB.seq.*
3: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq.*
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6: /cgn2_6/ptodata/1/pubpna/FCIUS_PUBCOMB.seq.*
7: /cgn2_6/ptodata/1/pubpna/US08_NEW_PUB.seq.*
8: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq.*
9: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq.*
10: /cgn2_6/ptodata/1/pubpna/US09_PUBCOMB.seq.*
11: /cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq.*
12: /cgn2_6/ptodata/1/pubpna/US10_PUBCOMB.seq.*
13: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq.*
14: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	229	100.0	229	9	US-09-092-296-2
2	228	99.6	239	9	US-09-092-296-1
3	218	95.2	413	9	US-09-092-296-6
4	218	95.2	422	9	US-09-992-598-362
5	218	95.2	422	9	US-09-989-293A-362
6	218	95.2	422	9	US-10-063-547-65
7	218	95.2	422	9	US-09-989-735-362
8	218	95.2	422	9	US-09-990-444-362
9	218	95.2	422	9	US-09-989-730-362
10	218	95.2	422	9	US-09-990-436-362
11	218	95.2	422	9	US-09-991-181-362
12	218	95.2	422	9	US-09-993-687-362
13	218	95.2	422	9	US-09-989-734-362
14	218	95.2	422	9	US-09-997-653-362
15	218	95.2	422	9	US-10-174-590-241
16	218	95.2	422	9	US-10-176-758-241
17	218	95.2	422	9	US-10-063-616-65
18	218	95.2	422	9	US-10-175-737-241
19	218	95.2	422	9	US-09-993-667-362

20 218 95.2 422 9 US-10-063-502-65 Sequence 65, Appl
21 218 95.2 422 9 US-10-173-706-241 Sequence 241, App
22 218 95.2 422 9 US-10-175-738-241 Sequence 241, App
23 218 95.2 422 9 US-10-175-752-241 Sequence 241, App
24 218 95.2 422 9 US-10-176-482-241 Sequence 241, App
25 218 95.2 422 9 US-10-176-757-241 Sequence 241, App
26 218 95.2 422 9 US-10-176-913-241 Sequence 241, App
27 218 95.2 422 9 US-10-180-552-241 Sequence 241, App
28 218 95.2 422 9 US-10-180-557-241 Sequence 241, App
29 218 95.2 422 9 US-09-990-438-362 Sequence 362, App
30 218 95.2 422 9 US-09-990-562-362 Sequence 362, App
31 218 95.2 422 9 US-09-997-428-362 Sequence 362, App
32 218 95.2 422 9 US-09-997-666-362 Sequence 362, App
33 218 95.2 422 9 US-10-173-700-241 Sequence 241, App
34 218 95.2 422 9 US-10-174-572-241 Sequence 241, App
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37 218 95.2 422 9 US-10-174-588-241 Sequence 241, App
38 218 95.2 422 9 US-10-175-739-241 Sequence 241, App
39 218 95.2 422 9 US-10-175-740-241 Sequence 241, App
40 218 95.2 422 9 US-10-175-743-241 Sequence 241, App
41 218 95.2 422 9 US-10-176-488-241 Sequence 241, App
42 218 95.2 422 9 US-10-176-492-241 Sequence 241, App
43 218 95.2 422 9 US-10-176-747-241 Sequence 241, App
44 218 95.2 422 9 US-10-176-750-241 Sequence 241, App
45 218 95.2 422 9 US-10-176-985-241 Sequence 241, App

ALIGNMENTS

RESULT 1
US-09-092-296-2
: Sequence 2, Application US/09092296
: Publication No. US20020188114A1
: GENERAL INFORMATION:
: APPLICANT: BILLING-MEDEL, PATRICIA
: APPLICANT: COHEN, MAURICE
: APPLICANT: COLPITTS, TRACEY L.
: APPLICANT: FRIEDMAN, PAULA N.
: APPLICANT: KLASS, MICHAEL R.
: APPLICANT: RUSSELL, JOHN C.
: APPLICANT: STROUPE, STEPHEN D.
: TITLE OF INVENTION: REAGENTS AND METHODS USEFUL
: TITLE OF INVENTION: FOR DETECTING DISEASES OF THE LUNG
: NUMBER OF SEQUENCES: 20
: CORRESPONDENCE ADDRESSES:
: ADDRESS: Abbott Laboratories
: STREET: 100 Abbott Park Road
: CITY: Abbott Park
: STATE: IL
: COUNTRY: USA
: ZIP: 60064-3500
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Diskette
: COMPUTER: IBM Compatible
: OPERATING SYSTEM: DOS
: SOFTWARE: FastSeq for Windows Version 2.0
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/09/092,296
: FILING DATE:
: CLASSIFICATION:
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: 60/048,810
: FILING DATE: 05-JUN-1997
: ATTORNEY/AGENT INFORMATION:
: NAME: Becker, Cheryl L.
: REGISTRATION NUMBER: 35,441
: REFERENCE/DOCKET NUMBER: 6104.US.01
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 847/935-1729
: TELEFAX: 847/938-2623
: TELEX:

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; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
;   LENGTH: 229 base pairs
;   TYPE: nucleic acid
;   STRANDEDNESS: single
;   TOPOLOGY: linear
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; US-09-092-296-2
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Best Local Similarity 100.0%; Pred. No. 4,1e-68;
Matches 229; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1 ACCGGGACTTCAGTGTCTCTCCATCCAGGAGCGGAGTGGCCACTATGCGGCTCGGGCT 60
   |||||||

QY 61 GCCCCTTGCTCCTCTTGGACCTCTTGGCAGCTCACATGGAACAGGCGGGGTATGAC 120
   |||||||
DB 61 GCCCCTTGCTCCTCTTGGACCTCTTGGCAGCTCACATGGAACAGGCGGGGTATGAC 120
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QY 121 TTGCAACTGAGCTGAAGGAGTCTTTTCTGACAAATTCCTCTATGAGTCCAGCTTCCT 180
   |||||||
DB 121 TTGCAACTGAGCTGAAGGAGTCTTTTCTGACAAATTCCTCTATGAGTCCAGCTTCCT 180
   |||||||

QY 181 GGAATTGCTGAAAGTCTGCCCTCTCCCTCCATCTCCCTTCAGGACCA 229
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DB 181 GGAATTGCTGAAAGTCTGCCCTCTCCCTCCATCTCCCTTCAGGACCA 229
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RESULT 2

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US-09-092-296-1
; Sequence 1, Application US/09092296
; Publication No. US20020188114A1
; GENERAL INFORMATION:
; APPLICANT: BILLING-MEDEL, PATRICIA
; APPLICANT: COHEN, MAURICE
; APPLICANT: COLPITTS, TRACEY L.
; APPLICANT: FRIEDMAN, PAULA N.
; APPLICANT: KLASS, MICHAEL R.
; APPLICANT: RUSSELL, JOHN C.
; APPLICANT: STROUPE, STEPHEN D.
; TITLE OF INVENTION: REAGENTS AND METHODS USEFUL
; FOR DETECTING DISEASES OF THE LUNG
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Abbott Laboratories
; STREET: 100 Abbott Park Road
; CITY: Abbott Park
; STATE: IL
; COUNTRY: USA
; ZIP: 60064-3500
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/092,296
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/048,810
; FILING DATE: 05-JUN-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Becker, Cheryl L.
; REGISTRATION NUMBER: 35,441
; REFERENCE/DOCKET NUMBER: 6104.US.01
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 847/935-1729
; TELEFAX: 847/938-2623
; TELEX:
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
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; LENGTH: 239 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: base polymorphism
; LOCATION: 200
; OTHER INFORMATION: /note= " N' represents an A or G or
; OTHER INFORMATION: T or C polymorphism at this position"
;
; US-09-092-296-1

Query Match          99.6%; Score 228; DB 9; Length 239;
Best Local Similarity 99.6%; Pred. No. 9,2e-68;
Matches 228; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ACCGGGACTTCAGTGTCTCTCCATCCAGGAGCGGAGTGGCCACTATGCGGCTCGGGCT 60
   |||||||
DB 5 ACCGGGACTTCAGTGTCTCTCCATCCAGGAGCGGAGTGGCCACTATGCGGCTCGGGCT 64
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QY 61 GCCCCTTGCTCCTCTTGGACCTCTTGGCAGCTCACATGGAACAGGCGGGGTATGAC 120
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DB 65 GCCCCTTGCTCCTCTTGGACCTCTTGGCAGCTCACATGGAACAGGCGGGGTATGAC 124
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QY 121 TTGCAACTGAGCTGAAGGAGTCTTTTCTGACAAATTCCTCTATGAGTCCAGCTTCCT 180
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QY 181 GGAATTGCTGAAAGTCTGCCCTCTCCCTCCATCTCCCTTCAGGACCA 229
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DB 185 GGAATTGCTGAAAGTCTGCCCTCTCCCTCCATCTCCCTTCAGGACCA 233
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RESULT 3

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US-09-092-296-6
; Sequence 6, Application US/09092296
; Publication No. US20020188114A1
; GENERAL INFORMATION:
; APPLICANT: BILLING-MEDEL, PATRICIA
; APPLICANT: COHEN, MAURICE
; APPLICANT: COLPITTS, TRACEY L.
; APPLICANT: FRIEDMAN, PAULA N.
; APPLICANT: KLASS, MICHAEL R.
; APPLICANT: RUSSELL, JOHN C.
; APPLICANT: STROUPE, STEPHEN D.
; TITLE OF INVENTION: REAGENTS AND METHODS USEFUL
; FOR DETECTING DISEASES OF THE LUNG
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Abbott Laboratories
; STREET: 100 Abbott Park Road
; CITY: Abbott Park
; STATE: IL
; COUNTRY: USA
; ZIP: 60064-3500
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/092,296
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/048,810
; FILING DATE: 05-JUN-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Becker, Cheryl L.
; REGISTRATION NUMBER: 35,441
; REFERENCE/DOCKET NUMBER: 6104.US.01
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 847/935-1729
; TELEFAX: 847/938-2623
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; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 413 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-09-092-296-6

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Best Local Similarity 99.6%  Pred. No. 2.7e-64;
Matches 229;  Conservative 0;  Mismatches 0;  Indels 1;  Gaps 1;

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DB   1  ACCGGAGCTTCAGTGTCTCCATCCAGGAGCGGAGTGGCCACTATGGGGTCTGGGCT 60
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QY  61  GCCCCTTGTCCTCTTGAACCTCTTGGCAGCTCACATGGAACAGGCCGGGTATGAC 120
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DB   61  GCCCCTTGTCCTCTTGAACCTCTTGGCAGCTCACATGGAACAGGCCGGGTATGAC 120
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QY  121  TTGCAACTGAAGCTGAAGAGCTCTTTCTGACAAATTCCTCTATGAGTCCAGCTTCCT 180
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QY  181  GGAATTGCTGAAAG-TCTGGCTCTCTCTCCATCTCCTTCAGGGACCA 229
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DB   181  GGAATTGCTGAAAGCTCTGCTCTCTCCATCTCCTTCAGGGACCA 230
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RESULT 4
US-09-992-598-362
; Sequence 362, Application US/09992598
; Patent No. US20020160384A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Bolstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Kijavlin, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tamas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P730P1C20
; CURRENT APPLICATION NUMBER: US/09/992, 598
; CURRENT FILING DATE: 2001-11-14
; PRIOR APPLICATION NUMBER: 60/049787
; PRIOR FILING DATE: 1997-06-16
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/065186
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; PRIOR APPLICATION NUMBER: 60/065311
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; PRIOR FILING DATE: 1997-11-24
; PRIOR APPLICATION NUMBER: 60/075945
; PRIOR FILING DATE: 1998-02-25
; PRIOR APPLICATION NUMBER: 60/078910
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/083322
; PRIOR FILING DATE: 1998-04-28
; PRIOR APPLICATION NUMBER: 60/084600
; PRIOR FILING DATE: 1998-05-07
; PRIOR APPLICATION NUMBER: 60/087106
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; PRIOR APPLICATION NUMBER: 60/087607
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; PRIOR APPLICATION NUMBER: 60/087609
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; PRIOR APPLICATION NUMBER: 60/087759
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; PRIOR FILING DATE: 1998-06-03
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; PRIOR FILING DATE: 1998-06-04
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; PRIOR FILING DATE: 1998-06-04
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; PRIOR FILING DATE: 1998-06-04
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; PRIOR FILING DATE: 1998-06-04
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; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/088655
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; PRIOR FILING DATE: 1998-06-10
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; PRIOR APPLICATION NUMBER: 60/088858
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; PRIOR APPLICATION NUMBER: 60/088876
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; PRIOR APPLICATION NUMBER: 60/089105
; PRIOR FILING DATE: 1998-06-12
; PRIOR APPLICATION NUMBER: 60/089440
; PRIOR FILING DATE: 1998-06-16
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; PRIOR FILING DATE: 1998-06-17
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; PRIOR APPLICATION NUMBER: 60/089538
; PRIOR FILING DATE: 1998-06-17
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; PRIOR FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: 60/090431
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; PRIOR FILING DATE: 1998-06-24
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; PRIOR APPLICATION NUMBER: 60/090696
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; PRIOR FILING DATE: 1998-07-01
; PRIOR APPLICATION NUMBER: 60/091478
; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/091544

; PRIOR FILING DATE: 1998-07-01
; PRIOR APPLICATION NUMBER: 60/091519
; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/091626
; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/091633
; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/091978
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/091982
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/092182
; PRIOR FILING DATE: 1998-07-09

Query Match 95.2%; Score 218; DB 9; Length 422;
Best Local Similarity 99.6%; Pred. No. 2.8e-64;
Matches 229; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 1 ACCGGGACTTCAGTGTCTCTCCATCCAGGAGCGAGTGGCCACTATGGGGTCTGGGCT 60
|||||
DB 12 ACCGGGACTTCAGTGTCTCTCCATCCAGGAGCGAGTGGGGTCTGGGCT 71
|||||
QY 61 GCCCTTGTCTCTCTTGACCTCTTGGCAGCTCAGATGGACAGGCGGGGTATGAC 120
|||||
DB 72 GCCCTTGTCTCTCTTGACCTCTTGGCAGCTCAGATGGACAGGCGGGGTATGAC 131
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QY 121 TTGCACTGAAGCTGAAGGAGTCTTTTCTGACAAATTCCTCTATGAGTCCAGCTTCCT 180
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DB 132 TTGCACTGAAGCTGAAGGAGTCTTTTCTGACAAATTCCTCTATGAGTCCAGCTTCCT 191
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QY 181 GGAATGCTTGAAAG-TCTGGCTCTCTCCATCTCCCTTCAGGGACCA 229
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DB 192 GGAATGCTTGAAAGCTCTGCTCTCTCTCCATCTCCCTTCAGGGACCA 241
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RESULT 5
US-09-989-293A-362
; Sequence 362, Application US/09989293A
; Patent No. US20020177164A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2730P1C66
; CURRENT APPLICATION NUMBER: US/09/989, 293A
; CURRENT FILING DATE: 2001-11-20
; PRIOR APPLICATION NUMBER: 60/049787
; PRIOR FILING DATE: 1997-06-16
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17

1	PRIOR APPLICATION NUMBER: 60/065186	2	PRIOR FILING DATE: 1998-06-16	3
2	PRIOR FILING DATE: 1997-11-12	4	PRIOR APPLICATION NUMBER: 60/089514	5
3	PRIOR APPLICATION NUMBER: 60/065311	6	PRIOR FILING DATE: 1998-06-16	7
4	PRIOR FILING DATE: 1997-11-13	8	PRIOR APPLICATION NUMBER: 60/089532	9
5	PRIOR APPLICATION NUMBER: 60/066770	10	PRIOR FILING DATE: 1998-06-17	11
6	PRIOR FILING DATE: 1997-11-24	12	PRIOR APPLICATION NUMBER: 60/089538	13
7	PRIOR APPLICATION NUMBER: 60/075945	14	PRIOR FILING DATE: 1998-06-17	15
8	PRIOR FILING DATE: 1998-02-25	16	PRIOR APPLICATION NUMBER: 60/089598	17
9	PRIOR APPLICATION NUMBER: 60/078910	18	PRIOR FILING DATE: 1998-06-17	19
10	PRIOR FILING DATE: 1998-03-20	20	PRIOR APPLICATION NUMBER: 60/089599	21
11	PRIOR APPLICATION NUMBER: 60/083322	22	PRIOR FILING DATE: 1998-06-17	23
12	PRIOR FILING DATE: 1998-04-28	24	PRIOR APPLICATION NUMBER: 60/089600	25
13	PRIOR APPLICATION NUMBER: 60/084600	26	PRIOR FILING DATE: 1998-06-17	27
14	PRIOR FILING DATE: 1998-05-07	28	PRIOR APPLICATION NUMBER: 60/089653	29
15	PRIOR APPLICATION NUMBER: 60/087106	30	PRIOR FILING DATE: 1998-06-17	31
16	PRIOR FILING DATE: 1998-05-28	32	PRIOR APPLICATION NUMBER: 60/089801	33
17	PRIOR APPLICATION NUMBER: 60/087607	34	PRIOR FILING DATE: 1998-06-18	35
18	PRIOR FILING DATE: 1998-06-02	36	PRIOR APPLICATION NUMBER: 60/089907	37
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20	PRIOR FILING DATE: 1998-08-02	40	PRIOR APPLICATION NUMBER: 60/089908	41
21	PRIOR APPLICATION NUMBER: 60/087759	42	PRIOR FILING DATE: 1998-06-18	43
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25	PRIOR APPLICATION NUMBER: 60/088021	50	PRIOR FILING DATE: 1998-06-19	51
26	PRIOR FILING DATE: 1998-06-04	52	PRIOR APPLICATION NUMBER: 60/089952	53
27	PRIOR APPLICATION NUMBER: 60/088025	54	PRIOR FILING DATE: 1998-06-19	55
28	PRIOR FILING DATE: 1998-08-04	56	PRIOR APPLICATION NUMBER: 60/090246	57
29	PRIOR APPLICATION NUMBER: 60/088026	58	PRIOR FILING DATE: 1998-06-22	59
30	PRIOR FILING DATE: 1998-06-04	60	PRIOR APPLICATION NUMBER: 60/090252	61
31	PRIOR APPLICATION NUMBER: 60/088028	62	PRIOR FILING DATE: 1998-06-22	63
32	PRIOR FILING DATE: 1998-06-04	64	PRIOR APPLICATION NUMBER: 60/090254	65
33	PRIOR APPLICATION NUMBER: 60/088029	66	PRIOR FILING DATE: 1998-06-22	67
34	PRIOR FILING DATE: 1998-06-04	68	PRIOR APPLICATION NUMBER: 60/090349	69
35	PRIOR APPLICATION NUMBER: 60/088030	70	PRIOR FILING DATE: 1998-06-23	71
36	PRIOR FILING DATE: 1998-06-04	72	PRIOR APPLICATION NUMBER: 60/090355	73
37	PRIOR APPLICATION NUMBER: 60/088033	74	PRIOR FILING DATE: 1998-06-23	75
38	PRIOR FILING DATE: 1998-06-04	76	PRIOR APPLICATION NUMBER: 60/090429	77
39	PRIOR APPLICATION NUMBER: 60/088326	78	PRIOR FILING DATE: 1998-06-24	79
40	PRIOR FILING DATE: 1998-06-04	80	PRIOR APPLICATION NUMBER: 60/090431	81
41	PRIOR APPLICATION NUMBER: 60/088167	82	PRIOR FILING DATE: 1998-06-24	83
42	PRIOR FILING DATE: 1998-06-05	84	PRIOR APPLICATION NUMBER: 60/090445	85
43	PRIOR APPLICATION NUMBER: 60/088202	86	PRIOR FILING DATE: 1998-06-24	87
44	PRIOR FILING DATE: 1998-06-05	88	PRIOR APPLICATION NUMBER: 60/090472	89
45	PRIOR APPLICATION NUMBER: 60/088212	90	PRIOR FILING DATE: 1998-06-24	91
46	PRIOR FILING DATE: 1998-06-05	92	PRIOR APPLICATION NUMBER: 60/090535	93
47	PRIOR APPLICATION NUMBER: 60/088217	94	PRIOR FILING DATE: 1998-06-24	95
48	PRIOR FILING DATE: 1998-06-05	96	PRIOR APPLICATION NUMBER: 60/090540	97
49	PRIOR APPLICATION NUMBER: 60/088655	98	PRIOR FILING DATE: 1998-06-24	99
50	PRIOR FILING DATE: 1998-06-09	100	PRIOR APPLICATION NUMBER: 60/090542	101
51	PRIOR APPLICATION NUMBER: 60/088734	102	PRIOR FILING DATE: 1998-06-24	103
52	PRIOR FILING DATE: 1998-06-10	104	PRIOR APPLICATION NUMBER: 60/090557	105
53	PRIOR APPLICATION NUMBER: 60/088738	106	PRIOR FILING DATE: 1998-06-24	107
54	PRIOR FILING DATE: 1998-06-10	108	PRIOR APPLICATION NUMBER: 60/090676	109
55	PRIOR APPLICATION NUMBER: 60/088742	110	PRIOR FILING DATE: 1998-06-25	111
56	PRIOR FILING DATE: 1998-06-10	112	PRIOR APPLICATION NUMBER: 60/090678	113
57	PRIOR APPLICATION NUMBER: 60/088810	114	PRIOR FILING DATE: 1998-06-25	115
58	PRIOR FILING DATE: 1998-06-10	116	PRIOR APPLICATION NUMBER: 60/090690	117
59	PRIOR APPLICATION NUMBER: 60/088824	118	PRIOR FILING DATE: 1998-06-25	119
60	PRIOR FILING DATE: 1998-06-10	120	PRIOR APPLICATION NUMBER: 60/090694	121
61	PRIOR APPLICATION NUMBER: 60/088826	122	PRIOR FILING DATE: 1998-06-25	123

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; PRIOR APPLICATION NUMBER: 60/091478
; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/091544
; PRIOR FILING DATE: 1998-07-01
; PRIOR APPLICATION NUMBER: 60/091519
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; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/091633
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; PRIOR APPLICATION NUMBER: 60/091978
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/091982
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/092182
; PRIOR FILING DATE: 1998-07-09

Query Match 95.2%; Score 218; DB 9; Length 422;

Best Local Similarity 99.6%; Pred. No. 2.8e-64; Mismatches 0; Indels 1; Gaps 1;
Matches 229; Conservative 0;

QY 1 ACCGGGACTTCAGTGTCTCTCCATCCAGGAGCGAGTGGCCACTATGSGGCTCTGGGCT 60
DB 12 ACCGGGACTTCAGTGTCTCTCCATCCAGGAGCGAGTGGCCACTATGSGGCTCTGGGCT 71
QY 61 GCCCCTTGCTCCTCTTGACCTCTTGCGAGCTCACATGGAACAGGCGGGGTATGAC 120
DB 72 GCCCCTTGCTCCTCTTGACCTCTTGCGAGCTCACATGGAACAGGCGGGGTATGAC 131
QY 121 TTGCAACTGAAGCTGAAGAGTCTTTTCTGACAAATTCCTCTATGAGTCCAGCTTCCT 180
DB 132 TTGCAACTGAAGCTGAAGAGTCTTTTCTGACAAATTCCTCTATGAGTCCAGCTTCCT 191
QY 181 GGAATTGCTTGAAGAAG-TCTGGCTCTCTCTCCATCTCCCTTCAGGGACCA 229
DB 192 GGAATTGCTTGAAGAAGCTCTGGCTCTCTCTCCATCTCCCTTCAGGGACCA 241

RESULT 6

US-10-063-547-65
; Sequence 65, Application US/10063547
; Publication No. US20020182638A1

; GENERAL INFORMATION:
; APPLICANT: Eaton, Dan L.
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3230R1C1
; CURRENT APPLICATION NUMBER: US/10/063.547
; CURRENT FILING DATE: 2002-05-02
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 170
; SEQ ID NO 65
; LENGTH: 422
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-063-547-65

Query Match 95.2%; Score 218; DB 9; Length 422;
Best Local Similarity 99.6%; Pred. No. 2.8e-64;
Matches 229; Conservative 0; Mismatches 0; Indels 1; Gaps 1;
QY 1 ACCGGGACTTCAGTGTCTCTCCATCCAGGAGCGAGTGGCCACTATGSGGCTCTGGGCT 60
DB 12 ACCGGGACTTCAGTGTCTCTCCATCCAGGAGCGAGTGGCCACTATGSGGCTCTGGGCT 71
QY 61 GCCCCTTGCTCCTCTTGACCTCTTGCGAGCTCACATGGAACAGGCGGGGTATGAC 120
DB 72 GCCCCTTGCTCCTCTTGACCTCTTGCGAGCTCACATGGAACAGGCGGGGTATGAC 131
QY 121 TTGCAACTGAAGCTGAAGAGTCTTTTCTGACAAATTCCTCTATGAGTCCAGCTTCCT 180
DB 132 TTGCAACTGAAGCTGAAGAGTCTTTTCTGACAAATTCCTCTATGAGTCCAGCTTCCT 191
QY 181 GGAATTGCTTGAAGAAG-TCTGGCTCTCTCTCCATCTCCCTTCAGGGACCA 229
DB 192 GGAATTGCTTGAAGAAGCTCTGGCTCTCTCTCCATCTCCCTTCAGGGACCA 241

US-09-989-735-362
; Sequence 362, Application US/09989735
; Publication No. US20020193299A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Borstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2730P1C61
; CURRENT APPLICATION NUMBER: US/09/989.735
; CURRENT FILING DATE: 2001-11-19
; PRIOR APPLICATION NUMBER: 60/049787
; PRIOR FILING DATE: 1997-06-16
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/065186
; PRIOR FILING DATE: 1997-11-12
; PRIOR APPLICATION NUMBER: 60/065311
; PRIOR FILING DATE: 1997-11-13
; PRIOR APPLICATION NUMBER: 60/066770
; PRIOR FILING DATE: 1997-11-24
; PRIOR APPLICATION NUMBER: 60/075945
; PRIOR FILING DATE: 1998-02-25
; PRIOR APPLICATION NUMBER: 60/078910
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/083322
; PRIOR FILING DATE: 1998-04-28
; PRIOR APPLICATION NUMBER: 60/084600
; PRIOR FILING DATE: 1998-05-07
; PRIOR APPLICATION NUMBER: 60/087106
; PRIOR FILING DATE: 1998-05-28
; PRIOR APPLICATION NUMBER: 60/087607
; PRIOR FILING DATE: 1998-06-02
; PRIOR APPLICATION NUMBER: 60/087609
; PRIOR FILING DATE: 1998-06-02


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Best Local Similarity 99.6%; Pred. No. 2.8e-64;
Matches 229; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 1 ACCGGACATGAGTCTCTCCATCCAGGAGCGAGTGGCCACTATGGGGTCTGGGCT 60
   |||||
Db 12 ACCGGACATGAGTCTCTCCATCCAGGAGCGAGTGGCCACTATGGGGTCTGGGCT 71
   |||||

QY 61 GCCCCTTGCTCTCTCTTGACCCCTCTTGGCAGCTCACATGGAACAGGCGCGGTATGAC 120
   |||||
Db 72 GCCCCTTGCTCTCTCTTGACCCCTCTTGGCAGCTCACATGGAACAGGCGCGGTATGAC 131
   |||||

QY 121 TTTCGAACCTGAAGCTGAAGAGTCTTTCTGACAAATTCCTCTATGAGTCCAGCTTCCT 180
   |||||
Db 132 TTTCGAACCTGAAGCTGAAGAGTCTTTCTGACAAATTCCTCTATGAGTCCAGCTTCCT 191
   |||||

QY 181 GGAATTGCTGAAAG-TCTGCTCTCTCTCCATCTCCCTCAGGACCA 229
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Db 192 GGAATTGCTGAAAGCTCTGCTCTCTCCATCTCCCTCAGGACCA 241
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RESULT 8
US-09-990-444-362
; Sequence 362, Application US/0990444
; Publication No. US20020193300A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Guiney, Austin L.
; APPLICANT: Kijavini, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2730P1C19
; CURRENT APPLICATION NUMBER: US/09/990,444
; CURRENT FILING DATE: 2001-11-14
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 ; PRIOR FILING DATE: 1998-07-02
 ; PRIOR APPLICATION NUMBER: 60/091633
 ; PRIOR FILING DATE: 1998-07-02
 ; PRIOR APPLICATION NUMBER: 60/091978
 ; PRIOR FILING DATE: 1998-07-07
 ; PRIOR APPLICATION NUMBER: 60/091982

; PRIOR FILING DATE: 1998-07-07
 ; PRIOR APPLICATION NUMBER: 60/092182
 ; PRIOR FILING DATE: 1998-07-09
 Query Match 95.28; Score 218; DB 9; Length 422;
 Best Local Similarity 99.6%; Pred. No. 2.8e-64; Indels 1; Gaps 1;
 Matches 229; Conservative 0; Mismatches 0
 QY 1 ACCGGGACTTTCAGTGTCTCCTCCATCCAGGAGCGCAGTGGCCACTATGGGGTCTGGGCT 60
 Db 12 ACCGGGACTTTCAGTGTCTCCTCCATCCAGGAGCGCAGTGGCCACTATGGGGTCTGGGCT 71
 QY 61 GCCCTTTGCTCCTCCTTGGACCTCTTGGCAGCTCACATGGACACAGGCGGGGTATGAC 120
 Db 72 GCCCTTTGCTCCTCCTCCTTGGACCTCTTGGCAGCTCACATGGACACAGGCGGGGTATGAC 131
 QY 121 TTGCAACTGAAGCTGAAGGAGTCTTTTCTTGACAAATTCCTCTATGAGTCCAGCTTCT 180
 Db 132 TTGCAACTGAAGCTGAAGGAGTCTTTTCTTGACAAATTCCTCTATGAGTCCAGCTTCT 191
 QY 181 GGAATTCCTTGAAGAAG-TCTGCCTCCTCCTCCATCTCCTTTCAGGGACCA 229
 Db 192 GGAATTCCTTGAAGAAGCTCGCTCCTCCTCCATCTCCTTTCAGGGACCA 241
 RESULT 9
 US-09-989-730-362
 ; Sequence 362, Application US/09989730
 ; Publication No. US20020197574A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Ashkenazi, Avi J.
 ; APPLICANT: Baker, Kevin P.
 ; APPLICANT: Botstein, David
 ; APPLICANT: Desnoyers, Luc
 ; APPLICANT: Eaton, Dan L.
 ; APPLICANT: Ferrara, Napoleone
 ; APPLICANT: Fong, Sherman
 ; APPLICANT: Gerber, Hanspeter
 ; APPLICANT: Gottard, Audrey
 ; APPLICANT: Godowski, Paul J.
 ; APPLICANT: Grimaldi, J. Christopher
 ; APPLICANT: Gurney, Austin L.
 ; APPLICANT: Kljavin, Ivar J.
 ; APPLICANT: Napier, Mary A.
 ; APPLICANT: Pan, James
 ; APPLICANT: Paoni, Nicholas F.
 ; APPLICANT: Roy, Margaret Ann
 ; APPLICANT: Stewart, Timothy A.
 ; APPLICANT: Tumas, Daniel
 ; APPLICANT: Watanabe, Colin K.
 ; APPLICANT: Williams, P. Mickey
 ; APPLICANT: Wood, William I.
 ; APPLICANT: Zhang, Zemin
 ; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
 ; FILE REFERENCE: P2730PIC69
 ; CURRENT APPLICATION NUMBER: US/09/989,730
 ; PRIOR FILING DATE: 2001-11-20
 ; PRIOR APPLICATION NUMBER: 60/049787
 ; PRIOR FILING DATE: 1997-06-15
 ; PRIOR APPLICATION NUMBER: 60/052250
 ; PRIOR FILING DATE: 1997-10-17
 ; PRIOR APPLICATION NUMBER: 60/055186
 ; PRIOR FILING DATE: 1997-11-12
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 ; PRIOR APPLICATION NUMBER: 60/075945
 ; PRIOR FILING DATE: 1998-02-25
 ; PRIOR APPLICATION NUMBER: 60/078910
 ; PRIOR FILING DATE: 1998-03-20

1	PRIOR APPLICATION NUMBER: 60/0083322
2	PRIOR FILING DATE: 1998-04-28
3	PRIOR APPLICATION NUMBER: 60/0084600
4	PRIOR FILING DATE: 1998-05-07
5	PRIOR APPLICATION NUMBER: 60/0087106
6	PRIOR FILING DATE: 1998-05-28
7	PRIOR APPLICATION NUMBER: 60/0087607
8	PRIOR FILING DATE: 1998-06-02
9	PRIOR APPLICATION NUMBER: 60/0087609
10	PRIOR FILING DATE: 1998-06-02
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33	PRIOR APPLICATION NUMBER: 60/0088202
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36	PRIOR FILING DATE: 1998-06-05
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39	PRIOR APPLICATION NUMBER: 60/0088655
40	PRIOR FILING DATE: 1998-06-09
41	PRIOR APPLICATION NUMBER: 60/0088734
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56	PRIOR FILING DATE: 1998-06-12
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58	PRIOR FILING DATE: 1998-06-16
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; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/092182
; PRIOR FILING DATE: 1998-07-09

Query Match          95.2%  Score 218;  DB 9;  Length 422;
Best Local Similarity 99.6%;  Pred. No. 2.8e-64;
Matches 229;  Conservative 0;  Mismatches 0;  Indels 1;  Gaps 1;

Oy 1  ACGGGACTTCAGTGTCTCTCCATCCAGGAGCGAGTGGCCACTATGGGGTCTGGGCT 60
Db 12 ACGGGACTTCAGTGTCTCTCCATCCAGGAGCGAGTGGCCACTATGGGGTCTGGGCT 71
Oy 61 GCCCCTTCTCTCTCTTTCACCTCTTTGGCAGCTCACATGGAACAGGGCCGGGTATGAC 120
Db 72 GCCCCTTCTCTCTCTTTCACCTCTCTTGGCAGCTCACATGGAACAGGGCCGGGTATGAC 131
Oy 121 TTGCAACTGAAGCTGAAGAGTCTTTTCGACAAATTCCTCATGATGTCAGCTTCTCT 180
Db 132 TTGCAACTGAAGCTGAAGAGTCTTTTCGACAAATTCCTCATGATGTCAGCTTCTCT 191
Oy 181 GGAATTGCTTGAAGAAG-TCTGCCTCTCTCTCCATCTCTCCCTTCAGGGACCA 229
Db 192 GGAATTGCTTGAAGAAGCTCTGCTCTCTCTCATCTCTCTTCAGGGACCA 241

RESULT 10
US-09-990-436-362
; Sequence 362, Application US/09990436
; Publication No. US20020198148A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnovers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gunney, Austin L.
; APPLICANT: Kijavlin, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tunas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2730P1C14
; CURRENT APPLICATION NUMBER: US/09/990,436
; CURRENT FILING DATE: 2001-11-14
; PRIOR APPLICATION NUMBER: 60/049787
; PRIOR FILING DATE: 1997-06-16
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
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; PRIOR APPLICATION NUMBER: 60/066770
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67	PRIOR APPLICATION NUMBER: 60/090863
68	PRIOR FILING DATE: 1998-06-26
69	PRIOR APPLICATION NUMBER: 60/091360
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; PRIOR APPLICATION NUMBER: 60/091978
; PRIOR FILING DATE: 1998-07-07
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; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/092182
; PRIOR FILING DATE: 1998-07-09

Query Match          95.28; Score 218; DB 9; Length 422;
Best Local Similarity 99.66; Pred. No. 2.8e-64;
Matches 229; Conservative 0; Mismatches 0; Indels 1; Gaps

QY 1 ACCGGAGCTTCAGTGTCTCTCCATCCAGGAGCGCAGTGGCCACTATGGGCTGGGGCT 120
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QY 61 GCCTCTGTCTCCTCTTGACCTCTTTGGCAGCTCAGTGGAAACAGGCGGGGTATGAC 120
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QY 121 TTGTGAAGCTGAAGAGAGTCTTTCTGCAAAATCTCTCTATGATCCAGCTTCCT 120
    |||||
Db 132 TTGTGAAGCTGAAGAGAGTCTTTCTGCAAAATCTCTCTATGATCCAGCTTCCT 131
    |||||

QY 181 GGAATTGCTTGAAGAAG-TCTGCCCTCTCTCCATCTCCCTTCAGGGACCA 229
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Db 192 GGAATTGCTTGAAGAAGCTCTGCCCTCTCTCCATCTCCCTTCAGGGACCA 241
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RESULT 11

US-09-991-181-362

Sequence 362, Application US/09991181

Publication No. US20020197615A1

GENERAL INFORMATION:

APPLICANT: Ashkenazi, Avi J.

APPLICANT: Baker, Kevin P.

APPLICANT: Botstein, David

APPLICANT: Desnoyers, Luc

APPLICANT: Eaton, Dan L.

APPLICANT: Ferrara, Napoleone

APPLICANT: Fong, Sherman

APPLICANT: Gerber, Hanspeter

APPLICANT: Gerritsen, Mary E.

APPLICANT: Goddard, Audrey

APPLICANT: Godowski, Paul J.

APPLICANT: Grimaldi, J. Christopher

APPLICANT: Gurney, Austin L.

APPLICANT: Kljavin, Ivar J.

APPLICANT: Napier, Mary A.

APPLICANT: Pan, James

APPLICANT: Paoni, Nicholas F.

APPLICANT: Roy, Margaret Ann

APPLICANT: Stewart, Timothy A.

APPLICANT: Tumas, Daniel

APPLICANT: Watanabe, Colin K.

APPLICANT: Williams, P. Mickey

APPLICANT: Wood, William I.

APPLICANT: Zhang, Zemin

TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic Acids Encoding the Same

FILE REFERENCE: P2730PIC53

CURRENT APPLICATION NUMBER: US/09/991,181

CURRENT FILING DATE: 2001-11-16

PRIOR APPLICATION NUMBER: 60/049787

PRIOR FILING DATE: 1997-06-16

PRIOR APPLICATION NUMBER: 60/062250

PRIOR FILING DATE: 1997-10-17

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8 PRIOR FILING DATE: 1998-02-25
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117 PRIOR APPLICATION NUMBER: 60/090444
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122 PRIOR FILING DATE: 1998-06-24
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146 PRIOR FILING DATE: 1998-06-26

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; PRIOR APPLICATION NUMBER: 60/091360
; PRIOR FILING DATE: 1998-07-01
; PRIOR APPLICATION NUMBER: 60/091478
; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/091544
; PRIOR FILING DATE: 1998-07-01
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; PRIOR APPLICATION NUMBER: 60/091633
; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/091978
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/091982
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/092182
; PRIOR FILING DATE: 1998-07-09

Query Match          95.2%; Score 218; DB 9; Length 422;
Best Local Similarity 99.6%; Pred. No. 2.8e-64;
Matches 229; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 1 ACCGGGACTTCAGTCTCTCCATCCAGGAGCCAGTGGCCACTATGGGCTCGGGCT 60
   |||||
Db 12 ACCGGGACTTCAGTCTCTCCATCCAGGAGCCAGTGGCCACTATGGGCTCGGGCT 71
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QY 61 GCCCCTTGTCCTCCTCTTGACCCCTCTGGCAGCICACATGGAACAGGCGCGGTATGAC 120
   |||||
Db 72 GCCCCTTGTCCTCCTCTTGACCCCTCTGGCAGCICACATGGAACAGGCGCGGTATGAC 131
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QY 121 TTTCGACGAGCTGAAGGAGTCTTTCTGACAAATTCCTCTATGAGTCCAGCTTCCT 180
   |||||
Db 132 TTTCGACGAGCTGAAGGAGTCTTTCTGACAAATTCCTCTATGAGTCCAGCTTCCT 191
   |||||

QY 181 GGAATTGCTTGAAGAAG-TCTGCCCTCCTCCTCCATCTCCCTTCAGGGACCA 229
   |||||
Db 192 GGAATTGCTTGAAGAAGCTCTGCCCTCCTCCTCCATCTCCCTTCAGGGACCA 241
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RESULT 12
US-09-993-687-362
; Sequence 362, Application US/09993687
; Publication No. US20020198149A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Destoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2730P1C11
; CURRENT APPLICATION NUMBER: US/09/993,687
; CURRENT FILING DATE: 2002-11-14
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; PRIOR APPLICATION NUMBER: 60/092182
; PRIOR FILING DATE: 1998-07-09

Query Match 95.2%; Score 218; DB 9; Length 422;
Best Local Similarity 99.6%; Pred. No. 2.8e-64;
Matches 229; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 1 ACCGGGACTTCAGTGTCTCTCCATCCAGGAGCGGAGTGCCCACTATGGGGTCTGGGCT 60
Db 12 ACCGGGACTTCAGTGTCTCTCCATCCAGGAGCGGAGTGCCCACTATGGGGTCTGGGCT 71

QY 61 GCCCTTGTCTCTCTCTTGACCCCTCTTGGCAGCTCACATGGAACAGGCGGGGTATGAC 120
Db 72 GCCCTTGTCTCTCTCTTGACCCCTCTTGGCAGCTCACATGGAACAGGCGGGGTATGAC 131

QY 121 TTGCACTGAAGCTGAAGGAGTCTTTCTGACAAATTCCTCTATGATCCAGCTTCT 180
Db 132 TTGCACTGAAGCTGAAGGAGTCTTTCTGACAAATTCCTCTATGATCCAGCTTCT 191

QY 181 GGAATTGCTTGAAGAAG-TCTGCTCTCTCTCCATCTCCCTTCAGGGACCA 229
Db 192 GGAATTGCTTGAAGAAGCTCTGCTCTCTCCATCTCCCTTCAGGGACCA 241

RESULT 13
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; Sequence 362, Application US/09989734
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; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
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; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.

;; APPLICANT: Zhang, Zemin
;; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
;; FILE OF INVENTION: Acids Encoding the Same
;; FILE REFERENCE: P2730P1C64
;; CURRENT APPLICATION NUMBER: US/09/989,734
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;; PRIOR APPLICATION NUMBER: 60/049787
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; PRIOR FILING DATE: 1998-07-09

Query Match 95.2%; Score 218; DB 9; Length 422;
Best Local Similarity 99.6%; Pred. No. 2.8e-64;
Matches 229; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 1 ACCGGAGCTCAGTGTCTCTCCATCCAGGAGCGAGTGGCCACTATGGGGTCTGGGCT 60
DB 12 ACCGGAGCTCAGTGTCTCTCCATCCAGGAGCGAGTGGCCACTATGGGGTCTGGGCT 71

QY 61 GCCCTTGTCTCTCTCTGACCTCTTGGCAGCTCACATGACAGCGCGGGTATGAC 120
DB 72 GCCCTTGTCTCTCTCTGACCTCTTGGCAGCTCACATGACAGCGCGGGTATGAC 131

QY 121 TTGCACTGAAGCTGAAGAGTCTTTTCTGACAAATCTCTATGATGCCAGCTTCT 180
DB 132 TTGCACTGAAGCTGAAGAGTCTTTTCTGACAAATCTCTATGATGCCAGCTTCT 191

QY 181 GGAATTGCTGAAAG-TCTGCTCTCTCTCCATCTCCCTTCAGGACCA 229
DB 192 GGAATTGCTGAAAGCTCTGCTCTCTCTCTCCATCTCCCTTCAGGACCA 241

RESULT 14
US-09-997-653-362
; Sequence 362, Application US/09997653
; Publication No. US20030008297A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
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; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2730PIC38
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; PRIOR FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: 60/090445
; PRIOR FILING DATE: 1998-06-24
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; PRIOR FILING DATE: 1998-06-24
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; PRIOR FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: 60/090540
; PRIOR FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: 60/090542
; PRIOR FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: 60/090557
; PRIOR FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: 60/090676

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; PRIOR FILING DATE: 1998-06-25
; PRIOR APPLICATION NUMBER: 60/090578
; PRIOR FILING DATE: 1998-06-25
; PRIOR APPLICATION NUMBER: 60/090590
; PRIOR FILING DATE: 1998-06-25
; PRIOR APPLICATION NUMBER: 60/090594
; PRIOR FILING DATE: 1998-06-25
; PRIOR APPLICATION NUMBER: 60/090595
; PRIOR FILING DATE: 1998-06-25
; PRIOR APPLICATION NUMBER: 60/090596
; PRIOR FILING DATE: 1998-06-25
; PRIOR APPLICATION NUMBER: 60/090862
; PRIOR FILING DATE: 1998-06-26
; PRIOR APPLICATION NUMBER: 60/090863
; PRIOR FILING DATE: 1998-06-26
; PRIOR APPLICATION NUMBER: 60/091360
; PRIOR FILING DATE: 1998-07-01
; PRIOR APPLICATION NUMBER: 60/091478
; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/091544
; PRIOR FILING DATE: 1998-07-01
; PRIOR APPLICATION NUMBER: 60/091519
; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/091626
; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/091633
; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/091978
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/091982
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/092182
; PRIOR FILING DATE: 1998-07-09
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Query Match 95.2%; Score 218; DB 9; Length 422;
Best Local Similarity 99.6%; Pred. No. 2.8e-64;
Matches 229; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

Qy 1 ACCGGAGCTTCAGTCTCTCTCCATCCAGGAGGAGTGGCCACTATGGGCTGGGCT 60
Db 12 ACCGGAGCTTCAGTCTCTCTCCATCCAGGAGGAGTGGCCACTATGGGCTGGGCT 71

Oy 61 GCCCCTTGCTCCTCTTGACCTCCTTGGCAGCTCACATGGAACAGGCGGGGTATGAC 120
Db 72 GCCCCTTGCTCCTCTTGACCTCCTTGGCAGCTCACATGGAACAGGCGGGGTATGAC 131

Oy 121 TTGTGAACCTGAAGCTGAAGGAGTCTTTTCTGACAAATTCCTCTATGAGTCCAGTTCCT 180
Db 132 TTGTGAACCTGAAGCTGAAGGAGTCTTTTCTGACAAATTCCTCTATGAGTCCAGTTCCT 191

Oy 181 GGAATTGCTTGAAAAG-TCTGGCTCCTCCTCCATCTCCCTTCAGGGACCA 229
Db 192 GGAATTGCTTGAAAAGCTCTGGCTCCTCCTCCATCTCCCTTCAGGGACCA 241

RESULT 15
US-10-174-590-241
; Sequence 241, Application US/10174590
; Publication No. US2003008352A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Chen, Jian
; APPLICANT: Desnoyers, Luc
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Smith, Victoria
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME


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; FILE REFERENCE: P3430RIC42
; CURRENT APPLICATION NUMBER: US/10/174,590
; CURRENT FILING DATE: 2002-06-18
; Prior application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 241
; LENGTH: 422
; TYPE: DNA
; ORGANISM: Homo Sapien
; US-10-174-590-241

Query Match      95.2%; Score 218; DB 9; Length 422;
Best Local Similarity 99.6%; Pred.No. 2.8e-64; Indels 1; Gaps 1;
Matches 229; Conservative 0; Mismatches 0;

Qy 1 ACCGGGACTTCAGTGTCTCTCCATCCAGGAGCGCAGTGGCCACTATGGGGTCTGGGCT 60
Db 12 ACCGGGACTTCAGTGTCTCTCCATCCAGGAGCGCAGTGGCCACTATGGGGTCTGGGCT 71
Qy 61 GCCCTTGTCTCTCTTGACCTCTTGGCAGCTCCATGGAACAGGCGCGGTATGAC 120
Db 72 GCCCTTGTCTCTCTTGACCTCTTGGCAGCTCCATGGAACAGGCGCGGTATGAC 131
Qy 121 TTGCAACTGAAGCTGAAGAGTCTTTCTGACAAATTCCTCTATGAGTCCAGCTTCT 180
Db 132 TTGCAACTGAAGCTGAAGAGTCTTTCTGACAAATTCCTCTATGAGTCCAGCTTCT 191
Qy 181 GGAATTGCTGAAAG-TCTGCTCTCTCTCCATCTCCCTTCAGGACCA 229
Db 192 GGAATTGCTGAAAGCTTGCTCTCTCTCCATCTCCCTTCAGGACCA 241

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Search completed: May 1, 2003, 05:17:10
Job time : 63.534 secs

GenCore version 5.1.5
Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucieic - nucleic search, using sw model

Run on: May 1, 2003, 03:08:45 ; Search time 1146.82 seconds
(without alignments)
3233.964 Million cell updates/sec

Title: US-09-092-296-2
Perfect score: 229
Sequence: 1 ACCGGGACCTTCAGTCTCC.....CCATCTCCCTTCAGGACCA 229

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 16154066 seqs, 8097743376 residues

Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST:*

1:	em_estba:*
2:	em_esthum:*
3:	em_esthum:*
4:	em_esthum:*
5:	em_estov:*
6:	em_estpl:*
7:	em_estro:*
8:	em_hic:*
9:	em_estl:*
10:	gb_est2:*
11:	gb_hic:*
12:	gb_est3:*
13:	gb_est4:*
14:	gb_est5:*
15:	em_estom:*
16:	em_estom:*
17:	gb_gss:*
18:	em_gss_hum:*
19:	em_gss_inv:*
20:	em_gss_pin:*
21:	em_gss_vrt:*
22:	em_gss_fun:*
23:	em_gss_mam:*
24:	em_gss_mus:*
25:	em_gss_other:*
26:	em_gss_pro:*
27:	em_gss_rod:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
c 1	216.4	94.5	449	10 AW293443	AW293443 UI-H-BI2-
c 2	216.4	94.5	830	13 BI759796	BI759796 603045679
c 3	215	93.9	456	12 BG506690	BG506690 601861290
c 4	213	93.0	422	12 BF002050	BF002050 7998c11 x
c 5	132.2	57.7	895	13 BI820029	BI820029 603037210
c 6	131	57.2	865	13 BI820110	BI820110 603037110

c 7	113	49.3	404	9	AI857998	AI857998 wj69b01.x
c 8	94	41.0	521	10	BB533837	BB533837 BB533837
c 9	94	41.0	522	10	BB664284	BB664284 BB664284
c 10	92.2	40.3	361	12	BF521842	BF521842 UI-R-C2p-
c 11	75.4	32.9	552	17	AQ718761	AQ718761 HS_55111_B
c 12	61.8	27.0	328	9	AI136523	AI136523 UI-R-C2p-
c 13	45.6	19.9	506	17	A2241329	A2241329 RPI-23-7
c 14	45.6	19.9	633	17	A2079350	A2079350 RPI-23-4
c 15	36	15.7	754	12	BG686317	BG686317 602638230
c 16	36	15.7	1020	13	BM477469	BM477469 AGENCOURT
c 17	35	15.3	348	14	F06958	F06958 HSC10C101 n
c 18	35	15.3	509	17	AQ838514	AQ838514 HS_5011_A
c 19	35	15.3	1019	13	BM474221	BM474221 AGENCOURT
c 20	34.6	15.1	261	10	BB411111	BB411111 BB411111
c 21	34.4	15.0	238	9	AA376266	AA376266 EST88915
c 22	34.4	15.0	264	14	BQ377407	BQ377407 IL5-UK007
c 23	34.4	15.0	412	9	AA769782	AA769782 ah71D05.s
c 24	34.4	15.0	458	9	AI632159	AI632159 ts89612.x
c 25	34.4	15.0	470	9	AI803529	AI803529 tc42H11.x
c 26	34.4	15.0	516	10	BE613876	BE613876 601504191
c 27	34.4	15.0	543	10	AW851149	AW851149 IL3-C7022
c 28	34.4	15.0	753	13	BI911665	BI911665 603064838
c 29	34.4	15.0	783	10	BE563718	BE563718 601335355
c 30	34.4	15.0	785	13	BI193645	BI193645 602948554
c 31	34.4	15.0	788	12	BG762871	BG762871 602735108
c 32	34.4	15.0	828	12	BG768039	BG768039 602743815
c 33	34.4	15.0	871	14	BQ956320	BQ956320 AGENCOURT
c 34	34.4	15.0	931	12	BF689789	BF689789 602186518
c 35	34.4	15.0	954	14	BQ220846	BQ220846 AGENCOURT
c 36	34.4	15.0	959	14	BQ940113	BQ940113 AGENCOURT
c 37	34.4	15.0	999	9	AL551231	AL551231 AL551231
c 38	34.4	15.0	1013	14	BQ953477	BQ953477 AGENCOURT
c 39	34.4	15.0	1061	14	BQ052186	BQ052186 AGENCOURT
c 40	34.4	15.0	1129	13	BM464458	BM464458 AGENCOURT
c 41	34.4	15.0	1138	13	BM564409	BM564409 AGENCOURT
c 42	34.4	15.0	1232	14	BM911289	BM911289 AGENCOURT
c 43	34.4	15.0	271	17	BH244391	BH244391 ATZEB57TF
c 44	34	14.8	637	17	BH244484	BH244484 ATZEE11TF
c 45	34	14.8	637	17	BH244484	BH244484 ATZEE11TF

ALIGNMENTS

RESULT 1
AW293443/c
LOCUS
DEFINITION
IMAGE:2727182 3', mRNA sequence.
ACCESSION
AW293443
VERSION
AW293443.1
KEYWORDS
EST.
SOURCE
human.
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 449)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
AUTHORS
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
TITLE
Tumor Gene Index
JOURNAL
Unpublished (1997)
COMMENT
Contact: Robert Strausberg, Ph.D.
Email: cgapbs@mail.nih.gov
The sequence contained an oligo-dT track that was present in the
oligonucleotide that was used to prime the synthesis of first
strand cDNA and therefore this may represent a bonafide poly A
tail. cDNA Library Preparation: M.B. Soares Lab Clone distribution:
NCI-CGAP clone distribution information can be found through the
I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/dbprr/image.html
Seq primer: M13 Forward
POLYA-res.

FEATURES

Location/Qualifiers

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source
1. 449
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="NCI_CGAP_Sub4"
/lab_host="DH10B (Life Technologies)"
/notes="vector: pT73D-Pac (Pharmacia) with a modified
polylinker; Site1: Not I; Site2: Eco RI; The
NCI_CGAP_Sub4 library is a subtracted library derived from
the NCI_CGAP_Sub2 library which is a subtracted library
derived from the NCI_CGAP_Sub1 library, which is a
subtracted library derived from B1. Bi constitutes a
mixture of 21 normalized or subtracted NCI_CGAP
libraries: NCI_CGAP_Co4, NCI_CGAP_Pr22, NCI_CGAP_Pr28,
NCI_CGAP_Kid10, NCI_CGAP_Co16, NCI_CGAP_Kid5,
NCI_CGAP_Kid12, NCI_CGAP_Kid3, NCI_CGAP_Kid11,
NCI_CGAP_Lym2, NCI_CGAP_Br2, NCI_CGAP_Co8, NCI_CGAP_CLL1,
NCI_CGAP_Le12, NCI_CGAP_Brn23, NCI_CGAP_Lu5,
NCI_CGAP_Lu24, NCI_CGAP_Lu19, NCI_CGAP_GC4, NCI_CGAP_GC6,
NCI_CGAP_Brn25. These 21 libraries were pooled and a
single-stranded DNA preparation of the resulting mixture
was used as a tracer in a subtractive hybridization with
a driver whose composition is detailed below:
NCI_CGAP_Kid3 pool 1 : LAM 3334-3337, 3682-3683,
3798-3803 (IMAGE CloneIDs 1322376-1323911,
1456008-1456775, 1500552-1502855) NCI_CGAP_Kid5 pool 1 :
LAM 3338-3342, 3722-3725, 3776-3778 (IMAGE CloneIDs
1323912-1325831, 1471368-1472003, 1492104-1493255)
NCI_CGAP_Lu5 pool 1 : LAM 3575-3582, 3851-3854 (IMAGE
CloneIDs 1414920-1417991, 1520904-1522439) NCI_CGAP_GC4
pool 1 : LAM 3164-3167, 3716-3720, 3733-3735 (IMAGE
CloneIDs 1257096-1258631, 1469064-1470983, 1475592-1476743
) NCI_CGAP_Pr22 pool 1 : LAM 2457-2459, 2758-2759,
3062-3068 (IMAGE CloneIDs 985608-986759, 1101192-1101959,
1217928-1220615) NCI_CGAP_Co10 pool 1 : LAM 2644-2653,
2871-2872 (IMAGE CloneIDs 1057416-1061255, 1144584-1145351
) Subtraction was performed as previously described
[Bonaldo, Lennon & Soares (1996): Normalization and
Subtraction: Two Approaches To Facilitate Gene Discovery.
Genome Research 6, 791-806.]
TAG_LIB=NCI_CGAP_Co4
TAG_TISSUE=COLON
TAG_SEQ=CTTGC"

BASE COUNT 104 a 108 c 134 g 103 t
ORIGIN

Query Match 94.5%; Score 216.4; DB 10; Length 449;
Best Local Similarity 99.1%; Pred. No. 1.1e-51;
Matches 228; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

QY 1 ACCGGACTTCAGTGTCTCTCCATCCAGAGCGCAGTGGCCACTATGGGTCTGGGCT 60
|||||
Db 433 ACCGGACTTCAGTGTCTCTCCATCCAGAGCGCAGTGGCCACTATGGGTCTGGGCT 374
|||||

QY 61 GCCCCTTGCTCCTCTTGACCTCTTGGCAGCTCAGATGGACAGGCGCGGTATGAC 120
|||||
Db 373 GCCCCTTGCTCCTCTTGACCTCTTGGCAGCTCAGATGGACAGGCGCGGTATGAC 314
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QY 121 TTTCGAACCTGAAGCTGAGGAGTCTTTTCTGACAAATTCCTCTATGAGTCCAGCTTCT 180
|||||
Db 313 TTTCGAACCTGAAGCTGAGGAGTCTTTTCTGACAAATTCCTCTATGAGTCCAGCTTCT 254
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QY 181 GGAATTCGTTGAAAAG-TCTGCCTCTCTCCATCTCCCTTCAGGACCA 229
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Db 253 GGAATTCGTTGAAAAGCTCTGCCTCTCTCCATCTCCCTTCAGGACCA 204
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RESULT 2
Bi759796 830 bp mRNA linear EST 25-SEP-2001
LOCUS 603045679F1 NIH_MGC_116 Homo sapiens cDNA clone IMAGE:5186107 5',
DEFINITION mRNA sequence.
ACCESSION Bi759796

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1. 449
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="NCI_CGAP_Sub4"
/lab_host="DH10B (Life Technologies)"
/notes="vector: pT73D-Pac (Pharmacia) with a modified
polylinker; Site1: Not I; Site2: Eco RI; The
NCI_CGAP_Sub4 library is a subtracted library derived from
the NCI_CGAP_Sub2 library which is a subtracted library
derived from the NCI_CGAP_Sub1 library, which is a
subtracted library derived from B1. Bi constitutes a
mixture of 21 normalized or subtracted NCI_CGAP
libraries: NCI_CGAP_Co4, NCI_CGAP_Pr22, NCI_CGAP_Pr28,
NCI_CGAP_Kid10, NCI_CGAP_Co16, NCI_CGAP_Kid5,
NCI_CGAP_Kid12, NCI_CGAP_Kid3, NCI_CGAP_Kid11,
NCI_CGAP_Lym2, NCI_CGAP_Br2, NCI_CGAP_Co8, NCI_CGAP_CLL1,
NCI_CGAP_Le12, NCI_CGAP_Brn23, NCI_CGAP_Lu5,
NCI_CGAP_Lu24, NCI_CGAP_Lu19, NCI_CGAP_GC4, NCI_CGAP_GC6,
NCI_CGAP_Brn25. These 21 libraries were pooled and a
single-stranded DNA preparation of the resulting mixture
was used as a tracer in a subtractive hybridization with
a driver whose composition is detailed below:
NCI_CGAP_Kid3 pool 1 : LAM 3334-3337, 3682-3683,
3798-3803 (IMAGE CloneIDs 1322376-1323911,
1456008-1456775, 1500552-1502855) NCI_CGAP_Kid5 pool 1 :
LAM 3338-3342, 3722-3725, 3776-3778 (IMAGE CloneIDs
1323912-1325831, 1471368-1472003, 1492104-1493255)
NCI_CGAP_Lu5 pool 1 : LAM 3575-3582, 3851-3854 (IMAGE
CloneIDs 1414920-1417991, 1520904-1522439) NCI_CGAP_GC4
pool 1 : LAM 3164-3167, 3716-3720, 3733-3735 (IMAGE
CloneIDs 1257096-1258631, 1469064-1470983, 1475592-1476743
) NCI_CGAP_Pr22 pool 1 : LAM 2457-2459, 2758-2759,
3062-3068 (IMAGE CloneIDs 985608-986759, 1101192-1101959,
1217928-1220615) NCI_CGAP_Co10 pool 1 : LAM 2644-2653,
2871-2872 (IMAGE CloneIDs 1057416-1061255, 1144584-1145351
) Subtraction was performed as previously described
[Bonaldo, Lennon & Soares (1996): Normalization and
Subtraction: Two Approaches To Facilitate Gene Discovery.
Genome Research 6, 791-806.]
TAG_LIB=NCI_CGAP_Co4
TAG_TISSUE=COLON
TAG_SEQ=CTTGC"

BASE COUNT 175 a 276 c 210 g 168 t 1 others
ORIGIN

Query Match 94.5%; Score 216.4; DB 13; Length 830;
Best Local Similarity 99.1%; Pred. No. 1.4e-51;
Matches 228; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

QY 1 ACCGGACTTCAGTGTCTCTCTCCATCCAGAGCGCAGTGGCCACTATGGGTCTGGGCT 60
|||||
Db 35 ACCGGACTTCAGTGTCTCTCTCCATCCAGAGCGCAGTGGCCACTATGGGTCTGGGCT 94
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QY 61 GCCCCTTGCTCCTCTTGACCTCTTGGCAGCTCAGATGGACAGGCGCGGTATGAC 120
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QY 121 TTTCGAACCTGAAGCTGAGGAGTCTTTTCTGACAAATTCCTCTATGAGTCCAGCTTCT 180
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Db 155 TTTCGAACCTGAAGCTGAGGAGTCTTTTCTGACAAATTCCTCTATGAGTCCAGCTTCT 214
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QY 181 GGAATTCGTTGAAAAG-TCTGCCTCTCTCCATCTCCCTTCAGGACCA 229
|||||
Db 215 GGAATTCGTTGAAAAGCTCTGCCTCTCTCCATCTCCCTTCAGGACCA 264
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RESULT 3
Bi759796 456 bp mRNA linear EST 27-MAR-2001
LOCUS 601861290F1 NIH_MGC_77 Homo sapiens cDNA clone IMAGE:407059 5',
DEFINITION mRNA sequence.
ACCESSION Bi759796
VERSION BG506690
KEYWORDS BG506690.1 GI:13468207
SOURCE EST.
ORGANISM Homo sapiens
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ORGANISM	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE	1. (bases 1 to 404)
AUTHORS	NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE	National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index
JOURNAL	Unpublished (1997)
COMMENT	Contact: Robert Strausberg, Ph.D. Email: cgaps@femail.nih.gov Tissue procurement: Christopher Moskaluk, M.D., Ph.D., Michael R. Emert-Buck, M.D., Ph.D. cDNA Library Preparation: M. Bento Soares, Ph.D. cDNA Library Arrayed by: Greg Lennon, Ph.D. DNA Sequencing by: Washington University Genome Sequencing Center Clone distribution: NCI-CGAP clone distribution found through the I.M.A.G.E. Consortium/LLNL at: www.bio.llnl.gov/bbrp/image/image.html Insert Length: 629 Std Error: 0.00 Seq primer: -400P from Gibco High quality sequence stop: 395. Location/Qualifiers 1..404 /organism="Homo sapiens" /db_xref="taxon:9606" /clone="IMAGE:2408041" /clone_lib="NCI_CGAP_Lu19"
FEATURES	source

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/dev_stage="adult"
/lab_host="DH10B (phage-resistant)"
/note="Organ: lung; Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; 1st strand cDNA was prepared from pooled lung tumor tissue, and was then primed with a Not I - oligo(dT) primer. Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT7T3 vector. Library went through one round of normalization. Library constructed by Bento Soares and M. Fatima Bonaldo."

BASE COUNT 97 a 105 c 117 g 84 t 1 others
ORIGIN
Query Match 49.3%; Score 113; DB 9; Length 404;
Best Local Similarity 98.4%; Pred. No. 5e-22;
Matches 124; Conservative 0; Mismatches 1; Indels 1; Gaps 1;
QY 105 CAGGCGCGGTATGACCTTTCGAACTGAAGAGTCTTTCTGCAAAATTCCTCT 164
Db 311 CAGGCGCGGTATGACCTTTCGAACTGAAGAGTCTTTCTGCAAAATTCCTCT 252
QY 165 ATGAGTCAGCTTCTCGAATTCCTGAAAG-TCTGCCTCTCTCTCCATCTCCTTCAG 223
Db 251 ATGAGTCAGCTTCTCGAATTCCTGAAAGCTTGCCTCTCTCCATCTCCTTCAG 192
QY 224 GGACCA 229
Db 191 GGACCA 186

RESULT 8
LOCUS BB533837
DEFINITION BB533837 RIKEN full-length enriched, 0 day neonate lung Mus
musculus cDNA clone E030032D13 3', mRNA sequence.
BB533837
EST. BB533837.2 GI:16446306
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 521)

Arakawa,T., Carninci,P., Fukuda,S., Furuno,M., Hanagaki,T., Hara,A., Hiramoto,K., Hori,F., Ishii,Y., Ito,M., Kawai,J., Konno,H., Kouda,M., Koya,S., Matsuyama,T., Miyazaki,A., Nomura,K., Ohno,M., Okazaki,Y., Okido,T., Saito,R., Sakai,C., Sakai,K., Sano,H., Sasaki,D., Shibata,K., Shinagawa,A., Shiraki,T., Sogabe,Y., Suzuki,H., Tagami,M., Tagawa,A., Takahashi,F., Takeda,Y., Tanaka,T., Toya,T., Muramatsu,M. and Hayashizaki,Y.
RIKEN Mouse ESTs (Arakawa,T., et al. 2001)
Unpublished (2001)
On Jul 29, 2000 this sequence version replaced gi:9585766.
Contact: Yoshihide Hayashizaki
Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
Tel: 81-45-503-9222
Fax: 81-45-503-9216
Email: genome-res@gsr.riken.go.jp,
URL:http://genome.gsc.riken.go.jp/
Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. Genome Res. 10 (10), 1617-1630 (2000)
wagi,K., Fujiwaki,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura

TITLE
JOURNAL
COMMENT

,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y.
RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000)
Konno,H., Fukunishi,Y., Shibata,K., Itoh,M., Carninci,P., Sugahara,Y. and Hayashizaki,Y.
Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)
Kondo,S., Shinagawa,A., Saito,T., Kiyosawa,H., Yamana,K.I., Aizawa,K., Fukuda,S., Hara,A., Itoh,M., Kawai,J., Shibata,K. and Hayashizaki,Y.
Computational Analysis of Full-Length Mouse cDNAs Compared with Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)
Please visit our web site (<http://genome.gsc.riken.go.jp/>) for further details.

cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.

FEATURES source

Location/Qualifiers
1..521
/organism="Mus musculus"
/db_xref="taxon:10090"
/clone_lib="E030032D13"
/clone_lib="RIKEN full-length enriched, 0 day neonate lung"
/tissue_type="lung"
/dev_stage="0 day neonate"
/lab_host="DH10B"
/note="Site 1: Sali; Site 2: BamHI; cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. 1st strand cDNA was primed with a primer [5'
GAGAGAGAGCGCGCGCACTCGAGTCTTTTCTTTTNN 3']. cDNA was prepared by using trehalose thermo-activated reverse transcriptase and subsequently enriched for full-length by cap-trapper. Second strand cDNA was prepared with the primer adapter of sequence [5'
GAGAGAGATTCGAGTTATTAATATCCGCCGCCGCC 3']. cDNA was cleaved with BamHI and XhoI. Vector: a modified pBluescript KS(+) after bulk excision from Lambda FLC 1."
BASE COUNT 119 a 163 c 125 g 114 t
ORIGIN

Query Match 41.0%; Score 94; DB 10; Length 521;
Best Local Similarity 73.3%; Pred. No. 1.5e-16;
Matches 148; Conservative 0; Mismatches 50; Indels 4; Gaps 2;
QY 29 AGGAGCGAGTGGCCATATGGGCTGGCGTGGCGCTTGTCTCTCTTGTACCCCTT 88
Db 156 AGAGCTGGGTAGCCACCATCTTTGATGGCTCTCTCTCTCTCTCTCTCTCT 215
QY 89 GGCAGCTCAGATGACAGCGCGGGTATGACTTGCACCTGAAGCTGAAGGAGTCTTT 148
Db 216 AGCAGCTCACAG---CAGGGCCAAAGGTGACTTTGAGGTAAGCTGACGAGACTTT 272
QY 149 CTGACAAATTCCTCTTCTGAGTTCAGCTTCTGGAATTCCTTGAAG-TCTGCCTCCTC 207
Db 273 CAGGACAGACCTCCCAAGACTCCAGTCTCTGACATGCTCCAAAGATCTGCTCTCTC 332
QY 208 CTCCTCTCTCTCTCAGGACCA 229
Db 333 CTCCTCTCTCTCTCAGGACCA 354

RESULT 9
BB664284

library, which is a subtracted library derived from the UI-R-C0 library. The UI-R-C0 library consisted of a mixture of individually tagged normalized libraries constructed from rat placenta, adult lung, brain, liver, kidney, heart, spleen, ovary, muscle, 8, 12 and 18-day embryo. The tag is a string of 3-5 nucleotides present between the Not I site and the oligo-dT track which allows identification of the library of origin of a clone within the mixture. The subtracted library (UI-R-C2p) was constructed as follows: PCR amplified cDNA inserts from UI-R-C1 clones from which 3' ESTs had been derived was used as a driver in a hybridization with the UI-R-C1 library in the form of single-stranded circles. The remaining single-stranded circles (subtracted library) was purified by hydroxyapatite column chromatography, converted to double-stranded circles and electroporated into DH10B bacteria (Life Technologies) to generate the UI-R-C2p library. This procedure has been previously described (Ronaldo, Lennon and Soares, Genome Research 6: 791-806, 1996).

BASE COUNT 79 a 121 c 91 g 70 t
ORIGIN

Query Match 40.3%; Score 92.2; DB 12; Length 361;
Best Local Similarity 68.8%; Pred. No. 4.5e-16;
Matches 141; Conservative 0; Mismatches 63; Indels 1; Gaps 1;

QY 26 CCAGAGCGCAGTGGCGCTATGGGTCTGGGCTGGCCCTTGTCTCTCTCTTGACCCCTC 85
DB 1 CAGAGGGTGAAGCGCGCCACATGGAGCTTCGATGTGCTCTCTCTCTCTGACCCCTC 60

QY 86 CTGGCAGCTCACATCGAACGCGCGGTATGACTTTGCAACTGAAGCTGAAGGAGTCT 145
DB 61 CTCGAGCTCACTCGAGGGCCACAAAGTGACTTCGAGTAAGTCAAGCGAGGCA 120

QY 146 TTCTGACAATTCCTCTATGATGCCAGCTTCTCGAATTCGTTGAAG-TCCTGCCTC 204
DB 121 TCTAGGCCAAGACTCCCAAGACTCCGGCTTCTCGACATCTCCAAAGATCTGCCTC 180

QY 205 CTCCTCATCTCCCTCTCAGGACCA 229
DB 181 CTCCTCCACCTCTCAGCGGGACCA 205

RESULT 11
A0718761/c
LOCUS
DEFINITION HS-5511_B2_F09_T7A RPCI-11 Human Male BAC Library Homo sapiens genomic clone Plate=1087 Col=18 Row=L, DNA sequence.

ACCESSION A0718761
VERSION A0718761.1 GI:5468077
KEYWORDS GSS.
SOURCE human.

ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 552)
AUTHORS Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T., Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D. and Hood,L.

TITLE Sequence-tagged connectors: A sequence approach to mapping and scanning the human genome
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999)
MEDLINE 99380589
COMMENT Contact: Mahairas GG, Wallace JC, Hood L
High Throughput Sequencing Center
University of Washington
401 Queen Anne Avenue North, Seattle, WA 98109, USA

Tel: (206) 616-3618
Fax: (206) 616-3887
Email: jwallace@u.washington.edu

Clones are derived from the human BAC library RPCI-11. For BAC library availability, please contact Pieter de Jong

(pieter@edjong.med.buffalo.edu). Clones may be purchased from BACPAC Resources (http://bacpac.med.buffalo.edu/ordering_bac.htm) or from Research Genetics (<http://www.htsc.washington.edu>)
Plate: 1087 row: L column: 18
Seq primer: T7
Class: BAC ends

High quality sequence stop: 552.

FEATURES
source
Location/Qualifiers
1..552
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="Plate=1087 Col=18 Row=L"
/clone_lib="RPCI-11 Human Male BAC Library"
/sex="male"
/note="Vector: pBACE3.6; Site_1: EcoRI; Site_2: EcoRI; Male blood DNA was isolated from one randomly chosen donor and partially digested with a combination of EcoRI and EcoRI-Methylase. Size selected DNA was cloned into the pBACE3.6 vector at EcoRI sites"

BASE COUNT 141 a 153 c 124 g 117 t 17 others
ORIGIN

Query Match 32.9%; Score 75.4; DB 17; Length 552;
Best Local Similarity 87.2%; Pred. No. 3.4e-11;
Matches 82; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

QY 103 ACAGGGCGGGTATGACTTTGCAACTGAAGCTGAAGGAGTCTTTTCGACAAATTCCTC 162
DB 474 AGCATGGCGAGGTATGACTTTGCANCTGAAGCTGAAGAGGTCTATTAGACAAATTCGTC 415

QY 163 CTATGAGTCCAGCTTCTCGAATTCGTTGAAAG 196
DB 414 TTATGAGTCCAGCTTCTCGAATTCGTTGAAG 381

RESULT 12
A1136523/c
LOCUS

DEFINITION A1136523 328 bp mRNA linear EST 11-FEB-1999
UI-R-C2p-nq-e-02-0-UI.s1 UI-R-C2p Rattus norvegicus cDNA clone
UI-R-C2p-nq-e-02-0-UI 3', mRNA sequence.

ACCESSION A1136523
VERSION A1136523.1 GI:3637300
KEYWORDS EST.
SOURCE Norway rat.

ORGANISM Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.
REFERENCE 1 (bases 1 to 328)
AUTHORS Ronaldo,M.F., Lennon,G. and Soares,M.B.

TITLE Normalization and subtraction: two approaches to facilitate gene discovery
JOURNAL Genome Res. 6 (9), 791-806 (1996)
MEDLINE 97044477
COMMENT Contact: Soares, MB
Program for Rat Gene Discovery and Mapping
University of Iowa
451 Eckstein Medical Research Building Iowa City, IA 52242, USA

Tel: 319 335 8250
Fax: 319 335 9565
Email: msoares@blue.weeg.uiowa.edu
The sequence tag present in the cDNA between the NotI site and the oligo-dT track served to identify it as a clone from the normalized adult Lung library. cDNA library preparation: M. Fatima Ronaldo, Ph.D. Clone distribution: clones will be available through Research Genetics

Seq primer: M13 Forward.
FEATURES
source
Location/Qualifiers
1..328
/organism="Rattus norvegicus"
/strain="Sprague-Dawley"
/db_xref="taxon:10116"

/clone="UI-R-C2p-nq-e-02-0-UI"
/clone_llb="UI-R-C2p"
/dev_stage="adult"

/lab_host="DH10B (Life Technologies)"
/note="Vector: p773D-Pac (Pharmacia) with a modified
polylinker; Site 1: Not I; Site 2: Eco RI; The UI-R-C2p
library is a subtracted library derived from the UI-R-C1
library, which is a subtracted library derived from the
UI-R-C0 library. The UI-R-C0 library consisted of a
mixture of individually tagged normalized libraries
constructed from rat placenta, adult lung, brain, liver,
kidney, heart, spleen, ovary, muscle, 8, 12 and 18-day
embryo. The tag is a string of 3-5 nucleotides present
between the Not I site and the oligo-dT track which allows
identification of the library of origin of a clone within
the mixture. The subtracted library (UI-R-C2p) was
constructed as follows: PCR amplified cDNA inserts from
UI-R-C1 clones from which 3' ESTs had been derived was
used as a driver in a hybridization with the UI-R-C1
library in the form of single-stranded circles. The
remaining single-stranded circles (subtracted library) was
purified by hydroxyapatite column chromatography,
converted to double-stranded circles and electroporated
into DH10B bacteria (Life Technologies) to generate the
UI-R-C2p library. This procedure has been previously
described (Bonaldo, Lemmon and Soares, Genome Research 6:
791-806, 1996)."

BASE COUNT 62 a 77 c 98 g 91 t
ORIGIN

Query Match 27.0%; Score 61.8; DB 9; Length 328;

Best Local Similarity 69.5%; Pred. No. 2.3e-07;

Matches 98; Conservative 0; Mismatches 42; Indels 1; Gaps 1;

Qy 90 GCAGCTCACATGGACAGCGCGGTATGACTTTGCAACTGAGCTGAGGAGTCTTTTC 149

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Db 327 GCAGCTCTACTGAGGCGCCACAAAGGTCCTTTCAGATGAATACACGAGGATCTC 268

||||||| | | | | | | | | | | | | | | | | | | | | | | | | | |

Qy 150 TGCAAAATTCCTCTATGATCCAGCTTCCTGGAAATGCTTGAAAAG-TCTGGCTCTCC 208

| | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

Db 267 AGGCCAAGACCTCCCAAGATCCGGCTTCTGGACATGCTCCAAAAGATCTGCTCTCC 208

| | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

Qy 209 TCCATCTCCCTTCAGGACCA 229

| | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

Db 207 TCCATCTCTACCGGGGACCA 187

| | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

RESULT 13
LOCUS AZ241329/c
DEFINITION RPCI-23-75C13.TJ RPCI-23 Mus musculus genomic clone RPCI-23-75C13,
DNA sequence.

ACCESSION AZ241329

VERSION AZ241329.1 GI:8554520

KEYWORDS GSS.

SOURCE house mouse.

ORGANISM Mus musculus

REFERENCE 1 (bases 1 to 506)

AUTHORS Zhao, S., Nierman, W., Feldblyum, T., Malek, J., Shatsman, S., Akinret

and Fraser, C.M.

TITLE Mouse BAC End Sequences from Library RPCI-23

JOURNAL Unpublished (1999)

COMMENT Other GSSs: RPCI-23-75C13.TV

Contact: Shaying Zhao

Department of Eukaryotic Genomics

The Institute for Genomic Research

9712 Medical Center Dr., Rockville, MD 20850, USA

Tel: 301 838 0200

Fax: 301 838 0208

Email: szhao@tigr.org

Clones are derived from the mouse BAC library RPCI-23. For BAC
library availability, please contact Pieter de Jong
(pieter@dejong.med.buffalo.edu). Clones may be purchased from
BACPAC Resources (http://bacpac.med.buffalo.edu/orderingframe.htm)
or from Resea ch Genetics (info@resgen.com). BAC end page:
http://www.tigr.org/tdb/bac_ends/mouse/bac_end_intro.html
Plate: 75 row: C column: 13
Seq primer: SF6
Class: BAC ends.

FEATURES

Source
Location/Qualifiers
1..506
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="RPCI-23-75C13"
/clone_llb="RPCI-23"
/sex="Female"
/lab_host="DH10B"
/note="Organ: Kidney/Brain; Vector: pBACE3.6; Site_1:
EcoRI; Site_2: EcoRI; Female C57BL/6J mouse kidney and/or
brain genomic DNA was isolated and partially digested
with a combination of EcoRI and EcoRI Methylase. Size
selected DNA was cloned into the pBACE3.6 vector at the
EcoRI sites. The ligation products were transformed into
DH10B electrocompetent cells (BRL Life Technologies)."

BASE COUNT 116 a 145 c 138 g 107 t

ORIGIN

Query Match 19.9%; Score 45.6; DB 17; Length 506;

Best Local Similarity 68.5%; Pred. No. 0.012;

Matches 63; Conservative 0; Mismatches 29; Indels 0; Gaps 0;

Qy 105 CAGGCGCGGTATGACTTTGCAACTGAGCTGAGGAGTCTTTTCACAAATCTCTCT 164

||||||| | | | | | | | | | | | | | | | | | | | | | | | | | |

Db 403 CAGGCGCAAGGTGACTTTGACAGTAAAGCTGACCGACATTTTCAGCAGACACCTCCC 344

||||||| | | | | | | | | | | | | | | | | | | | | | | | | | |

Qy 165 ATGAGTCAGAGCTTCCTGGAAATGCTTGAAAAG 196

| | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

Db 343 AGAAGTCCAGTCTGCGACATGCTCCAAAAG 312

| | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

RESULT 14

AZ079350/c

LOCUS AZ079350

DEFINITION RPCI-23-438H19.TV RPCI-23 Mus musculus genomic clone RPCI-23-438H19

, DNA sequence.

ACCESSION AZ079350

VERSION AZ079350.1 GI:7372249

KEYWORDS GSS.

SOURCE house mouse.

ORGANISM Mus musculus

REFERENCE 1 (bases 1 to 633)

AUTHORS Zhao, S., Nierman, W., Feldblyum, T., Malek, J., Shatsman, S., Akinret

, B., Levins, M., McGann, S., Tsegaye, G., Geer, K., Krol, M., de Jong, P.

and Fraser, C.M.

TITLE Mouse BAC End Sequences from Library RPCI-23

JOURNAL Unpublished (1999)

COMMENT Other GSSs: RPCI-23-438H19.TJ

Contact: Shaying Zhao

Department of Eukaryotic Genomics

The Institute for Genomic Research

9712 Medical Center Dr., Rockville, MD 20850, USA

Tel: 301 838 0200

Fax: 301 838 0208

Email: szhao@tigr.org

Clones are derived from the mouse BAC library RPCI-23. For BAC

library availability, please contact Pieter de Jong

(pieter@dejong.med.buffalo.edu). Clones may be purchased from

BACPAC Resources (http://bacpac.med.buffalo.edu/orderingframe.htm)

or from Resea ch Genetics (info@resgen.com). BAC end page:

http://www.tigr.org/tdb/bac_ends/mouse/bac_end_intro.html

Plate: 438 row: H column: 19

Seq primer: T7

Class: BAC ends.

Location/Qualifiers

1. .633
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone_lib="RPCI-23-438H19"
/sex="Female"
/lab_host="DH10B"

/note="Organ: Kidney/Brain; Vector: pBACE3.6; Site_1: EcoRI; Site_2: EcoRI; Female C57BL/6J mouse kidney and/or brain genomic DNA was isolated and partially digested with a combination of EcoRI and EcoRI Methylase. Size selected DNA was cloned into the pBACE3.6 vector at the EcoRI sites. The ligation products were transformed into DH10B electrocompetent cells (BRL Life Technologies)."

BASE COUNT 138 a 191 c 161 g 143 t
ORIGIN

Query Match 19.9%; Score 45.6; DB 17; Length 633;
Best Local Similarity 68.5%; Pred. No. 0.013;
Matches 63; Conservative 0; Mismatches 29; Indels 0; Gaps 0;

QY 105 CAGGCGCGGTATGACTTGCACCTGAAGCTGAGGAGTCTTTCTGACAAATTCCTCT 164

Db 403 CAGGCGCAAGGTACTTTCGAGTGAAGCTGACCGAGACTTTTCAGGACAAACCTCCC 344

QY 165 ATGAGTCCAGCTCTCTGGAATTCCTGAAAG 196

Db 343 AGAACTCCAGTGTCTGGACATGCTCCAAAG 312

RESULT 15

LOCUS BG686317 754 bp mRNA linear EST 01-MAY-2001
DEFINITION 602638230F1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4765975 5', mRNA sequence.

ACCESSION BG686317

VERSION BG686317.1 GI:13917714

KEYWORDS EST.

SOURCE human.

ORGANISM

Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 754)

NIH-MGC <http://mgi.nci.nih.gov/>.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgaps-f@mail.nih.gov

Tissue Procurement: Louis M. Staudt, M.D., Ph.D.

cDNA Library Preparation: Ling Hong/Rubin Laboratory

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

<http://image.llnl.gov>

Plate: LCN1625 row: 1 column: 08

High quality sequence stop: 750.

Location/Qualifiers

1. .754

/organism="Homo sapiens"

/db_xref="taxon:9606"

/clone="IMAGE:4765975"

/clone_lib="NIH_MGC_48"

/tissue_type="Primary B-cells from tonsils (cell line)"

/lab_host="DH10B (phage-resistant)"

/note="Organ: B-cells; Vector: pOTB7; Site_1: XhoI;

Site_2: EcoRI; cDNA made by oligo-dT priming.

Directionally cloned into EcoRI/XhoI sites using the

following 5' adaptor: GGCACGAG(G). Size-selected >500bp
for average insert size 1.8kb. Library constructed by Ling
Hong in the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA Synthesis kit
(Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH_MGC Library."

BASE COUNT 166 a 206 c 201 g 181 t
ORIGIN

Query Match 15.7%; Score 36; DB 12; Length 754;

Best Local Similarity 64.3%; Pred. No. 7.8; Indels 0; Gaps 0;

Matches 54; Conservative 0; Mismatches 30;

QY 14 TGTCTCTCCATCCAGGAGCGCAGTGGCCACTATGGGTCTGGGCTGCCCTTGCTC 73

Db 249 TGTTCCTCCCTCCAGGATCCCTTTGGTGAGTATGTTCCAGGATGCACCATCACCAC 308

QY 74 CTCTTGACCTCTCTTGGCAGTCA 97

Db 309 CTCTAGATACCTTCAGGCACACA 332

Search completed: May 1, 2003, 05:10:04

Job time : 1150.32 secs

GenCore version 5.1.5
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OM nucleic - nucleic search, using sw model

Run on: May 1, 2003, 03:53:25 ; Search time 41.542 Seconds
(without alignments)
1690.556 Million cell updates/sec

Title: US-09-092-296-2

Perfect score: 229

Sequence: 1 ACCGGGACTTCAGTGTCTCC.....CCATCTCCTTCAGGGAACA 229

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 441362 seqs, 153338381 residues

Total number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0

Maximum DB seq length: 20000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Issued_Patents_NA:*
1: /cgn2_6/ptodata/2/ina/5A_COMB.seq:*
2: /cgn2_6/ptodata/2/ina/5B_COMB.seq:*
3: /cgn2_6/ptodata/2/ina/6A_COMB.seq:*
4: /cgn2_6/ptodata/2/ina/6B_COMB.seq:*
5: /cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*
6: /cgn2_6/ptodata/2/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	30.8	13.4	16063	4	US-09-801-052-3
C 2	30.4	13.3	580	2	US-08-627-610-7
C 3	30.4	13.3	580	3	US-08-581-918A-7
C 4	30.4	13.3	580	4	US-08-346-147B-7
C 5	30.4	13.3	580	4	US-08-822-936-7
C 6	30.4	13.3	580	4	US-08-497-214D-7
C 7	30.4	13.3	580	5	PCN-US95-04636-7
C 8	30.4	13.3	1515	4	US-08-928-383B-25
C 9	30	13.1	3358	3	US-09-248-571-2
C 10	30	13.1	3358	4	US-09-553-736-2
C 11	29.8	13.0	3509	2	US-08-817-436A-1
C 12	29.6	12.9	7218	1	US-08-232-463-14
C 13	29.4	12.8	1091	4	US-09-219-194-2
C 14	29	12.7	1157	1	US-07-709-949-1
C 15	29	12.7	1316	4	US-09-056-105-24
C 16	29	12.7	2259	6	5185254-3
C 17	28.8	12.6	1785	3	US-08-729-416C-8
C 18	28.4	12.4	2095	1	US-08-405-230-8
C 19	28.4	12.4	2095	2	US-08-910-990-8
C 20	28.4	12.4	2564	3	US-08-276-968A-19
C 21	28.4	12.4	3218	4	US-09-369-364A-6
C 22	27.8	12.1	1396	4	US-09-328-174A-2
C 23	27.8	12.1	2870	4	US-09-221-017B-850
C 24	27.8	12.1	8396	4	US-09-328-174A-1
C 25	27.8	12.1	8409	4	US-09-167-681-37
C 26	27.6	12.1	3088	1	US-08-418-444A-1
C 27	27.6	12.1	5102	1	US-08-494-168-1

c 28	27.4	12.0	3941	4	US-09-408-865-2	Sequence 2, Appl 1
c 29	27.2	11.9	1295	4	US-09-219-194-3	Sequence 3, Appl 1
c 30	27.2	11.9	2122	1	US-08-485-449-1	Sequence 1, Appl 1
c 31	27.2	11.9	3398	5	PCT-US95-08493-12	Sequence 12, Appl 1
c 32	27.2	11.9	152331	3	US-09-128-155-16	Sequence 16, Appl 1
c 33	27.2	11.9	176373	3	US-09-128-155-17	Sequence 17, Appl 1
c 34	27	11.8	312	4	US-09-060-756-506	Sequence 506, App
c 35	27	11.8	956	4	US-09-641-638-36	Sequence 36, Appl 1
c 36	27	11.8	956	4	US-09-641-638-37	Sequence 37, Appl 1
c 37	27	11.8	956	4	US-09-641-638-38	Sequence 38, Appl 1
c 38	27	11.8	1001	4	US-09-641-638-39	Sequence 39, Appl 1
c 39	27	11.8	1294	2	US-08-665-647-4	Sequence 628, App
c 40	27	11.8	1554	1	US-08-469-486-1	Sequence 4, Appl 1
c 41	27	11.8	1554	2	US-08-469-486-1	Sequence 1, Appl 1
c 42	27	11.8	1554	2	US-08-469-486-1	Sequence 1, Appl 1
c 43	26.8	11.7	1674	3	US-09-059-369-17	Sequence 17, Appl 1
c 44	26.8	11.7	2090	3	US-09-059-369-1	Sequence 1, Appl 1
c 45	26.8	11.7	2703	2	US-08-288-508C-1	Sequence 1, Appl 1

ALIGNMENTS

RESULT 1
US-09-801-052-3/c
; Sequence 3, Application US/09801052
; Patent No. 6368842
; GENERAL INFORMATION:
; APPLICANT: BEASLEY, Ellen
; TITLE OF INVENTION: ISOLATED HUMAN PHOSPHOLIPASE PROTEINS,
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN PHOSPHOLIPASE
; TITLE OF INVENTION: PROTEINS, AND USES THEREOF
; FILE REFERENCE: CL001045
; CURRENT APPLICATION NUMBER: US/09/801.052
; CURRENT FILING DATE: 2001-03-08
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 16063
; TYPE: DNA
; ORGANISM: Human
US-09-801-052-3

Query Match 13.4%; Score 30.8; DB 4; Length 16063;
Best Local Similarity 55.7%; Pred. No. 2.1;
Matches 59; Conservative 0; Mismatches 47; Indels 0; Gaps 0;
Qy 36 CAGTGGCCACTATGGGTCTGGGCTGCCCTTGCTCTCTTGGACCCCTCTTGGCAGCT 95
Db 7189 CACTCCCGAGTGTGTCTGTCTTCCCTGCTCCACAGTACCCTCCACCCAGCT 7130
Oy 96 CACATGGAACAGGCGGGTATGACTTTGCAACTGAAGCTGAAGGA 141
Db 7129 CCATAGCTAAGTCTCTAGATGATATCAACTTAAGTTTGATGA 7084

RESULT 2
US-08-627-610-7/c
; Sequence 7, Application US/08627610
; Patent No. 5919997
; GENERAL INFORMATION:
; APPLICANT: Beach, David H.
; APPLICANT: Serrano, Manuel
; APPLICANT: DePinho, Ronald A.
; TITLE OF INVENTION: Transgenic Animals Having Modified Cell-Cycle
; TITLE OF INVENTION: Regulation
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD
; STREET: 60 State Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA

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; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII(text)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/627,610
; FILING DATE: 04-APR-1996
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Vincent, Matthew P.
; REGISTRATION NUMBER: 36,709
; REFERENCE/DOCKET NUMBER: CSI-001CP6
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 227-7400
; TELEFAX: (617) 227-5941
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 580 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 91..480
; US-08-627-610-7

Query Match 13.38; Score 30.4; DB 2; Length 580;
Best Local Similarity 57.3%; Pred. No. 0.64; Mismatches 41; Indels 0; Gaps 0;
Matches 55; Conservative 0;

QY 35 GCAGTGGCCACTATGGGTCTGGGCTGCCCTTGTCTCTTGTGACCTCTCTTGGCAGC 94
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Db 128 GCGGTGGCCAGGCCGCGTCACTGCTGCCGCCAACATGCGCTTGTCCCGGCTGTGTGC 69

QY 95 TCACATGGAACAGGCCGCGGTATGACTTTGCAACTG 130
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Db 68 AGAATGGTCTTCGCCGCCGTGAGATTGCTACAG 33

RESULT 3
US-08-581-918A-7/c
; Sequence 7, Application US/08581918A
; Patent No. 6043030
; GENERAL INFORMATION:
; APPLICANT: Beach, David H.
; APPLICANT: Demetrick, Douglas J.
; APPLICANT: Serrano, Manuel
; APPLICANT: Hannon, Gregory J.
; TITLE OF INVENTION: Cell-Cycle Regulatory Proteins, and Uses
; TITLE OF INVENTION: Related Thereto
; NUMBER OF SEQUENCES: 39
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley, Hoag & Eliot
; STREET: One Post Office Square
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WordPad
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/581,918A
; FILING DATE: 02-JAN-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/497,214
; FILING DATE: 30-JUN-1995
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; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/346,147
; FILING DATE: 29-NOV-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/306,511
; FILING DATE: 14-SEP-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/248,812
; FILING DATE: 25-MAY-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/227,371
; FILING DATE: 14-APR-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/154,915
; FILING DATE: 18-NOV-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/991,997
; FILING DATE: 17-DEC-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Vincent, Matthew P.
; REGISTRATION NUMBER: 36,709
; REFERENCE/DOCKET NUMBER: MIV-071.06
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 832-1299
; TELEFAX: (617) 832-7000
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 580 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 91..480
; US-08-581-918A-7

Query Match 13.38; Score 30.4; DB 3; Length 580;
Best Local Similarity 57.3%; Pred. No. 0.64; Mismatches 41; Indels 0; Gaps 0;
Matches 55; Conservative 0;

QY 35 GCAGTGGCCACTATGGGTCTGGGCTGCCCTTGTCTCTTGTGACCTCTCTTGGCAGC 94
|| ||||| || ||||| || ||||| || ||||| || ||||| || ||||| || |||||
Db 128 GCGGTGGCCAGGCCGCGTCACTGCTGCCGCCAACATGCGCTTGTCCCGGCTGTGTGC 69

QY 95 TCACATGGAACAGGCCGCGGTATGACTTTGCAACTG 130
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Db 68 AGAATGGTCTTCGCCGCCGTGAGATTGCTACAG 33

RESULT 4
US-08-346-147B-7/c
; Sequence 7, Application US/08346147B
; Patent No. 6211334
; GENERAL INFORMATION:
; APPLICANT: Beach, David H.
; APPLICANT: Demetrick, Douglas J.
; APPLICANT: Serrano, Manuel
; APPLICANT: Hannon, Gregory J.
; TITLE OF INVENTION: Cell-Cycle Regulatory Proteins, and Uses
; TITLE OF INVENTION: Related Thereto
; NUMBER OF SEQUENCES: 47
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley, Hoag & Eliot
; STREET: One Post Office Square
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
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SOFTWARE: Wordpad
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/346,147B
FILING DATE: 29-NOV-1994
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: US 08/306,511
FILING DATE: 14-SEP-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/248,812
FILING DATE: 25-MAY-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/227,371
FILING DATE: 14-APR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/154,915
FILING DATE: 18-NOV-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/991,997
FILING DATE: 17-DEC-1992
ATTORNEY/AGENT INFORMATION:
NAME: Vincent, Matthew P.
REGISTRATION NUMBER: 36,709
REFERENCE/DOCKET NUMBER: MIV-071.04
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 832-1299
TELEFAX: (617) 832-7000
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 580 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
TOPOLOGY: linear
MOLECULE TYPE: gDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 91..480
US-08-346-147B-7

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	Query Match	13.3%	Score 30.4;	DB 4;	Length 580;
	Best Local Similarity	57.3%;	Pred. No. 0.64;		
	Matches 35;	Conservative 0;	Mismatches 41;	Indels 0;	Gaps 0;
QY	35	GCAGTGGCCACTATGGGGTCTGGGTGCGCCCTTTGCTCTCTTTGACCCCTCCTTTGGCAGC	94		
DB	128	GGCGTGGCCAGCCCGCGTCACTGCTGCGCCCAACATGCCCTTTGCCCGCTCTGTGGC	69		
QY	95	TCACATGGAAACGGCGGGTATGACTTTGTCAACTG	130		
DB	68	AGAAATGGTCTTTCGCGCGCGCTGAGATGCTACAG	33		

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RESULT 5
US-08-822-936-7/c
; Sequence 7, Application US/08822936
; Patent NO. 6242575
; GENERAL INFORMATION:
; APPLICANT: Massague, Joan
; APPLICANT: Roberts, James M.
; APPLICANT: Koif, Andrew
; APPLICANT: Polyak, Kornelia
; TITLE OF INVENTION: Isolated p27 Protein, Nucleic Acid
; TITLE OF INVENTION: Molecules Encoding Same, Methods of Identifying Agents Acting
; TITLE OF INVENTION: And Uses of Said Agents
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley, Hoag & Eliot, LLP
; STREET: One Post Office Square
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02109-2170
; COMPUTER READABLE FORM:

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; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/822,936
; FILING DATE: 21-FEBRUARY-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Vincent, Matthew P.
; REGISTRATION NUMBER: 36,709
; REFERENCE/DOCKET NUMBER: MIV-079, 05
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 832-1000
; TELEFAX: (617) 832-7000
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 580 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: linear
; MOLECULE TYPE: cdna
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 91...480
US-08-822-936-7

Query Match 13.3%; Score 30.4; DB 4; Length 580;
Best Local Similarity 57.3%; Pred. No. 0.64;
Matches 55; Conservative 0; Mismatches 41; Indels 0; Gaps 0;

QY 35 CGACGTGCACACTATGTGGGTCGTGGGTCGCCCTTGTCTCTCTGTACCCCTCTTGGCAGC 94
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 128 CGGTGGCCAGCCGGCGGTCACTGTCGCCGCCCMACATCCCTGTCTCCGGTCTGTGGC 69
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY 95 TCACATGGAAACAGGCCCGGGTATGACTTTGCAACTG 130
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 68 AGAAATGGTCCTTCGCGCGCGGTGAGATTGCTACAG 33
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RESULT 6
US-08-497-214D-7/c
; Sequence 7, Application US/08497214D
; Patent No. 6331390
; GENERAL INFORMATION:
; APPLICANT: Beach, David H.
; APPLICANT: Demetrick, Douglas J.
; APPLICANT: Serrano, Manuel
; APPLICANT: Hannon, Gregory J.
; TITLE OF INVENTION: Cell-Cycle Regulatory Proteins, and Uses
; TITLE OF INVENTION: Related Thereto
; NUMBER OF SEQUENCES: 47
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley, Hoag & Elliot
; STREET: One Post Office Square
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WordPad
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/497.214D
; FILING DATE: 30-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/346.147
; FILING DATE: 29-NOV-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/306.511
; FILING DATE: 14-SEP-1994

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FILING DATE: 14-APR-1994

US-08-928-383B-25


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Query Match      13.3%; Score 30.4; DB 4; Length 1515;
Best Local Similarity 61.2%; Pred. No. 0.99; 31; Indels 0; Gaps 0;
Matches 49; Conservative 0; Mismatches 31; Indels 0; Gaps 0;

QY 29 AGGAGCGCAGTGGCCACTATGGGCTTGGGCTGGCCCTTGTCTCTCTTGGACCTCCTT 88
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Db 712 ACATCGCGGGCGCGTCATAGGACGCTGTGCGCCCTTGTCTCTATCGGGGCGATCCTC 771
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QY 89 GGCAGCTCACATGGACAGG 108
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Db 772 TTCTGTGTACAGGAACG 791
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RESULT 9
US-09-248-571-2
; Sequence 2, Application US/09248571
; Patent No. 6136539
; GENERAL INFORMATION:
; APPLICANT: BASBAUM, CAROL
; APPLICANT: GALLUP, MARIANNE
; APPLICANT: DAIZONG, LI
; APPLICANT: GEBREMICHAEL, ASSEFA
; APPLICANT: GENSGH, ERIN
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR INHIBITION OF MUC-5 MUCIN
; TITLE OF INVENTION: GENE EXPRESSION
; FILE REFERENCE: UCSF12/02
; CURRENT APPLICATION NUMBER: US/09/248,571
; CURRENT FILING DATE: 1999-02-11
; EARLIER APPLICATION NUMBER: 60/074,398
; EARLIER FILING DATE: 1998-02-11
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 3358
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-248-571-2

Query Match      13.1%; Score 30; DB 3; Length 3358;
Best Local Similarity 61.5%; Pred. No. 1.9; 30; Indels 0; Gaps 0;
Matches 48; Conservative 0; Mismatches 30; Indels 0; Gaps 0;

QY 17 CTCCTCCATCCAGCGCAGTGGCCACTATGGGCTTGGGCTGGCCCTTGTCTCTCTCCTC 76
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Db 552 CTCATTACAGACGACGACGTACACCAAGTGGAGCGCAGGCTGGGCTTGTCTCTCATG 611
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 77 TTGACCTCTTGGCAGC 94
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Db 612 TGGACACGATGACAGC 629
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RESULT 10
US-09-553-736-2
; Sequence 2, Application US/09553736
; Patent No. 6440672
; GENERAL INFORMATION:
; APPLICANT: BASBAUM, CAROL
; APPLICANT: GALLUP, MARIANNE
; APPLICANT: DAIZONG, LI
; APPLICANT: GEBREMICHAEL, ASSEFA
; APPLICANT: GENSGH, ERIN
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE INHIBITION OF MUC-5
; TITLE OF INVENTION: MUCIN GENE EXPRESSION
; FILE REFERENCE: UCSF-012/03US
; CURRENT APPLICATION NUMBER: US/09/553,736
; CURRENT FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 09/248,571
; PRIOR FILING DATE: 1999-02-11
; PRIOR APPLICATION NUMBER: US 60/074,398
; PRIOR FILING DATE: 1998-02-11
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
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; LENGTH: 3358
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-553-736-2

Query Match      13.1%; Score 30; DB 4; Length 3358;
Best Local Similarity 61.5%; Pred. No. 1.9; 30; Indels 0; Gaps 0;
Matches 48; Conservative 0; Mismatches 30; Indels 0; Gaps 0;

QY 17 CTCCTCCATCCAGCGCAGTGGCCACTATGGGCTTGGGCTGGCCCTTGTCTCTCTCCTC 76
    ||||| ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 552 CTCATTACAGACGACGACGTACACCAAGTGGAGCGCAGGCTGGGCTTGTCTCTCATG 611
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 77 TTGACCTCTTGGCAGC 94
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 612 TGGACACGATGACAGC 629
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RESULT 11
US-08-817-436A-1
; Sequence 1, Application US/08817436A
; Patent No. 5882880
; GENERAL INFORMATION:
; APPLICANT: Canaan1, Dan
; TITLE OF INVENTION: Human Checkpoint Gene and Gene for
; TITLE OF INVENTION: Antisense RNA thereof
; NUMBER OF SEQUENCES: 3
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Wigman, Cohen, Leitner & Myers
; STREET: 900 17th Street, N.W., Suite 1000
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.
; ZIP: 20006
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette 3.5 inch, 1.44Mb storage
; COMPUTER: IBM compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: ASCII
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/817,436A
; FILING DATE: 11-JUN-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/12445
; FILING DATE: 11-OCT-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Cohen, Herbert
; REGISTRATION NUMBER: 25,109
; REFERENCE/DOCKET NUMBER: 0744,066
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-463-7700
; TELEFAX: 202-463-6915
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3509 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA to mRNA
; HYPOTHEetical: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
; CELL LINE: ESTABLISHED XERODERMA PIGMENTOSUM GM2096-SV3
; IMMEDIATE SOURCE:
; CLONE: RAP-1 cDNA
US-08-817-436A-1

Query Match      13.0%; Score 29.8; DB 2; Length 3509;
Best Local Similarity 51.9%; Pred. No. 2.3; 62; Indels 0; Gaps 0;
Matches 67; Conservative 0; Mismatches 62; Indels 0; Gaps 0;
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GenCore version 5.1.5
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OM nucleic - nucleic search, using sw model

Run on: May 1, 2003, 02:55:40 ; Search time 157.34 Seconds

(without alignments)

3277.661 Million cell updates/sec

Title: US-09-092-296-2

Perfect score: 229

Sequence: 1 ACCGGGACTTCAGTCTCC.....CCATCTCCTTCAGGACCA 229

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Searched: 2185239 seqs, 1125999159 residues

Total number of hits satisfying chosen parameters: 4370478

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

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- 7: /SID52/gcgdata/geneseq/geneseq-emb1/NA1986.DAT.*
- 8: /SID52/gcgdata/geneseq/geneseq-emb1/NA1987.DAT.*
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- 12: /SID52/gcgdata/geneseq/geneseq-emb1/NA1991.DAT.*
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- 21: /SID52/gcgdata/geneseq/geneseq-emb1/NA2000.DAT.*
- 22: /SID52/gcgdata/geneseq/geneseq-emb1/NA2001A.DAT.*
- 23: /SID52/gcgdata/geneseq/geneseq-emb1/NA2001B.DAT.*
- 24: /SID52/gcgdata/geneseq/geneseq-emb1/NA2002.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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3	218	95.2	422	22	AAZ65087
4	218	95.2	422	22	AAZ65087
5	218	95.2	422	22	AAZ65087
6	218	95.2	422	22	AAZ65087
7	114	49.8	624	20	AAZ65087
8	109.8	47.9	729	23	AAZ65087
9	34.4	15.0	2923	20	AAZ65087

10	34.4	15.0	3417	22	AAK94567	Human full-length
11	34	14.8	27082	22	AAK70447	Human immune/haema
12	32.8	14.3	361	21	AAC30979	Human secreted pro
13	32.4	14.1	6855	24	ABN83971	Human gene sequenc
14	32	14.0	1128	19	AAV28846	Mouse coxsackievir
15	31.8	13.9	1251	24	ABK09969	Eastern cottonmout
16	31.6	13.8	11749	22	AAK36066	Human musculoskele
17	31.6	13.8	11749	22	AAK36066	Human musculoskele
18	31.6	13.8	11749	22	AAK36066	Human musculoskele
19	31.6	13.8	11749	22	AAK36066	Human musculoskele
20	31.6	13.8	11749	22	AAK36066	Human musculoskele
21	31.6	13.8	11749	22	AAK36066	Human musculoskele
22	31.6	13.8	11749	22	AAK36066	Human musculoskele
23	31.6	13.8	11749	22	AAK36066	Human musculoskele
24	31.6	13.8	11749	22	AAK36066	Human musculoskele
25	31.2	13.6	6096	23	ABL09866	Drosophila melanog
26	31.2	13.6	16596	22	AAK93767	Human immune/haema
27	31	13.5	1243	22	AAK93767	Human immune/haema
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30	30.6	13.4	377	22	AAH42526	Nucleotide sequenc
31	30.6	13.4	377	22	AAH42526	Human digestive sy
32	30.6	13.4	705	22	AAH03213	Human digestive sy
33	30.6	13.4	2135	22	AAH13650	Human cDNA clone (
34	30.4	13.3	580	16	AAK02964	Human cDNA sequenc
35	30.4	13.3	580	20	AAK02964	Cell-cycle regulat
36	30.4	13.3	580	24	AAK13099	Mouse ink-4 protei
37	30.4	13.3	580	24	AAK13099	Murine cell cycle
38	30.4	13.3	1301	19	AAV50430	Mouse cDNA encodin
39	30.4	13.3	1318	21	AAK04640	Mouse coxsackievir
40	30.4	13.3	2387	21	AAK04640	Arabidopsis thalia
41	30.4	13.3	3036	23	AAK04640	Human membrane-ass
42	30.4	13.3	3334	23	AAK04640	DNA encoding novel
43	30.4	13.3	3874	23	AAK04640	DNA encoding novel
44	30.4	13.3	3875	23	AAK04640	DNA encoding novel
45	30	13.1	4013	24	AAK04640	Human ORFX ORF695
			180	24	ABL99631	Toxicologically re

ALIGNMENTS

RESULT 1

AAZ65087
ID AAZ65087 standard; cDNA; 422 BP.

AC AAZ65087;

DT 05-APR-2000 (first entry)

DE Membrane-bound protein PRO1098 encoding cDNA.

DE Membrane-bound polypeptide; PRO polypeptide; LDL receptor; TIE ligand;
pharmaceutical; receptor immunoadhesin; gene mapping; ss.

OS Homo sapiens.

PN WO963088-A2.

PD 09-DEC-1999.

PF 02-JUN-1999; 99WO-US12252.

PR 02-JUN-1998; 98US-0087607.

PR 02-JUN-1998; 98US-0087609.

PR 02-JUN-1998; 98US-0087759.

PR 03-JUN-1998; 98US-0087827.

PR 04-JUN-1998; 98US-0088021.

PR 04-JUN-1998; 98US-0088025.

PR 04-JUN-1998; 98US-0088028.

PR 04-JUN-1998; 98US-0088029.

PR 04-JUN-1998; 98US-0088030.

PR 04-JUN-1998; 98US-0088033.

PR 04-JUN-1998; 98US-0088326.

PR 05-JUN-1998; 98US-0088167.
PR 05-JUN-1998; 98US-0088202.
PR 05-JUN-1998; 98US-0088212.
PR 05-JUN-1998; 98US-0088217.
PR 05-JUN-1998; 98US-0088217.
PR 09-JUN-1998; 98US-0088655.
PR 10-JUN-1998; 98US-0088722.
PR 10-JUN-1998; 98US-0088730.
PR 10-JUN-1998; 98US-0088734.
PR 10-JUN-1998; 98US-0088738.
PR 10-JUN-1998; 98US-0088740.
PR 10-JUN-1998; 98US-0088741.
PR 10-JUN-1998; 98US-0088742.
PR 10-JUN-1998; 98US-0088810.
PR 10-JUN-1998; 98US-0088811.
PR 10-JUN-1998; 98US-0088824.
PR 10-JUN-1998; 98US-0088825.
PR 10-JUN-1998; 98US-0088826.
PR 11-JUN-1998; 98US-0088858.
PR 11-JUN-1998; 98US-0088861.
PR 11-JUN-1998; 98US-0088863.
PR 11-JUN-1998; 98US-0088876.
PR 12-JUN-1998; 98US-0089090.
PR 12-JUN-1998; 98US-0089105.
PR 16-JUN-1998; 98US-0089440.
PR 16-JUN-1998; 98US-0089512.
PR 16-JUN-1998; 98US-0089514.
PR 17-JUN-1998; 98US-0089532.
PR 17-JUN-1998; 98US-0089538.
PR 17-JUN-1998; 98US-0089598.
PR 17-JUN-1998; 98US-0089599.
PR 17-JUN-1998; 98US-0089600.
PR 17-JUN-1998; 98US-0089653.
PR 18-JUN-1998; 98US-0089801.
PR 18-JUN-1998; 98US-0089807.
PR 18-JUN-1998; 98US-0089908.
PR 19-JUN-1998; 98US-0089947.
PR 19-JUN-1998; 98US-0089948.
PR 19-JUN-1998; 98US-0089952.
PR 22-JUN-1998; 98US-0090246.
PR 22-JUN-1998; 98US-0090252.
PR 22-JUN-1998; 98US-0090254.
PR 23-JUN-1998; 98US-0090349.
PR 23-JUN-1998; 98US-0090355.
PR 24-JUN-1998; 98US-0090429.
PR 24-JUN-1998; 98US-0090431.
PR 24-JUN-1998; 98US-0090435.
PR 24-JUN-1998; 98US-0090444.
PR 24-JUN-1998; 98US-0090445.
PR 24-JUN-1998; 98US-0090461.
PR 24-JUN-1998; 98US-0090472.
PR 24-JUN-1998; 98US-0090535.
PR 24-JUN-1998; 98US-0090538.
PR 24-JUN-1998; 98US-0090540.
PR 24-JUN-1998; 98US-0090557.
PR 25-JUN-1998; 98US-0090676.
PR 25-JUN-1998; 98US-0090678.
PR 25-JUN-1998; 98US-0090688.
PR 25-JUN-1998; 98US-0090690.
PR 25-JUN-1998; 98US-0090691.
PR 25-JUN-1998; 98US-0090694.
PR 25-JUN-1998; 98US-0090695.
PR 25-JUN-1998; 98US-0090696.
PR 26-JUN-1998; 98US-0090862.
PR 26-JUN-1998; 98US-0090863.
PR 01-JUL-1998; 98US-0091358.
PR 01-JUL-1998; 98US-0091360.
PR 01-JUL-1998; 98US-0091544.
PR 02-JUL-1998; 98US-0091478.
PR 02-JUL-1998; 98US-0091486.
PR 02-JUL-1998; 98US-0091519.
PR 02-JUL-1998; 98US-0091626.
PR 02-JUL-1998; 98US-0091628.
PR 02-JUL-1998; 98US-0091633.
PR 02-JUL-1998; 98US-0091633.
PR 02-JUL-1998; 98US-0091646.
PR 02-JUL-1998; 98US-0091673.
PR 07-JUL-1998; 98US-0091978.
PR 07-JUL-1998; 98US-0091982.
PR 09-JUL-1998; 98US-0092182.
PR 10-JUL-1998; 98US-0092472.
PR 20-JUL-1998; 98US-0093339.
PR 30-JUL-1998; 98US-0094651.
PR 04-AUG-1998; 98US-0095282.
PR 04-AUG-1998; 98US-0095285.
PR 04-AUG-1998; 98US-0095301.
PR 04-AUG-1998; 98US-0095302.
PR 04-AUG-1998; 98US-0095318.
PR 04-AUG-1998; 98US-0095321.
PR 04-AUG-1998; 98US-0095325.
PR 10-AUG-1998; 98US-0095916.
PR 10-AUG-1998; 98US-0095929.
PR 10-AUG-1998; 98US-0096012.
PR 11-AUG-1998; 98US-0096143.
PR 11-AUG-1998; 98US-0096146.
PR 12-AUG-1998; 98US-0096329.
PR 17-AUG-1998; 98US-0096757.
PR 17-AUG-1998; 98US-0096766.
PR 17-AUG-1998; 98US-0096768.
PR 17-AUG-1998; 98US-0096773.
PR 17-AUG-1998; 98US-0096791.
PR 17-AUG-1998; 98US-0096867.
PR 17-AUG-1998; 98US-0096891.
PR 17-AUG-1998; 98US-0096894.
PR 17-AUG-1998; 98US-0096895.
PR 17-AUG-1998; 98US-0096897.
PR 18-AUG-1998; 98US-0096949.
PR 18-AUG-1998; 98US-0096950.
PR 18-AUG-1998; 98US-0096959.
PR 18-AUG-1998; 98US-0096960.
PR 18-AUG-1998; 98US-0097022.
PR 19-AUG-1998; 98US-0097141.
PR 20-AUG-1998; 98US-0097218.
PR 24-AUG-1998; 98US-0097661.
PR 26-AUG-1998; 98US-0097951.
PR 26-AUG-1998; 98US-0097952.
PR 26-AUG-1998; 98US-0097954.
PR 26-AUG-1998; 98US-0097955.
PR 26-AUG-1998; 98US-0097971.
PR 26-AUG-1998; 98US-0097974.
PR 26-AUG-1998; 98US-0097978.
PR 26-AUG-1998; 98US-0097979.
PR 26-AUG-1998; 98US-0097986.
PR 26-AUG-1998; 98US-0098014.
PR 31-AUG-1998; 98US-0098325.
PR 16-SEP-1998; 98US-0100634.
PR 12-JAN-1999; 99US-0115565.
XX
XX (GETH) GENENTECH INC.
XX Baker K, Chen J, Goddard A, Gurney AL, Smith V, Watanabe CK;
PI Wood WI, Yuan J;
XX WPI; 2000-072883/06.
DR P-PSDB; AAY66741.
XX
XX Membrane-bound proteins and related nucleotide sequences -
XX Claim 2; Fig 257; 822pp; English.
XX The invention provides membrane-bound PRO polypeptides and
CC polynucleotides encoding them. The PRO sequences of the invention were
CC identified based on extracellular domain homology screening. The PRO
CC sequences have homology with proteins including LDL receptors, TIE
CC ligands and various enzymes. The membrane-bound proteins and receptor
CC molecules are useful as pharmaceutical and diagnostic agents. Receptor
CC immunoadhesins, for instance, can be used as therapeutic agents to block
CC receptor-ligand interactions. The membrane-bound proteins can also be

employed for screening of potential peptide or small molecule inhibitors of the relevant receptor/ligand interaction. The PRO encoding sequences are useful as hybridization probes, in chromosome and gene mapping and in the generation of antisense RNA and DNA. PRO nucleic acid sequences will also be useful for the preparation of PRO polypeptides, especially by recombinant techniques.

Sequence 422 BP; 84 A; 134 C; 104 G; 100 T; 0 other;

Query Match 95.2%; Score 218; DB 21; Length 422;
Best Local Similarity 99.6%; Pred. No. 2.1e-60;
Matches 229; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

Qy		1	ACCGGAGACTTCAGTCTCTCCTCCATCCCAAGAGAGCGCATGTGGCCATATATGGGGCTCTGGGCT	60
Dd		12	ACCGGAGACTTCAGTCTCTCCTCCATCCCAAGAGAGCGCATGTGGCCATATATGGGGCTCTGGGCT	71
Qy		61	GCCGCCTGTGCCCTCCTTTGACCCTCCTTGCGCAGCTCACATGGAACAGGCCGCGGTATGAC	120
Dd		72	GCCGCCTGTGCCCTCCTTTGACCCTCCTTGCGCAGCTCACATGGAACAGGCCGCGGTATGAC	131
Qy		121	TTTGCAACTGAAGCTGAAGGAGCTTTTTCTGACAAATTCCTCCTATGAGTCCAGCTTCCT	180
Dd		132	TTTGCAACTGAAGCTGAAGGAGCTTTTTCTGACAAATTCCTCCTATGAGTCCAGCTTCCT	191
Qy		181	GGAAATTGCTGAAAAG-TC TGGCCTCCTCCTCCAICTCCCTTCAGGGACCA	229
Dd		192	GGAAATTGCTGAAAAG-TC TGGCCTCCTCCTCCAICTCCCTTCAGGGACCA	241

RESULT 2

RESOL 2
AAS46045

AA040045
ID AAS46045 standard; cDNA: 422 BP.

AC AAS46045;

XX
DT 18-DEC-2001 (first entry)

Human DNA encoding PRO polypeptide sequence #121:

xx PRO polypeptide; mammal; tumour; cancer; human; prostate; sheep; ss:
 KW dog; cat; pig; goat; rabbit; tumour necrosis factor alpha; TNF-alpha;
 KW blood; chondrocyte cell; cell proliferation; cell differentiation; colon;
 KW adrenal; lung; breast; prostate; rectum; cervix; liver; genetic disorder;
 KW PCR primer.

XX
05 Homo sapiens

XX PN WQ200168848-A2

XX
PD 20-SEP-2001

XX
PF
28-FEB-2001: 2001WO-US06520.

XX	01 -MAR-2000;	2000OWO-US05601.
PR	02 -MAR-2000;	2000OWO-US05684.
PR	03 -MAR-2000;	2000US-1872020;
PR	06 -MAR-2000;	2000US-186968P;
PR	14 -MAR-2000;	2000US-1893200;
PR	14 -MAR-2000;	2000US-189328P;
PR	15 -MAR-2000;	2000OWO-US06884.
PR	21 -MAR-2000;	2000US-1908280;
PR	21 -MAR-2000;	2000US-191007P;
PR	21 -MAR-2000;	2000US-191048P;
PR	21 -MAR-2000;	2000US-191314P;
PR	28 -MAR-2000;	2000US-192655P;
PR	29 -MAR-2000;	2000US-193032P;
PR	29 -MAR-2000;	2000US-193053P;
PR	30 -MAR-2000;	2000OWO-US0843P;
PR	04 -APR-2000;	2000US-194445P;
PR	04 -APR-2000;	2000US-194647P;
PR	11 -APR-2000;	2000US-195975P;
PR	11 -APR-2000;	2000US-196000P;

[illegible]

AA
PA (GETH) GENENTECH INC.

AA Baker KP, Chen J, Desnoyers L, Goddard A, Godowski PJ, Gurney AL;
PI Pan J, Smith V, Watanabe CK, Wood WI, Zhang Z;
PI

XX
DR WPI: 2001-602746/68.

DR WPI; 2001-802748/
DR P-PSDB; AAU29144.

Novel nucleic acids encoding PRO polypeptides, used to diagnose the presence of tumours, such as prostate and breast tumours, in mammals and to screen for modulators of the compounds -

XX
PS
Claim 2: Fig 241: 774pp: English.

Sequences AAS45925-AAS46231 represent DNA molecules encoding and PCR primers for PRO polypeptides of the invention. The sequences of the invention can be used to detect the presence of a tumour in a mammal by comparing the level of expression of a PRO polypeptide in a test sample of cells from the animal and a control sample of normal cells, whereby a higher level of expression in the test sample indicates the presence of a tumour in the mammal. Mammals include dogs, cats, cattle, horses, sheep, pigs, goats and rabbits but are preferably human. The polypeptides can be used to stimulate tumour necrosis factor (TNF) alpha release from human blood, when contacted with it. A specific polypeptide can be used to stimulate the proliferation or differentiation of chondrocyte cells. The PRO proteins can be used to determine the presence of tumours and also susceptibility to tumour development, particularly adrenal, lung, colon, breast, prostate, rectal, cervical, or liver tumours, in mammalian subjects. The oligonucleotide probes specific for the PRO nucleic acids can be used for genetic analysis of individuals with genetic disorders.

Sequence 422 BP: 84 A: 134 C: 104 G: 100 T: 0 other: XX
SQ

Query Match	95.28;	Score 218;	DB 22;	Length 422;
Best Local Similarity	99.68;	Pred. No. 2.1e-60;		

QY	1	ACCGGGA	CTTCAGTGTCTCTCCATCCAGGAGCGCAGTGGCCACATATGGGCTCTGGGCT	60
Db	12	ACCGGGA	CTTCAGTGTCTCTCCATCCAGGAGCGCAGTGGCCACATATGGGCTCTGGGCT	71
QY	61	GCCTCTGTCTCTCTTGTAGCCCTCTTGGCAGCTCACATGGACACAGGCGGGGTATGAC		120
Db	72	GCCTCTGTCTCTCTTGTAGCCCTCTTGGCAGCTCACATGGACACAGGCGGGGTATGAC		131
QY	121	TTTGCAC	TCAAGCTGAAGGAGTCTTTTCTGTGACAAATTCCTCTCTATGAGTCCACAGCTTCCT	180
Db	132	TTTGCAC	TCAAGCTGAAGGAGTCTTTTCTGTGACAAATTCCTCTCTATGAGTCCACAGCTTCCT	191
QY	181	GGAAATG	CTTGAAG - TCTGCCTCTCTCCATCTCCTTCAGGACCA	229
Db	192	GGAAATG	CTTGAAGAGCTCTGCCTCTCTCCATCTCCTTCAGGACCA	241

RESULT 3

AAF92090
ID AAF92090 standard; cDNA; 422 BP.

XX AC AAF92090;

XX XX 15-MAY-2001 (first entry)

XX DE Human PRO1098 cDNA.

XX KW Human; PRO protein; mapping; ss.

XX OS Homo sapiens.

XX PN WO200116318-A2.

XX PD 08-MAR-2001.

XX PF 24-AUG-2000; 2000WO-US23328.

XX PR 01-SEP-1999; 99WO-US20111.

XX PR 15-SEP-1999; 99WO-US21090.

XX PR 07-DEC-1999; 99US-0169495.

XX PR 09-DEC-1999; 99US-0170262.

XX PR 11-JAN-2000; 2000US-0175481.

XX PR 18-FEB-2000; 2000WO-US04341.

XX PR 22-FEB-2000; 2000WO-US04414.

XX PR 01-MAR-2000; 2000WO-US05601.

XX PR 03-MAR-2000; 2000US-0187202.

XX PR 25-APR-2000; 2000US-0193997.

XX PR 22-MAY-2000; 2000WO-US14042.

XX PR 05-JUN-2000; 2000US-0209832.

XX PA (GETH) GENENTECH INC.

XX PI Eaton DL, Filvaroff E, Gerritsen ME, Goddard A, Godowski PJ;

XX PI Grimaldi CJ, Gurney AL, Watanabe CK, Wood WI;

XX XX WPI; 2001-183260/18.

XX DR P-PSDB; AAB87558.

XX PT Eighty four nucleic acids encoding PRO polypeptides, useful in

XX PT molecular biology, including use as hybridization probes, and in

XX PS chromosome and gene mapping.

XX PS Claim 2; Fig 65; 278pp; English.

XX CC The present sequence is the coding sequence for a human PRO polypeptide

XX CC (secreted and transmembrane). The PRO protein, and PRO agonists, PRO

XX CC antagonists or anti-PRO antibodies are useful for preparation of a

XX CC medicament useful in the treatment of a condition which is responsive to

XX CC the PRO protein, agonists, antagonists or anti-PRO antibodies. The PRO

XX CC protein may also be employed as molecular weight markers for protein

XX CC electrophoresis. The PRO coding sequence has applications in molecular

XX CC biology, including use as hybridisation probes, and in chromosome and

XX CC gene mapping.

XX SQ Sequence 422 BP; 84 A; 134 C; 104 G; 100 T; 0 other;

Query Match

Best Local Similarity 99.6%; Score 218; DB 22; Length 422;

Matches 229; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 1 ACCGGGACTTCAGTGTCTCTCCATCCAGGAGCGGAGTGGCCACTATGGGCTTGGGCT 60

Db |||||||

QY 12 ACCGGGACTTCAGTGTCTCTCCATCCAGGAGCGGAGTGGCCACTATGGGCTTGGGCT 71

Db |||||||

QY 61 GCCCGTGTCTCTCTTGGACCTCTTGGACCTCACATGGAACAGGCGCGGTATGAC 120

Db |||||||

QY 72 GCCCGTGTCTCTCTTGGACCTCTTGGACCTCACATGGAACAGGCGCGGTATGAC 131

Db |||||||

QY 121 TTTCGAAGCTGAAGCTGAAGGAGCTTTTCTGACAAATTCCTCTATGAGTCCAGCTTCT 180

Db |||||||

QY 132 TTTCGAAGCTGAAGCTGAAGGAGCTTTTCTGACAAATTCCTCTATGAGTCCAGCTTCT 191

Db |||||||

QY 181 GGAATTGCTTGAAGAAG-TCTGCCTCTCTCTCCATCTCCCTTCAGGACCA 229

Db |||||||

QY 192 GGAATTGCTTGAAGAAGCTCTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 241

Db |||||||

QY 192 GGAATTGCTTGAAGAAGCTCTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 241

Db |||||||

QY 192 GGAATTGCTTGAAGAAGCTCTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 241

Db |||||||

QY 192 GGAATTGCTTGAAGAAGCTCTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 241

Db |||||||

QY 192 GGAATTGCTTGAAGAAGCTCTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 241

Db |||||||

QY 192 GGAATTGCTTGAAGAAGCTCTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 241

Db |||||||

QY 192 GGAATTGCTTGAAGAAGCTCTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 241

Db |||||||

QY 192 GGAATTGCTTGAAGAAGCTCTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 241

Db |||||||

QY 192 GGAATTGCTTGAAGAAGCTCTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 241

Db |||||||

QY 192 GGAATTGCTTGAAGAAGCTCTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 241

Db |||||||

QY 192 GGAATTGCTTGAAGAAGCTCTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 241

Db |||||||

QY 192 GGAATTGCTTGAAGAAGCTCTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 241

Db |||||||

QY 192 GGAATTGCTTGAAGAAGCTCTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 241

Db |||||||

QY 192 GGAATTGCTTGAAGAAGCTCTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 241

Db |||||||

QY 192 GGAATTGCTTGAAGAAGCTCTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 241

Db |||||||

QY 192 GGAATTGCTTGAAGAAGCTCTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 241

Db |||||||

QY 192 GGAATTGCTTGAAGAAGCTCTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 241

Db |||||||

QY 192 GGAATTGCTTGAAGAAGCTCTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 241

Db |||||||


```

XX OS Homo sapiens.
XX FH
XX FT Location/Qualifiers
XX CDS 75..311
XX FT /tag=a
XX FT /note="cDNA comprising the coding region (minus
XX the stop codon) is claimed (Claim 3)"
XX PN WO9855508-A2.
XX XX
XX PD 10-DEC-1998.
XX PF
XX PP 03-JUN-1998; 98WO-JP02445.
XX PR 03-JUN-1997; 97JP-0144948.
XX XX
XX PA (PROT-) PROTEGENE INC.
XX PA (SAGA ) SAGAMI CHEM RES CENTRE.
XX PI
XX PI Kato S., Sekine S., Yamaguchi T;
XX DR WPI; 1999-045730/04.
XX DR P-FSDB: AAW88498.
XX XX
XX PT New human proteins containing transmembrane domains and their
XX encoding sequences - useful in the preparation of antibodies and
XX large-scale protein production, gene diagnosis, and gene therapy
XX PS
XX PS Claim 4; Page 135; 178pp; English.
XX CC
XX CC This is the nucleotide sequence of cDNA clone HPI0408, which
XX includes a coding region (also claimed) for a novel human
XX transmembrane protein (see AAW88498). The clone was isolated from a
XX stomach cancer cDNA library using a signal sequence detection
XX method, and by protein synthesis by in vitro translation. The
XX encoded protein has a putative signal sequence and a putative
XX internal transmembrane domain. The invention provides nucleotide
XX sequences (see AAW84359-76) coding for 18 transmembrane proteins
XX (see AAW88491-508), vectors containing such polynucleotides, and
XX eukaryotic cells containing the vectors. The proteins can be
XX used as antigens or as compositions in the preparation of
XX antibodies against the proteins. The polynucleotides can be used
XX as probes for gene diagnosis, and as gene sources for gene therapy
XX and large-scale production of proteins encoded by the cDNA. The
XX host cells are used for the detection of ligands corresponding to
XX the expressed proteins, and the screening of low mol.wt. medicines.
XX SQ Sequence 439 BP; 89 A; 137 C; 109 G; 104 T; 0 other;

Query Match 95.2%; Score 218; DB 20; Length 439;
Best Local Similarity 99.6%; Pred. No. 2.le-60;
Matches 229; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 1 ACCGGGACATTCAGTGTCTCTCCATCCAGAGGCGAGTGGCCACTATGGGGTCTGGGCT 60
Db 29 ACCGGGACATTCAGTGTCTCTCCATCCAGAGGCGAGTGGCCACTATGGGGTCTGGGCT 88
QY 61 GCCCCTGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 120
Db 89 GCCCCTGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 148
QY 121 TTTCGAAGTGAAGTGAAGGAGTCTTTTCTGACAAATTCCTATGAGTCCAGCTTCCT 180
Db 149 TTTCGAAGTGAAGTGAAGGAGTCTTTTCTGACAAATTCCTATGAGTCCAGCTTCCT 208
QY 181 GGAATTCCTGAAAG-TCTGCGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 229
Db 209 GGAATTCCTGAAAGTCTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 258

```

RESULT 7
ABK81818

```

ID ABK81818 standard; DNA; 624 BP.
XX AC
XX AC ABK81818;
XX DT 13-AUG-2002 (first entry)
XX DE
XX DE DNA representing lung specific gene #4.
XX KW Lung specific gene; gene therapy; vaccine; lung cancer;
XX KW cancer staging; cancer monitoring; cancer diagnosis;
XX KW imaging lung cancer; metastases; gene; ss.
XX OS Homo sapiens.
XX PN WO200218576-A2.
XX PD 07-MAR-2002.
XX PF 27-AUG-2001; 2001WO-US26684.
XX PR 28-AUG-2000; 2000US-228378P.
XX PA (DIAD-) DIADEXUS INC.
XX PI Chen S., Macina RA, Sun Y, Recipon H;
XX DR WPI; 2002-434904/46.
XX XX
XX PT New lung specific genes and their encoded proteins, useful in gene
XX therapy or as a vaccine for treating lung cancer, as well as for
XX PT measuring metastases of lung cancer, or staging, monitoring, diagnosing
XX PT or imaging lung cancer -
XX PS Claim 1; Page 161; 206pp; English.
XX CC The invention describes a new lung specific gene and it's variants. The
XX CC lung specific gene proteins and genes are useful in gene therapy or as a
XX CC vaccine for treating lung cancer. Lung specific genes are also useful for
XX CC staging, monitoring, diagnosing or imaging lung cancer, as well as for
XX CC measuring metastases of lung cancer. This sequence represents a lung
XX CC specific gene described in the invention.
XX SQ Sequence 624 BP; 129 A; 175 C; 182 G; 138 T; 0 other;

Query Match 49.8%; Score 114; DB 24; Length 624;
Best Local Similarity 99.2%; Pred. No. 9.2e-27;
Matches 125; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 105 CAGGGCCGGGTATGACTTTGCAACTGCAAGCTGAAGGAGTCTTTTCTGACAAATTCCTCT 164
Db 314 CAGGGCCGGGTATGACTTTGCAACTGCAAGCTGAAGGAGTCTTTTCTGACAAATTCCTCT 373
QY 165 ATGAGTCCAGCTTCTCGAATTGTTGAAAAG-TCTGCGCTCTCTCTCTCTCTCTCTCTCT 223
Db 374 ATGAGTCCAGCTTCTCGAATTGTTGAAAAGTCTGCGCTCTCTCTCTCTCTCTCTCTCT 433
QY 224 GGACCA 229
Db 434 GGACCA 439

RESULT 8
AAS65519
ID AAS65519 standard; cDNA; 729 BP.
XX AC
XX AC AAS65519;
XX DT 13-FEB-2002 (first entry)
XX DE
XX DE DNA encoding novel human diagnostic protein #1323.
XX KW Human; chromosome mapping; gene mapping; gene therapy; forensic;
XX KW food supplement; medical imaging; diagnostic; genetic disorder; ss.

```

XX Homo sapiens.
OS WO200175067-A2.
PW 11-OCT-2001.
XX 30-MAR-2001; 2001WO-US08631.
XX 31-MAR-2000; 2000US-0540217.
XX 23-AUG-2000; 2000US-0649167.
XX (HYSE-) HYSEQ INC.
XX Drmanac RT, Liu C, Tang YT;
XX WPI; 2001-639362/73.
XX P-PSDB; ABG01332.
XX New isolated polynucleotide and encoded polypeptides, useful in
PT diagnostics, gene mapping, identification of mutations
PT responsible for genetic disorders or other traits and to assess
PT biodiversity
XX Claim 1; SEQ ID NO 1323; 103pp; English.
XX The invention relates to isolated polynucleotide (I) and
CC polypeptide (II) sequences. (I) is useful as hybridisation probes,
CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome
CC and gene mapping, and in recombinant production of (II). The
CC polynucleotides are also used in diagnostics as expressed sequence tags
CC for identifying expressed genes. (I) is useful in gene therapy techniques
CC to restore normal activity of (II) or to treat disease states involving
CC (II). (II) is useful for generating antibodies against it, detecting or
CC quantitating a polypeptide in tissue, as molecular weight markers and as
CC a food supplement. (II) and its binding partners are useful in medical
CC imaging of sites expressing (II). (I) and (II) are useful for treating
CC disorders involving aberrant protein expression or biological activity.
CC The polypeptide and polynucleotide sequences have applications in
CC diagnostics, forensics, gene mapping, identification of mutations
CC responsible for genetic disorders or other traits to assess biodiversity
CC and to produce other types of data and products dependent on DNA and
CC amino acid sequences. AA56197-AA594564 represent novel human
CC diagnostic coding sequences of the invention.
CC Note: the sequence data for this patent did not appear in the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences.
XX
XX Sequence 729 BP; 187 A; 169 C; 152 G; 146 T; 75 other;
SQ
Query Match 47.9%; Score 109.8; DB 23; Length 729;
Best Local Similarity 98.2%; Pred. No. 2.2e-25;
Matches 111; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Oy 30 GGAGCGCAGTGGCCACTATGGGTCTGGCTGCCCTTCTCTCTGTGACCTCTTTG 89
Dy 8 GGAGCGCAGAGCCACTATGGGTCTGGCTGCCCTTCTCTCTGTGACCTCTTTG 67
Oy 90 GCAGCTCACATGGACAGCGCGGTATGACTTTGCACTGAAGCTGAAGGAG 142
Dy 68 GCAGCTCACATGGACAGCGCGGTATGACTTTGCACTGAAGCTGAAGGAG 120
RESULT 9
AA04326
ID AA04326 standard; DNA; 2923 BP.
XX
XX AA04326;
AC
XX 13-APR-1999 (first entry)
DT
XX Human secreted protein gene 16 clone HSHBQ68.
XX

KW Human; secreted protein; fusion protein; gene therapy; protein therapy;
KW diagnosis; tissue; cancer; tumour; neurodegenerative disorder; leukaemia;
KW developmental abnormality; foetal deficiency; blood; allergy; renal; ds;
KW immune system; schuma; lymphocytic disease; brain; hepatic; lymphoma;
KW inflammation; ischaemic shock; Alzheimer's disease; restenosis; AIDS;
KW cognitive disorder; schizophrenia; prostate; obesity; osteoclast; thymus;
KW osteoporosis; arthritis; testis; lung; thyroiditis; thyroid; digestion;
KW endocrine; metabolism; regulation; malabsorption; gastritis; neoplasm.
XX
OS Homo sapiens.
XX WO9856804-A1.
XX 17-DEC-1998.
XX 11-JUN-1998; 98WO-US12125.
XX 02-OCT-1997; 97US-0061060.
XX 13-JUN-1997; 97US-0049547.
XX 13-JUN-1997; 97US-0049548.
XX 13-JUN-1997; 97US-0049549.
XX 13-JUN-1997; 97US-0049550.
XX 13-JUN-1997; 97US-0049606.
XX 13-JUN-1997; 97US-0049607.
XX 13-JUN-1997; 97US-0049608.
XX 13-JUN-1997; 97US-0049609.
XX 13-JUN-1997; 97US-0049610.
XX 13-JUN-1997; 97US-0049611.
XX 13-JUN-1997; 97US-0050566.
XX 13-JUN-1997; 97US-0050901.
XX 13-JUN-1997; 97US-0052989.
XX 08-JUL-1997; 97US-0051919.
XX 18-AUG-1997; 97US-0055984.
XX 12-SEP-1997; 97US-0058665.
XX 12-SEP-1997; 97US-0058668.
XX 12-SEP-1997; 97US-0058669.
XX 12-SEP-1997; 97US-0058750.
XX 12-SEP-1997; 97US-0058971.
XX 12-SEP-1997; 97US-0058972.
XX 12-SEP-1997; 97US-0058975.
XX 02-OCT-1997; 97US-0060834.
XX 02-OCT-1997; 97US-0060841.
XX 02-OCT-1997; 97US-0060844.
XX 02-OCT-1997; 97US-0060865.
XX 02-OCT-1997; 97US-0061059.
XX (HUMA-) HUMAN GENOME SCI INC.
XX Brever LA, Ebner R, Ferrie AM, Feng P, Greene JM, Lafleur DW;
PI Moore PA, N1 J, Olsen HS, Rosen CA, Ruben SM, Shi Y, Young P;
PI Yu GL;
XX WPI; 1999-080881/07.
XX P-PSDB; AAW78141.
XX New isolated human genes and the secreted polypeptides they encode -
XX useful for diagnosis and treatment of e.g. cancers, neurological
XX disorders, immune diseases, inflammation or blood disorders
XX
XX Claim 1; Page 180-182; 380pp; English.
XX This sequence represents a nucleic acid molecule which encodes a
XX secreted human protein. The gene number, and the clone it is derived
XX from, are detailed in the descriptor line. The gene can be used to
XX generate fusion proteins by linking to the gene to a human immunoglobulin
XX Fc portion (e.g. AAX04302) for increasing the stability of the fused
XX protein as compared to the human protein only.
XX The invention relates to 86 novel genes and their fragments (nucleic
XX acid sequences: AAX04311-x04410; amino acid sequences AAW78126-w78225)
XX which are useful for preventing, treating or ameliorating medical
XX conditions e.g. by protein or gene therapy. Also, pathological
XX conditions can be diagnosed by determining the amount of the new
XX polypeptides in a sample or by determining the presence of mutations in

PR	05-SEP-2000;	2000US-0229513	PR
PR	06-SEP-2000;	2000US-0230437	PR
PR	06-SEP-2000;	2000US-0230438	PR
PR	08-SEP-2000;	2000US-0231242	PR
PR	08-SEP-2000;	2000US-0231243	PR
PR	08-SEP-2000;	2000US-0231244	PR
PR	08-SEP-2000;	2000US-0231341	PR
PR	08-SEP-2000;	2000US-0231414	PR
PR	08-SEP-2000;	2000US-0232080	PR
PR	08-SEP-2000;	2000US-0232081	PR
PR	12-SEP-2000;	2000US-0231968	PR
PR	14-SEP-2000;	2000US-0232397	PR
PR	14-SEP-2000;	2000US-0232398	PR
PR	14-SEP-2000;	2000US-0232399	PR
PR	14-SEP-2000;	2000US-0232400	PR
PR	14-SEP-2000;	2000US-0232401	PR
PR	14-SEP-2000;	2000US-0232403	PR
PR	14-SEP-2000;	2000US-0232406	PR
PR	14-SEP-2000;	2000US-0232406	PR
PR	14-SEP-2000;	2000US-0232406	PR
PR	21-SEP-2000;	2000US-0232423	PR
PR	21-SEP-2000;	2000US-0234274	PR
PR	25-SEP-2000;	2000US-0234997	PR
PR	25-SEP-2000;	2000US-0234998	PR
PR	25-SEP-2000;	2000US-0234998	PR
PR	26-SEP-2000;	2000US-0235484	PR
PR	27-SEP-2000;	2000US-0235834	PR
PR	27-SEP-2000;	2000US-0235836	PR
PR	29-SEP-2000;	2000US-0236327	PR
PR	29-SEP-2000;	2000US-0236327	PR
PR	29-SEP-2000;	2000US-0236368	PR
PR	29-SEP-2000;	2000US-0236369	PR
PR	29-SEP-2000;	2000US-0236370	PR
PR	02-OCT-2000;	2000US-0236802	PR
PR	02-OCT-2000;	2000US-0237037	PR
PR	02-OCT-2000;	2000US-0237039	PR
PR	02-OCT-2000;	2000US-0237039	PR
PR	02-OCT-2000;	2000US-0237040	PR
PR	13-OCT-2000;	2000US-0239935	PR
PR	13-OCT-2000;	2000US-0239937	PR
PR	20-OCT-2000;	2000US-0240960	PR
PR	20-OCT-2000;	2000US-0241221	PR
PR	20-OCT-2000;	2000US-0241785	PR
PR	20-OCT-2000;	2000US-0241786	PR
PR	20-OCT-2000;	2000US-0241787	PR
PR	20-OCT-2000;	2000US-0241808	PR
PR	20-OCT-2000;	2000US-0241809	PR
PR	20-OCT-2000;	2000US-0241826	PR
PR	01-NOV-2000;	2000US-0246171	PR
PR	08-NOV-2000;	2000US-0246474	PR
PR	08-NOV-2000;	2000US-0246475	PR
PR	08-NOV-2000;	2000US-0246476	PR
PR	08-NOV-2000;	2000US-0246477	PR
PR	08-NOV-2000;	2000US-0246478	PR
PR	08-NOV-2000;	2000US-0246523	PR
PR	08-NOV-2000;	2000US-0246524	PR
PR	08-NOV-2000;	2000US-0246525	PR
PR	08-NOV-2000;	2000US-0246526	PR
PR	08-NOV-2000;	2000US-0246527	PR
PR	08-NOV-2000;	2000US-0246528	PR
PR	08-NOV-2000;	2000US-0246532	PR
PR	08-NOV-2000;	2000US-0246609	PR
PR	08-NOV-2000;	2000US-0246610	PR
PR	08-NOV-2000;	2000US-0246613	PR
PR	17-NOV-2000;	2000US-0249207	PR
PR	17-NOV-2000;	2000US-0249208	PR
PR	17-NOV-2000;	2000US-0249209	PR
PR	17-NOV-2000;	2000US-0249210	PR
PR	17-NOV-2000;	2000US-0249211	PR
PR	17-NOV-2000;	2000US-0249212	PR
PR	17-NOV-2000;	2000US-0249213	PR
PR	17-NOV-2000;	2000US-0249214	PR
PR	17-NOV-2000;	2000US-0249215	PR
PR	17-NOV-2000;	2000US-0249216	PR

PR	17-NOV-2000;	2000US-0249217.
PR	17-NOV-2000;	2000US-0249218.
PR	17-NOV-2000;	2000US-0249219.
PR	17-NOV-2000;	2000US-0249224.
PR	17-NOV-2000;	2000US-0249225.
PR	17-NOV-2000;	2000US-0249264.
PR	17-NOV-2000;	2000US-0249265.
PR	17-NOV-2000;	2000US-0249297.
PR	17-NOV-2000;	2000US-0249299.
PR	17-NOV-2000;	2000US-0249300.
PR	01-DEC-2000;	2000US-0250160.
PR	01-DEC-2000;	2000US-0250391.
PR	05-DEC-2000;	2000US-0251030.
PR	05-DEC-2000;	2000US-0251988.
PR	05-DEC-2000;	2000US-0256719.
PR	06-DEC-2000;	2000US-0251479.
PR	08-DEC-2000;	2000US-0251856.
PR	08-DEC-2000;	2000US-0251868.
PR	08-DEC-2000;	2000US-0251869.
PR	08-DEC-2000;	2000US-0251989.
PR	11-DEC-2000;	2000US-0251990.
PR	11-DEC-2000;	2000US-0254097.
PR	05-JAN-2001;	2001US-0259678.
XX	(HUMA-)	HUMAN GENOME SCI INC.
XX	Rosen CA,	Barash SC, Ruben SM;
XX	WPI;	2001-483426/52.
XX	Nucleic acids encoding human immune/hematopoietic antigen polypeptides,	
PT	useful for preventing, diagnosing and/or treating cancers and	
PT	metastasis -	
PS	Disclosure; SEQ ID NO 25259; 3071pp + Sequence Listing; English.	
XX	AAK54951 to AAK64702 encode the human Immune/haematopoietic antigen (I)	
CC	amino acid sequences given in AAM2170 to AAM91921. (I) have cytostatic	
CC	activity, and can be used in gene therapy and vaccine production. (I)	
CC	proteins and polynucleotides may be used in the prevention, diagnosis and	
CC	treatment of diseases associated with inappropriate (I) expression. For	
CC	example, they may be used to treat disorders associated with decreased	
CC	expression by rectifying mutations or deletions in a patient's genome	
CC	that affect the activity of (I) by expressing inactive proteins or to	
CC	supplement the patients own production of (I). Additionally, (I)	
CC	polynucleotides may be used to produce the secreted (I), by inserting	
CC	the nucleic acids into a host cell and culturing the cell to express the	
CC	protein. (I) proteins and polynucleotides may be used to prevent,	
CC	diagnose and treat Immune/haematopoietic-related diseases, especially	
CC	cancers and cancer metastases of haematopoietic-derived cells. AAK64703	
CC	to AAK87694 represent human immune/haematopoietic antigen genomic	
CC	sequences from the present invention. AAK54942 to AAK54950 and AAM82169	
CC	represent sequences used in the exemplification of the present invention.	
XX	Sequence 27082 BP; 5963 A; 7786 C; 7711 G; 5622 T; 0 other;	
SQ	Query Match	14.8%; Score 34; DB 22; Length 27082;
	Best Local Similarity	54.9%; Pred. No. 2.7;
	Matches	67; Conservative
	0; Mismatches	55; Indels
	0; Gaps	0
Qy	15	GTCCTCTCATCCAGGACGCAGTGGCCACTATGTGGGTCTCGGCCCTTGCTCCTCC 74
Db	13016	GCGTACTCTTAGGATAAGCCCGCGTCCCPCATCCCTGGCCAGTGCTCCGTGACCCCA 13075
Qy	75	TCTTGACCCTCTTGGCAGCTCATGTGAACAGGCGCGGTATGACTTTGCACTGACG 134
Db	13076	TCTACTCTTCTTGGGGACTTCTCAGCCACGAGGCTGGGCCCTTGACATTCACTGACG 13135
Qy	135	TG 136
Db	13136	TG 13137

KW pancreatic infection; acute pancreatitis; gastrointestinal tract;
KW diabetes mellitus; ss.
XX
OS Mus sp.
XX
FH Key Location/Qualifiers
KW CDS 1..1128
FT /tag= a
FT /product= "coxsackievirus and adenovirus receptor"
FT /transl_except= (pos:1096..1098,aa:Xaa)
FT /note= "Xaa= a stop codon, the sequence is shown as
FT continuing but gets unclear"
XX
XX WO9811221-A2.
XX
XX 19-MAR-1998.
XX
XX 12-SEP-1997; 97WO-US16189.
XX
XX 13-SEP-1996; 96US-0026100.
XX
XX (DAND) DANA FARMER CANCER INST INC.
XX
XX Bergelson JM, Finberg RW, Horowitz MS;
XX WPI; 1998-207384/18.
XX P-PSDB; AAW57213.
XX
XX DNA encoding coxsackie virus and adenovirus receptor - useful for
XX modulation of e.g. cardiac, pancreatic or gastrointestinal infection
XX
XX Disclosure; Fig 14; 104pp; English.
XX
XX The present sequence encodes mouse coxsackievirus and adenovirus
XX receptor (CAR). The present invention also describes: (1) a method for
XX modulating CAR expression comprising contacting the cell with an agent
XX which modulates CAR protein activity or CAR nucleic acid expression,
XX such that a cell associated activity is altered relative to a cell
XX associated activity of the cell in the absence of the agent; and (2) a
XX method for detecting the presence of CAR in a biological sample
XX comprising contacting a biological sample with an agent capable of
XX detecting CAR protein or mRNA such that the presence of CAR is detected.
XX Modulation of CAR is useful for treatment of cardiac infection, e.g.
XX myocarditis, pericarditis or dilated cardiomyopathy, or infection of the
XX central nervous system, e.g. a non-specific febrile illness or
XX meningoencephalitis, or pancreatic infection, e.g. acute pancreatitis,
XX or infection of the respiratory or gastrointestinal tract or childhood
XX onset diabetes mellitus. Probes derived from CAR nucleic acids are
XX useful for hybridisation assays, and antibodies raised against CAR
XX protein are useful for blocking CAR expression. Cell-free assays which
XX include combining CAR protein and a candidate/test compound are useful
XX in screening for drugs which interact with CAR protein.
XX
SQ Sequence 1128 BP; 297 A; 286 C; 288 G; 257 T; 0 other;

Query Match 14.0%; Score 32; DB 19; Length 1128;
Best Local Similarity 62.5%; Pred. No. 3.4;
Matches 50; Conservative 0; Mismatches 30; Indels 0; Gaps 0;

QY 29 AGGAGCGCAGTGGCGACTGTGGGTGGCGCTGCTCTCTTGACCCCTCCTT 88
Db 712 ACGATCGGCGCGCGCTACAGGACGCTGCTGCGCCCTGTCTCTCTGCGGCGCCATCCTC 771

QY 89 GGCAGCTCACATGAGCAAGG 108
Db 772 TTCTGCTGTACAGGAAGG 791

RESULT 15
ABK09969
ID ABK09969 standard; cDNA; 1251 BP.
XX
AC ABK09969;

XX 21-MAY-2002 (first entry)
XX Eastern cottonmouth snake zsnk1 gene sequence.
XX
XX Eastern cottonmouth snake; zsnk1; gene; snake venom; blood pressure;
KW vascular permeability; heparin binding; cell proliferation; mitogenesis;
KW hypotensive; cytostatic; antirheumatic; antiarthritic; antidiabetic;
KW vasotropic; antiarteriosclerotic; vulnerary; antitumor; hepatotropic;
KW antiinflammatory; vaccine; gene therapy; angiogenesis regulator;
KW neurite outgrowth; organ development; organ regeneration; cancer; ss.
XX
XX Agkistrodon piscivorus piscivorus.
XX
XX Key Location/Qualifiers
FH CDS 201..638
FT /tag= a
FT /product= "Eastern cottonmouth snake zsnk1 protein"
FT misc_feature 201..435
FT /tag= b
FT /note= "Used to make snake venom polypeptide.
FT Specifically claimed in claim 2d"
FT
FT sig_peptide 201..263
FT /tag= c
FT sig_peptide 201..254
FT /tag= d
FT /note= "Alternative signal peptide #1"
FT sig_peptide 201..248
FT /tag= e
FT /note= "Alternative signal peptide #2"
FT misc_feature 249..435
FT /tag= f
FT /note= "Used to make snake venom polypeptide.
FT Specifically claimed in claim 2c"
FT
FT mat_peptide 249..635
FT /tag= g
FT /note= "Alternative mature peptide #2"
FT mat_peptide 255..635
FT /tag= h
FT /note= "Alternative mature peptide #1"
FT misc_feature 255..435
FT /tag= i
FT /note= "Used to make snake venom polypeptide.
FT Specifically claimed in claim 2b"
FT
FT mat_peptide 264..635
FT /tag= j
FT misc_feature 264..435
FT /tag= k
FT /note= "Used to make snake venom polypeptide.
FT Specifically claimed in claim 2a"
XX
XX WO200212334-A2.
XX
XX 14-FEB-2002.
XX
XX 07-AUG-2001; 2001WO-US24999.
XX
XX 07-AUG-2000; 2000US-223164P.
XX
XX (ZYMO) ZYMOGENETICS INC.
XX Sheppard PO;
XX
XX WPI; 2002-217178/27.
XX P-PSDB; AAU76683.
XX
XX New snake venom zsnk1 polypeptide and polynucleotide, useful for
XX decreasing blood pressure, causing vascular permeability, binding
XX heparin and inducing proliferation or mitogenesis in cells
XX
XX Claim 2; Page 98-99; 103pp; English.
XX
XX The present invention relates to a new snake venom zsnk1 polypeptide
XX

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OM nucleic - nucleic search, using sw model

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Title: US-09-092-296-2
Perfect score: 229
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Total number of hits satisfying chosen parameters: 4109280

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Maximum Match 100%
Listing first 45 summaries

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10: gb_ro.*
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41: em_htgo_other.*

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score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query %	Match	Length	DB	ID	Description
1	218	95.2	422	6	AX092334	AX092334	Sequence
2	218	95.2	422	6	AX376174	AX376174	Sequence
3	218	95.2	422	6	AX03475	AX03475	Sequence
4	216.4	94.5	484	9	AX102070	AX102070	Homo sapi
5	114	49.8	624	6	AX472955	AX472955	Sequence
6	109.4	47.8	47323	9	AC005937	AC005937	Homo sapi
c 7	109.4	47.8	84474	9	AL662854	AL662854	Human DNA
8	109.4	47.8	104154	2	AL773541	AL773541	Homo sapi
c 9	109.4	47.8	156272	9	AL669830	AL669830	Human DNA
10	109.4	47.8	178688	2	AL713893	AL713893	Homo sapi
11	109.4	47.8	192650	9	AB023048	AB023048	Homo sapi
12	109.4	47.8	200000	9	AF000511	AF000511	Homo sapi
c 13	66	28.8	349980	6	AX344553	AX344553	Sequence
c 14	66	28.8	349980	6	AX344554	AX344554	Sequence
15	62.2	27.2	349980	6	AX344571	AX344571	Sequence
c 16	45.6	19.9	175345	2	AC022301	AC022301	Mus muscu
17	44.8	19.6	132977	2	RN510D20	AL603723	Rattus no
18	44.8	19.6	337832	2	AC099175	AC099175	Rattus no
c 19	38.2	16.7	130742	2	AF005653	AF005653	Oryza sat
c 20	37.8	16.5	185154	2	AC127110	AC127110	Rattus no
21	36	15.7	155406	2	AC105514	AC105514	Rattus no
22	35.8	15.6	196840	9	AC104435	AC104435	Homo sapi
c 23	35.8	15.6	203773	9	AC097369	AC097369	Homo sapi
24	35.4	15.5	146399	9	AC025835	AC025835	Homo sapi
c 25	34.8	15.2	176994	2	AC118783	AC118783	Rattus no
26	34.8	15.2	188082	2	AC121784	AC121784	Rattus no
27	34.8	15.2	197344	2	AC102613	AC102613	Mus muscu
28	34.8	15.2	243644	2	AC097608	AC097608	Rattus no
29	34.4	15.0	2032	9	AK025566	AK025566	Homo sapi
c 30	34.4	15.0	77322	9	HSDJ14C9	AL096774	Human DNA
31	34.4	15.0	141272	9	AP001976	AP001976	Homo sapi
c 32	34.4	15.0	154937	2	AP002382	AP002382	Homo sapi
c 33	34.4	15.0	183887	9	AC017033	AC017033	Homo sapi
c 34	34.4	15.0	187027	2	AC019078	AC019078	Homo sapi
c 35	34.4	15.0	202895	2	AC019134	AC019134	Homo sapi
c 36	34.4	15.0	333841	2	AL161641	AL161641	Homo sapi
37	34.2	14.9	188406	2	AC079560	AC079560	Mus muscu
c 38	34.2	14.9	203155	2	AC079473	AC079473	Mus muscu
39	34.2	14.9	292172	2	AC125207	AC125207	Mus muscu
40	34	14.8	1801	8	OSU25430	U25430	Oryza sativ
41	34	14.8	3753	8	AF245483	AF245483	Oryza sativ
42	34	14.8	36676	9	HSJ858B16	AL096768	Human DNA
43	34	14.8	77691	9	AC120118	AC120118	Homo sapi
44	34	14.8	100521	9	AC113397	AC113397	Homo sapi
45	34	14.8	149610	8	AF003244	AF003244	Oryza sat

ALIGNMENTS

RESULT 1
AX092334
LOCUS AX092334
DEFINITION Sequence 65 from Patent WO0116318.
ACCESSION AX092334
VERSION AX092334.1 GI:13444481
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 422)
AUTHORS Eaton,D.L., Filvaroff,E., Gerritsen,M.E., Goddard,A.,
Godowski,P.J., Grimaldi,C.J., Gurney,A.L., Watanabe,C.K. and
Wood,W.I.

AX092334 AX092334 422 bp DNA linear PAT 21-MAR-2001
Sequence 65 from Patent WO0116318.

TITLE Secrated and transmembrane polypeptides and nucleic acids encoding
the same
JOURNAL Patent: WO 0116318-A 65 08-MAR-2001;
Genentech, Inc. (US)
FEATURES Location/Qualifiers
source
1..422
/organism="Homo sapiens"
/db_xref="taxon:9606"
BASE COUNT 84 a 134 c 104 g 100 t
ORIGIN
Query Match 95.2%; Score 218; DB 6; Length 422;
Best Local Similarity 99.6%; Pred. No. 4.9e-58;
Matches 229; Conservative 0; Mismatches 0; Indels 1; Gaps 1;
QY 1 ACCGGGACITTCAGTGTCTCTCCATCCAGGAGCGCAGTGGCCACIATGGGGTCTGGGCT 60
Db 12 ACCGGGACITTCAGTGTCTCTCCATCCAGGAGCGCAGTGGCCACIATGGGGTCTGGGCT 71
QY 61 GCCCCTTGCTCCTCTTGACCCCTCTTGGAGCTCAGTGGACAGCGCGGGTATGAC 120
Db 72 GCCCCTTGCTCCTCTTGACCCCTCTTGGAGCTCAGTGGACAGCGCGGGTATGAC 131
QY 121 TTGCAACTGAAGCTGAAGGAGTCTTTCTGACAAATTCCTCTATGATCCAGCTTCCT 180
Db 132 TTGCAACTGAAGCTGAAGGAGTCTTTCTGACAAATTCCTCTATGATCCAGCTTCCT 191
QY 181 GGAATTGCTGAAAAG-TCTGCCTCTCTCCATCTCCCTTCAGGAGCA 229
Db 192 GGAATTGCTGAAAAGCTGTGCTCTCTCCATCTCCCTTCAGGAGCA 241
RESULT 2
AX376174 422 bp DNA linear PAT 01-MAR-2002
LOCUS AX376174
DEFINITION Sequence 241 from Patent WO0168848.
ACCESSION AX376174
VERSION AX376174.1 GI:19170479
KEYWORDS human.
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
1
AUTHORS Baker, K.P., Chen, J., Desnoyers, L., Goddard, A., Godowski, P.J.,
Gurney, A.L., Pan, J., Smith, V., Watanabe, C.K., Wood, W.I. and
Zhang, Z.
TITLE Secrated and transmembrane polypeptides and nucleic acids encoding
the same
JOURNAL Patent: WO 0168848-A 241 20-SEP-2001;
Genentech, Inc. (US)
FEATURES Location/Qualifiers
source
1..422
/organism="Homo sapiens"
/db_xref="taxon:9606"
BASE COUNT 84 a 134 c 104 g 100 t
ORIGIN
Query Match 95.2%; Score 218; DB 6; Length 422;
Best Local Similarity 99.6%; Pred. No. 4.9e-58;
Matches 229; Conservative 0; Mismatches 0; Indels 1; Gaps 1;
QY 1 ACCGGGACITTCAGTGTCTCTCCATCCAGGAGCGCAGTGGCCACIATGGGGTCTGGGCT 60
Db 12 ACCGGGACITTCAGTGTCTCTCCATCCAGGAGCGCAGTGGCCACIATGGGGTCTGGGCT 71
QY 61 GCCCCTTGCTCCTCTTGACCCCTCTTGGAGCTCAGTGGACAGCGCGGGTATGAC 120
Db 72 GCCCCTTGCTCCTCTTGACCCCTCTTGGAGCTCAGTGGACAGCGCGGGTATGAC 131
QY 121 TTGCAACTGAAGCTGAAGGAGTCTTTCTGACAAATTCCTCTATGATCCAGCTTCCT 180
Db 132 TTGCAACTGAAGCTGAAGGAGTCTTTCTGACAAATTCCTCTATGATCCAGCTTCCT 191

QY 181 GGAATTGCTGAAAAG-TCTGCCTCTCTCCATCTCCCTTCAGGAGCA 229
Db 192 GGAATTGCTGAAAAGCTGTGCTCTCTCCATCTCCCTTCAGGAGCA 241
RESULT 3
AX403475 422 bp DNA linear PAT 14-JUN-2002
LOCUS AX403475
DEFINITION Sequence 362 from Patent WO0073454.
ACCESSION AX403475
VERSION AX403475.1 GI:21436973
KEYWORDS human.
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
1
AUTHORS Ashkenazi, A.J., Baker, K.P., Botstein, D., Desnoyers, L., Eaton, D.,
Ferrara, N., Gerber, H., Griffioen, M., Goddard, A., Godowski, P.,
Grimaldi, C.J., Gurney, A.L., Kljavin, I., Napier, M.A., Pan, J.,
Paoni, N.F., Roy, M., Stewart, T.A., Tumas, D., Watanabe, C.K.,
Williams, P., Wood, W.I. and Zhang, Z.
TITLE Secrated and transmembrane polypeptides and nucleic acids encoding
the same
JOURNAL Patent: WO 0073454-A 362 07-DEC-2000;
Genentech Inc. (US)
FEATURES Location/Qualifiers
source
1..422
/organism="Homo sapiens"
/db_xref="taxon:9606"
BASE COUNT 84 a 134 c 104 g 100 t
ORIGIN
Query Match 95.2%; Score 218; DB 6; Length 422;
Best Local Similarity 99.6%; Pred. No. 4.9e-58;
Matches 229; Conservative 0; Mismatches 0; Indels 1; Gaps 1;
QY 1 ACCGGGACITTCAGTGTCTCTCCATCCAGGAGCGCAGTGGCCACIATGGGGTCTGGGCT 60
Db 12 ACCGGGACITTCAGTGTCTCTCCATCCAGGAGCGCAGTGGCCACIATGGGGTCTGGGCT 71
QY 61 GCCCCTTGCTCCTCTTGACCCCTCTTGGAGCTCAGTGGACAGCGCGGGTATGAC 120
Db 72 GCCCCTTGCTCCTCTTGACCCCTCTTGGAGCTCAGTGGACAGCGCGGGTATGAC 131
QY 121 TTGCAACTGAAGCTGAAGGAGTCTTTCTGACAAATTCCTCTATGATCCAGCTTCCT 180
Db 132 TTGCAACTGAAGCTGAAGGAGTCTTTCTGACAAATTCCTCTATGATCCAGCTTCCT 191
QY 181 GGAATTGCTGAAAAG-TCTGCCTCTCTCCATCTCCCTTCAGGAGCA 229
Db 192 GGAATTGCTGAAAAGCTGTGCTCTCTCCATCTCCCTTCAGGAGCA 241
RESULT 4
AY102070 484 bp mRNA linear PRI 18-JUN-2002
LOCUS AY102070
DEFINITION Homo sapiens surfactant associated protein G mRNA, partial
sequence.
ACCESSION AY102070
VERSION AY102070.1 GI:21464498
KEYWORDS human.
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
1 (bases 1 to 484)
AUTHORS Walker, M.G. and Spiro, P.
TITLE Genes co-expressed with pulmonary surfactants
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 484)
AUTHORS Walker, M.G. and Spiro, P.

TITLE Direct Submission
JOURNAL Submitted (07-MAY-2002) Incyte Genomics, 1475 Flamingo Way,
Sunnyvale, CA 94087-3405, USA

FEATURES

source
Location/Qualifiers
l..484
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="236582"
c1..>484
/gene="surfactant associated protein G"
/note="SFTPG"

BASE COUNT 124 a 149 c 110 g 101 t

ORIGIN

Query Match 94.5%; Score 216.4; DB 9; Length 484;

Best Local Similarity 99.1%; Pred. No. 1.6e-57;

Matches 228; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

QY 1 ACCGGACTTCAGTGTCTCTCCATCCAGGAGCGCAGTGGCCACTATGGGGTCTGGGCT 60

Db 9 ACCGGACTTCAGTGTCTCTCCATCCAGGAGCGCAGTGGCCACTATGGGGTCTGGGCT 68

QY 61 GCCCCTGTCTCTCTCTGACCTCTCTGGCAGCTCACATGGAACAGCGCGGTATGAC 120

Db 69 GCCCCTGTCTCTCTCTGACCTCTCTGGCAGCTCACATGGAACAGCGCGGTATGAC 128

QY 121 TTGCAACTGAAGCTGAAGAGCTTTCTGACAAATTCCTGATGATCCAGCTTCCT 180

Db 129 TTGCAACTGAAGCTGAAGAGCTTTCTGACAAATTCCTGATGATCCAGCTTCCT 188

QY 181 GGAATGCTTGAAGAAG-ICTGCTCTCTCTCCATCTCCCTTCAGGGACCA 229

Db 189 GGAATGCTTGAAGAAGCTCTGCTCTCTCCATCTCCCTTCAGGGACCA 238

RESULT 5

AX472955

LOCUS

AX472955

DEFINITION

Sequence 4 from Patent WO0218576.

AX472955

VERSION

AX472955.1 GI:22207742

KEYWORDS

human.

ORGANISM

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE

Chen, S.Y., Macina, R.A., Sun, Y. and Recipon, H.

Compositions and methods relating to lung specific genes

Patent: WO 0218576-A 4 07-MAR-2002;

Diadexus, Inc. (US)

FEATURES

Location/Qualifiers

l..624

/organism="Homo sapiens"

/db_xref="taxon:9606"

BASE COUNT 129 a 175 c 182 g 138 t

ORIGIN

Query Match 49.8%; Score 114; DB 6; Length 624;

Best Local Similarity 99.2%; Pred. No. 4.4e-25;

Matches 125; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 105 CAGGCGGGATGACATTCGACCTGAAGAGTCTTTCTGACAAATTCCTTCCT 164

Db 314 CAGGCGGGATGACATTCGACCTGAAGAGTCTTTCTGACAAATTCCTTCCT 373

QY 165 ATGAGTCCAGCTTCCTGGAATTCGTAAG-TCTGCTCTCTCTCCATCTCCCTTCAG 223

Db 374 ATGAGTCCAGCTTCCTGGAATTCGTAAGAGCTCTGCTCTCTCTCCATCTCCCTTCAG 433

QY 224 GGACCA 229

Db 434 GGACCA 439

RESULT 6

AC005937

LOCUS

AC005937

DEFINITION

Homo sapiens clone UWGC:370M23.002 from 6p21, complete sequence.

AC005937

ACCESSION

AC005937.1 GI:3845393

VERSION

HTG.

KEYWORDS

Homo sapiens.

SOURCE

Homo sapiens.

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE

1 (Bases 1 to 47323)

JANER, M., Guillaudoux, T., Vu, Q., Kutyavin, T., Harter, H. and

Geraghty, D.E.

Large scale sequence analysis of the human MHC class I region

Unpublished (1998)

Fred Hutchinson Cancer Research Center

The Clinical Research Division

1100 Fairview Ave. N., P.O. Box 19024

Seattle, WA 98109-1024

2 (Bases 1 to 47323)

Geraghty, D.E. and Olson, M.V.

Direct Submission

Submitted (05-NOV-1998) Human Genome Center, University of

Washington, Box 352145, Seattle, WA 98195, USA

University of Washington Human Genome Center

Box 352145 Seattle, WA 98195

Contact: Daniel E. Geraghty (geraghty@fhcrc.org)

Overlapping Sequences:

5': UWGC:370M23.013 (Genbank Accession: AC005530)

3': UWGC:y67c112 (Genbank Accession: AC004211)

Sequence Quality Assessment:

This entry has been annotated with sequence quality

estimates computed by the Phrap assembly program.

All manually edited bases have been reduced to quality zero.

Quality levels above 40 are expected to have less than

1 error in 10,000 bp.

Base-by-base quality values are not generally visible from the

GenBank flat file format but are available as part

of this entry's ASN.1 file.

Double stranded (DS) coverage: 75.5%

DS or two chemistry coverage: 98.9%

Single stranded regions: 3

Sequence Validation:

This sequence has been validated by Multiple Complete Digest

Mapping. Comparison of the experimentally derived map digest

fragments with sequence-predicted fragments is given below.

Small fragments below a variable cutoff (approximately 400-600bp)

are not mapped and hence do not appear in the table. There are no

significant remaining discrepancies between the experimental and

predicted values. Uniquely ordered fragment groups are separated

by dashed lines.

BglIII

Map Seq Map Seq

1069.11 1050.00 889.55 866.00 30541.40 30653.00

20320.67 20855.00 1050.18 1015.00 3279.08 3231.00

2171.50 2147.00 7268.78 7196.00

2560.20 2531.00 10085.80 9992.00

4335.42 4269.00 11212.78 11131.00

2698.62 2628.00

1927.50 1887.00

variation	47240..47256	/note="clonal variation with 3' overlapping clone - insertion of 17bp repeat"
BASE COUNT	11556 a 11489 c 12284 g 11994 t	
ORIGIN		
Query Match	47.8%; Score 109.4; DB 9; Length 47323;	
Best Local Similarity	95.0%; Pred. No. 1.6e-23;	
Matches 113;	Conservative 0; Mismatches 6; Indels 0; Gaps 0;	
QY 1	ACCGGACATTCAGTGTCTCTCCATCCAGGAGCGCAGTGCACATGATGGGTCTGGGCT 60	
Db 35121	ACCGGACTTCAGTGTCTCTCCATCCAGGAGCGCAGTGCACATGATGGGTCTGGGCT 35180	
QY 61	GCCCCCTTCCTCTTGACCTCTTGCGAGCTCACATGGAACAGCCCGGTATGA 119	
Db 35181	GCCCCCTTCCTCTTGACCTCTTGCGAGCTCACATGGAACAGGTGAGGGCTAGA 35239	
RESULT 7		
AL662854/c		
LOCUS	Human DNA sequence from clone XHbac-105N19 on chromosome 6,	
DEFINITION	Complete sequence.	
ACCESSION	AL662854	
VERSION	AL662854.7 GI:20068660	
KEYWORDS	HTG.	
SOURCE	human.	
ORGANISM	Homo sapiens	
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	
AUTHORS	Tracey A.	
TITLE	Direct Submission	
JOURNAL	Submitted (23-APR-2002) Wellcome Trust Sanger Institute, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk On Apr 7, 2002 this sequence version replaced gi:19031750. During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.	
COMMENT	This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest. The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em: ENBL; Sw: SWISSPROT; Tr: TREMBL; Wp: WORMPEP; Information on the WORMPEP database can be found at http://www.sanger.ac.uk/Projects/C_elegans/wormpep XHbac-105N19 is from a CHORI-502 human bac - COX cell line library VECTOR: PTARBAC2.1	
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source	1..84474	/location/Qualifiers
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		/db_xref="taxon:9606"
		/chromosome="6"
		/clone="XHbac-105N19"
		/clone_lib="CHORI-502"
BASE COUNT	19363 a 22004 c 21777 g 21330 t	
ORIGIN		
Query Match	47.8%; Score 109.4; DB 9; Length 84474;	
repeat_region	3130.46 3090.00	/note="clonal variation with 3' overlapping clone"
repeat_region	2166.69 2129.00	/note="clonal variation with 3' overlapping clone"
repeat_region	2044.67 2005.00	/note="clonal variation with 3' overlapping clone"
FEATURES		
source		
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		/db_xref="taxon:9606"
		/chromosome="6"
		/sub_clone="UMGC:370M23.002"
		/clone_lib="Research Genetics BAC Library"
	3647..3932	/rpt_family="Alu"
	complement(4999..5277)	/rpt_family="Alu"
	6285..6572	/rpt_family="Alu"
	complement(6972..7050)	/rpt_family="Alu"
	7286..7584	/rpt_family="Alu"
	complement(8164..8609)	/rpt_family="Alu"
	complement(21287..21895)	/rpt_family="Alu"
	22715..22957	/rpt_family="Alu"
	25510..25802	/rpt_family="Alu"
	27835..28010	/rpt_family="Alu"
	31285..31594	/rpt_family="MER20"
	33515..33767	/rpt_family="Alu"
	34223..34290	/rpt_family="Alu"
	37372..37648	/rpt_family="MIR"
	38526..38700	/rpt_family="Alu"
	39583..40010	/rpt_family="MER3"
	40046..40156	/rpt_family="Alu"
	43194..43372	/rpt_family="Alu"
	43325	/rpt_family="MER5"
	44149	/note="clonal variation with 3' overlapping clone"
	4451	/note="clonal variation with 3' overlapping clone"
	44537	/note="clonal variation with 3' overlapping clone"
	44814	/note="clonal variation with 3' overlapping clone"
	44965	/note="clonal variation with 3' overlapping clone"
	45760	/note="clonal variation with 3' overlapping clone"
	45900	/note="clonal variation with 3' overlapping clone"
	46851	/note="clonal variation with 3' overlapping clone"
	46859	/note="clonal variation with 3' overlapping clone"
	47032	/note="clonal variation with 3' overlapping clone"
		/note="clonal variation with 3' overlapping clone"

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Best Local Similarity 95.0%; Pred. No. 1.7e-23;
Matches 113; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 ACCGGGACTTCAGTGTCTCTCCATCCAGGAGCGCAGTGGCCACTATGGGCTCTGGGCT 60
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Db 56560 ACCGGGACTTCAGTGTCTCTCCATCCAGGAGCGCAGTGGCCACTATGGGCTCTGGGCT 56501
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QY 61 GCCCCTTGCTCTCTCTGACCCCTCTTGGCAGCTCAGTGGCAACAGCGCGGTATGGA 119
|||||
Db 56500 GCCCCTTGCTCTCTCTGACCCCTCTTGGCAGCTCAGTGGCAACAGCGGTAGGCTAGA 56442
|||||

RESULT 8
AL773541
LOCUS 104154 bp DNA linear HTG 09-AUG-2002
DEFINITION Homo sapiens chromosome 6 clone XXbac-11J22, *** SEQUENCING IN
ACCESSION AL773541
VERSION 1
KEYWORDS HTG; HTGS_PHASE2; HTGS_ACTIVEPIN; HTGS_DRAFT; HTGS_FULLTOP.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
Almeida, J.
Direct Submission
Submitted (31-JUL-2002) Wellcome Trust Sanger Institute, Hinxton,
Cambridgeshire, CB10 1SA, UK. E-mail enquiries:
humquerry@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
On Aug 11, 2002 this sequence version replaced gi:21621737.
----- Genome Center
Center: Wellcome Trust Sanger Institute
Center code: SC
Web site: http://www.sanger.ac.uk
Contact: humquerry@sanger.ac.uk
----- Project Information
Center project name: B0B1J22
----- Summary Statistics
Assembly program: XGAP4; version 4.5
Chemistry: Dye-terminator; 100% of reads
Consensus quality: 104135 bases at least Q40
Consensus quality: 104142 bases at least Q30
Consensus quality: 104145 bases at least Q20
Insert size: 110727; 1.1% error; agarose-fp
Quality coverage: 19.52x in Q20 bases; sum-of-contigs Quality
coverage: 18.64x in Q20 bases; agarose-fp
-----
* NOTE: This is a 'working draft' sequence.
* This sequence will be replaced
* by the finished sequence as soon as it is available and
* the accession number will be preserved.
FEATURES
source
Location/Qualifiers
1..104154
/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="6"
/clone="XXbac-11J22"
/clone_lib="DNA-arts-BAC.1-QBL.1"
misc_feature
1..104154
/note="assembly_fragment:00090"
BASE COUNT 26560 a 25418 c 26093 g 26083 t
ORIGIN
Query Match 47.8%; Score 109.4; DB 2; Length 104154;
Best Local Similarity 95.0%; Pred. No. 1.7e-23;
Matches 113; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 ACCGGGACTTCAGTGTCTCTCCATCCAGGAGCGCAGTGGCCACTATGGGCTCTGGGCT 60
|||||
Db 67502 ACCGGGACTTCAGTGTCTCTCCATCCAGGAGCGCAGTGGCCACTATGGGCTCTGGGCT 67561
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```

```

QY 61 GCCCCTTGCTCTCTCTGACCCCTCTTGGCAGCTCAGTGGCAACAGCGCGGTATGGA 119
|||||
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|||||

RESULT 9
AL669830/c
LOCUS 156272 bp DNA linear PRI 24-APR-2002
DEFINITION Human DNA sequence from clone XXbac-118E17 on chromosome 6,
complete sequence.
ACCESSION AL669830
VERSION 1
KEYWORDS HTG.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
Johnson, C.
Direct Submission
Submitted (23-APR-2002) Wellcome Trust Sanger Institute, Hinxton,
Cambridgeshire, CB10 1SA, UK. E-mail enquiries:
humquerry@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
On Apr 10, 2002 this sequence version replaced gi:20067510.
During sequence assembly data is compared from overlapping clones.
Where differences are found these are annotated as variations
together with a note of the overlapping clone name. Note that the
variation annotation may not be found in the sequence submission
corresponding to the overlapping clone, as we submit sequences with
only a small overlap as described above.
This sequence was finished as follows unless otherwise noted: all
regions were either double-stranded or sequenced with an alternate
chemistry or covered by high quality data (i.e., phred quality >=
30); an attempt was made to resolve all sequencing problems, such
as compressions and repeats; all regions were covered by at least
one plasmid subclone or more than one M13 subclone; and the
assembly was confirmed by restriction digest. The following
abbreviations are used to associate primary accession numbers given
in the feature table with their source databases: En:, EMBL; SW:,
SWISSPROT; Tr:, TREMBL; Wp:, WORMPEP; Information on the WORMPEP
database can be found at
http://www.sanger.ac.uk/Projects/C_elegans/wormpep/XXbac-118E17 is
from a CHORI-501 human bac - PGF cell line library VECTOR:
PTARBAC2.1
This sequence was generated from part of bacterial clone contigs
constructed by the MHC Haplotype Consortium and collaborators.
Further information can be found at
http://www.sanger.ac.uk/HGP/Chr6/MHC.
FEATURES
source
Location/Qualifiers
1..156272
/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="6"
/clone="XXbac-118E17"
/clone_lib="CHORI-501"
BASE COUNT 41135 a 37989 c 36907 g 40241 t
ORIGIN
Query Match 47.8%; Score 109.4; DB 9; Length 156272;
Best Local Similarity 95.0%; Pred. No. 1.8e-23;
Matches 113; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 ACCGGGACTTCAGTGTCTCTCCATCCAGGAGCGCAGTGGCCACTATGGGCTCTGGGCT 60
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Db 25902 ACCGGGACTTCAGTGTCTCTCCATCCAGGAGCGCAGTGGCCACTATGGGCTCTGGGCT 25843
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QY 61 GCCCCTTGCTCTCTCTGACCCCTCTTGGCAGCTCAGTGGCAACAGCGCGGTATGGA 119
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Db 25842 GCCCCTTGCTCTCTCTGACCCCTCTTGGCAGCTCAGTGGCAACAGCGGTAGGCTAGA 25784
|||||

RESULT 10
AL713893

```

LOCUS AL713893 178688 bp DNA linear HTG 28-MAR-2002
DEFINITION Homo sapiens chromosome 6 clone XXbac-307M4, *** SEQUENCING IN
PROGRESS ***, 6 unordered pieces.
ACCESSION AL713893
VERSION AL713893.5 GI:19847952
KEYWORDS HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_FULLTOP.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1
Sims.S.
REFERENCE Direct Submission
AUTHORS Submitted (26-MAR-2002) Wellcome Trust Sanger Institute, Hinxton,
TITLE Cambridgeshire, CB10 1SA, UK. E-mail enquiries:
JOURNAL humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
COMMENT On Mar 29, 2002 this sequence version replaced gi:19773907.
----- Genome Center
Center: Wellcome Trust Sanger Institute
Center code: SC
Web site: http://www.sanger.ac.uk
Contact: humquery@sanger.ac.uk
----- Project Information
Center project name: bpG307M4
----- Summary Statistics
Assembly program: XGAP4; version 4.5
Chemistry: Dye-terminator Big Dye; 100% of reads
Consensus quality: 177277 bases at least Q40
Consensus quality: 177708 bases at least Q30
Consensus quality: 177956 bases at least Q20
Insert size: 178188; sum-of-contigs
Insert size: 192613; 0.9% error; agarose-fp
Quality coverage: 8.57x in Q20 bases; sum-of-contigs Quality
coverage: 8.00x in Q20 bases; agarose-fp

* NOTE: This is a 'working draft' sequence. It currently
* consists of 6 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
*
* 37410: contig of 37410 bp in length
* 37411 37510: gap of 100 bp
* 37511 82372: contig of 44862 bp in length
* 82373 82472: gap of 100 bp
* 82473 142457: contig of 59985 bp in length
* 142458 142557: gap of 100 bp
* 142558 152859: contig of 10302 bp in length
* 152860 152959: gap of 100 bp
* 152960 172054: contig of 19095 bp in length
* 172055 172154: gap of 100 bp
* 172155 178688: contig of 6534 bp in length.
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/chromosome="6"
/clone="XXbac-307M4"
/clone.lib="CHORI-501"
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37511..82372
/note="assembly-fragment:00918
fragment_chain:1"
82473..142457
/note="assembly-fragment:03231
fragment_chain:1"
142558..152859
/note="assembly-fragment:03008
fragment_chain:1"

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/note="assembly-fragment:04309
fragment_chain:1"
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fragment_chain:1
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Best Local Similarity 95.0%; Pred. No. 1.8e-23;
Matches 113; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
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Db 173451 ACCGGGACATTCAGTCTCTCCATCCAGGAGCGCAGTGGGCTCTGGGCT 173510
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QY 61 GCCCTTGTCTCTCTCTGACCTCTGCGAGCTCAGATGGAGCGCGGCTATGA 119
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Db 173511 GCCCTTGTCTCTCTCTGACCTCTGCGAGCTCAGATGGAGCGCGGCTATGA 173569
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RESULT 11
AB023048 192650 bp DNA linear PRI 20-NOV-1999
LOCUS Homo sapiens genomic DNA, chromosome 6p21.3, HLA class I region,
DEFINITION clone:53L9, complete sequence.
ACCESSION AB023048
VERSION AB023048.1 GI:5672603
KEYWORDS HTG.
SOURCE Homo sapiens cell_line:978SK DNA, clone:53L9.
ORGANISM Homo sapiens
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (sices)
Shiina,T., Tamiya,G., Oka,A., Takishima,N., Yamagata,T.,
Kikkawa,E., Iwata,K., Tomizawa,M., Okuaki,N., Kuwano,Y.,
Watanabe,K., Fukuzumi,Y., Itakura,S., Sugawara,C., Ono,A.,
Yamazaki,M., Tashiro,H., Ando,A., Ikemura,T., Soeda,E., Kimura,M.,
Bahram,S. and Inoko,H.
Molecular dynamics of MHC genesis unraveled by sequence analysis of
the 1,796,938-bp HLA class I region
Proc. Natl. Acad. Sci. U.S.A. 96 (23), 13282-13287 (1999)
20027539
2 (bases 1 to 192650)
Shiina,T. and Takishima,N.
Direct Submission
Submitted (29-JAN-1999) Takashi Shiina, Tokai University School of
Medicine, Department of Molecular Life Science 2; Bohseidai,
Isehara, Kanagawa 259-1193, Japan
(E-mail: tshiina@is.icc.u-tokai.ac.jp, Tel:81-463-93-1121,
Fax:81-463-94-8884)
FEATURES
Location/Qualifiers
1. .192650
/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="6"
/map="6p21.3"
/clone="53L9"
/cell_line="978SK"
BASE COUNT 49862 a 44743 c 45833 g 52212 t
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Query Match 47.8%; Score 109.4; DB 9; Length 192650;
Best Local Similarity 95.0%; Pred. No. 1.8e-23;
Matches 113; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
QY 1 ACCGGGACATTCAGTCTCTCCATCCAGGAGCGCAGTGGGCTCTGGGCT 60
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/note="SHG-16870:The location is between each flanking
site of PCR primers."
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of PCR primers."
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complement(142479..142740)
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site of PCR primers."
/db_xref="GDB:675281"
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148667..148818,148927..149022,149548..149794,
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148667..148818,148927..149022,149548..149794,
149902..150089,150614..150712,150972..151119,
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/gene="DDR"
/codon_start=1
/product="Receptor tyrosine kinase"
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/translation="MGPEALSSLLLLLVASGDAMKHFDPKCYALGMQDRTPID
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QGRHAGLKEFSRSLRYLRDGRMMGKRWQVEYISGNEDESVYKDLGPPVY
ARLYFTPRADRYMSVCLRYELGCLRWDGLSYTPVGOTMYLSEAVYINDSTYDGH
TVGLQGLGLADVGLDQDFRKQELRVMPGYDVGWNSHSFSSGVYEMEFEDR
LRATQAMOVHNMHTLGLARLPGVGECRRPGRPMANWEGEPMRNLGNGLPDPRARV
SVPLGGVARFLQCRFLPAGPMLLSEIFSDIVYNNSSPALGTFPPAPMPDGPDP
TNFSLELPRGQGVAKAEGSPAILIGLIVAILILLIITALLMLWHLWRLLSKL
ERRVLELTVHLSVPGDTILINNRGPREPPYQEPNRPNGNPPHAPCVNGSALLL
SNPYALLLTYAPRPGPPTPAWAKPTNTQAYSGDMEPEKPGAPLLPPPPQNSV
PHYAEDIVTLQCVTGGNTYAVPALPGAVGDPVDFPFRSLRFEKELGREGVEY
HLCEVSQDPLVSLDFLNVKRGHLLVAVKLRPDATKNARDELKVKIMSRLLDP
NIIELVGQDDPLCMITDYMNDLNOFLSAHQEDKAEAGPDGQAQGPITYY
PMLHVAQIASCGRMYLATNFVHRLATRNCLVGNFTIKIADFGMSRLNYAGDYR
VQGLRALPIKMAWECILMGKFTTASDVWAFGVTLWEVLMICRAQPFGLTDEQVFN
AGEFERDGRQVYLSRRPACPGQLYELMLRCNSRESEQRPFSQLHFLAEALNTV"
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144949..145076
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/number=13
145225..145469
/gene="DDR"
/number=12

Query Match 47.8%; Score 109.4; DB 9; Length 200000;
Best Local Similarity 95.0%; Pred. No. 1.8e-23;
Matches 113; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
QY 1 ACCGGGACTTCAGTCTCTCTTGCACCTTCATGCAAGAGCGGCGGCTGGGCT 60
Db 109962 ACCGGGACTTCAGTCTCTCTTGCACCTTCATGCAAGAGCGGCGGCTGGGCT 110021
QY 61 GCCCCTTGCTCTCTTGCACCTTCATGCAAGAGCGGCGGCTGGGCT 119
Db 110022 GCCCCTTGCTCTCTTGCACCTTCATGCAAGAGCGGCGGCTGGGCT 110080

RESULT 13
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LOCUS 349980 bp DNA linear PAT 01-FEB-2002
DEFINITION Sequence 4 from Patent WO0200932.
ACCESSION AX344553
VERSION AX344553.1 GI:18492439
KEYWORDS
SOURCE synthetic construct.
ORGANISM synthetic construct.
REFERENCE 1
AUTHORS Olek,A., Piepenbrock,C. and Berlin,K.
TITLE Diagnosis of known genetic parameters within the mhc
JOURNAL Patent: WO 0200932-A 4 03-JAN-2002;
EpiGenomics AG (DE)
FEATURES
Location/Qualifiers
source
1. 349980
/organism="synthetic construct"
/db_xref="taxon:32630"
/note="chemically treated genomic DNA (Homo sapiens)-Original length of seq 1: 3.673778 <223>-split as follows--seq 01 0.000.001 TO 0.349.980-seq 02 0.300.001 649.980-seq 03 600.001 949.980-seq 04 900.001 1.249.980-seq 05 1.200.001 1.549.980-seq 06 1.500.001 1.849.980-seq 07 1.800.001 2.149.980-seq 08 2.100.001 2.449.980-seq 09 2.400.001 2.749.980-seq 10 2.700.001 3.049.980-seq 11 3.000.001 3.349.980-seq 12 3.300.001 3.649.980-seq 13 3.600.001 3.673.778 <223>-Original length of seq 2: 3.673778 <223>-split as follows--seq 14 0.000.001 TO 0.349.980-seq 15 0.300.001 649.980-seq 16 600.001 949.980-seq 17 900.001 1.249.980-seq 18 1.200.001 1.549.980-seq 19 1.500.001 1.849.980-seq 20 1.800.001 2.149.980-seq 21 2.100.001 2.449.980-seq 22 2.400.001 2.749.980-seq 23 2.700.001 3.049.980-seq 24 3.000.001 3.349.980-seq 25 3.300.001 3.649.980-seq 26 3.600.001 3.673.778"
BASE COUNT 86682 a 5859 c 85073 g 172166 t
ORIGIN
Query Match 28.8%; Score 66; DB 6; Length 349980;
Best Local Similarity 76.4%; Pred. No. 1e-09;
Matches 81; Conservative 0; Mismatches 25; Indels 0; Gaps 0;
QY 1 ACCGGGACTTCAGTCTCTCTTGCACCTTCATGCAAGAGCGGCGGCTGGGCT 60
Db 319857 ACCGAACTTCATCTCTCTCCCAAGCAATTAACCTATAAATCTAACT 319798
QY 61 GCCCCTTGCTCTCTTGCACCTTCATGCAAGAGCGGCGGCTGGGCT 106
Db 319797 ACCCCTTATCTCTTAACTCTTAACTCTTAACTCTTAACTCTTAACT 319752
RESULT 14
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LOCUS 349980 bp DNA linear PAT 01-FEB-2002
DEFINITION Sequence 5 from Patent WO0200932.
ACCESSION AX344554
VERSION AX344554.1 GI:18492440
KEYWORDS
SOURCE synthetic construct.
ORGANISM synthetic construct.
REFERENCE 1
AUTHORS Olek,A., Piepenbrock,C. and Berlin,K.
TITLE Diagnosis of known genetic parameters within the mhc
JOURNAL Patent: WO 0200932-A 5 03-JAN-2002;
EpiGenomics AG (DE)
FEATURES
Location/Qualifiers
source
1. 349980
/organism="synthetic construct"
/db_xref="taxon:32630"

BASE COUNT
ORIGIN

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	Best Local Similarity	76.4%	Pred. No. 1e-09		
	Matches 81	Conservative	0	Mismatches 25	Indels 0
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DB	19857	ACCGAAACTCAATATCTCTCCATCCGAAAAACGCAATACCACTATAAAATCTTAAACT	19798		
QY	61	GCCCCTTGGCTCTCTCTTGGACCTCTTGGCAGCTCACATGGAACA	106		
DB	19797	ACCCCTTATCTCTCTCTTAACTCCTTAACTCACTACATAAAACA	19752		

BASE COUNT	91992 a	5703 c	86514 g	165771 t
ORIGIN				
Query Match	27.2%		Score 62.2	DB 6; Length 349980;

GenCore version 5.1.5
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OM nucleic - nucleic search, using sw model

Run on: May 1, 2003, 04:34:36 : Search time 64.2211 Seconds
(without alignments)
4397.425 Million cell updates/sec

Title: US-09-092-296-1

Perfect score: 239

Sequence: 1 GCCACCGGAGTTCAGTGT.....CCCTTAGGACCGACGCTCA 239

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 746064 seqs, 590810554 residues

Total number of hits satisfying chosen parameters: 1492128

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications NA.*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	238	99.6	239	9	US-09-092-296-1
2	228	95.4	229	9	US-09-092-296-2
3	227	95.0	422	9	US-09-992-598-362
4	227	95.0	422	9	US-09-989-293A-362
5	227	95.0	422	9	US-10-063-547-65
6	227	95.0	422	9	US-09-989-735-362
7	227	95.0	422	9	US-09-990-444-362
8	227	95.0	422	9	US-09-989-730-362
9	227	95.0	422	9	US-09-990-436-362
10	227	95.0	422	9	US-09-991-181-362
11	227	95.0	422	9	US-09-993-687-362
12	227	95.0	422	9	US-09-997-653-362
13	227	95.0	422	9	US-09-989-734-362
14	227	95.0	422	9	US-10-174-590-241
15	227	95.0	422	9	US-10-176-758-241
16	227	95.0	422	9	US-10-063-616-65
17	227	95.0	422	9	US-10-175-737-241
18	227	95.0	422	9	US-09-993-667-362
19	227	95.0	422	9	US-10-063-502-65

20	227	95.0	422	9	US-10-173-706-241
21	227	95.0	422	9	US-10-175-738-241
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23	227	95.0	422	9	US-10-176-482-241
24	227	95.0	422	9	US-10-176-757-241
25	227	95.0	422	9	US-10-176-913-241
26	227	95.0	422	9	US-10-180-552-241
27	227	95.0	422	9	US-10-180-557-241
28	227	95.0	422	9	US-09-990-438-362
29	227	95.0	422	9	US-09-990-562-362
30	227	95.0	422	9	US-09-997-428-362
31	227	95.0	422	9	US-09-997-666-362
32	227	95.0	422	9	US-10-173-700-241
33	227	95.0	422	9	US-10-174-572-241
34	227	95.0	422	9	US-10-174-579-241
35	227	95.0	422	9	US-10-174-582-241
36	227	95.0	422	9	US-10-174-588-241
37	227	95.0	422	9	US-10-175-739-241
38	227	95.0	422	9	US-10-175-740-241
39	227	95.0	422	9	US-10-175-743-241
40	227	95.0	422	9	US-10-176-488-241
41	227	95.0	422	9	US-10-176-492-241
42	227	95.0	422	9	US-10-176-747-241
43	227	95.0	422	9	US-10-176-750-241
44	227	95.0	422	9	US-10-176-985-241
45	227	95.0	422	9	US-10-176-987-241

ALIGNMENTS

RESULT 1
US-09-092-296-1
; Sequence 1, Application US/09092296
; Publication No. US20020188114A1
; GENERAL INFORMATION:
; APPLICANT: BILLING-MEDEL, PATRICIA
; APPLICANT: COHEN, MAURICE
; APPLICANT: COLPITTS, TRACEY L.
; APPLICANT: FRIEDMAN, PAULA N.
; APPLICANT: KLASS, MICHAEL R.
; APPLICANT: RUSSELL, JOHN C.
; APPLICANT: STROUPE, STEPHEN D.
; TITLE OF INVENTION: REAGENTS AND METHODS USEFUL
; FOR DETECTING DISEASES OF THE LUNG
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Abbott Laboratories
; STREET: 100 Abbott Park Road
; CITY: Abbott Park
; STATE: IL
; COUNTRY: USA
; ZIP: 60064-3500
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/092,296
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/048,810
; FILING DATE: 05-JUN-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Becker, Cheryl L.
; REGISTRATION NUMBER: 35,441
; REFERENCE/DOCKET NUMBER: 6104.US.01
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 847/935-1729
; TELEFAX: 847/938-2623
; TELEX:

INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 239 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
FEATURE:
NAME/KEY: base_polymorphism
LOCATION: 200
OTHER INFORMATION: /note= " N' represents an A or G or
OTHER INFORMATION: T or C polymorphism at this position"
US-09-092-296-1

Query Match 99.6%; Score 238; DB 9; Length 239;
Best Local Similarity 100.0%; Pred. No. 8.4e-71;
Matches 239; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 GCCACCGGACTTCAGTCTCCCTCCATCCAGAGCGCAGTGGCCACTATGGGCTCG 60
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QY 61 GGCTGCCCTTGTCTCTCTTGAACCTCTTGGCAGCTCACATGGAACAGGCCGGGTA 120
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Db 61 GGCTGCCCTTGTCTCTCTTGAACCTCTTGGCAGCTCACATGGAACAGGCCGGGTA 120
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QY 121 TGACTTTGCAACTGAAAGCTGAAGGAGTCTTTTCTGACAAATTCCTCTATGAGTCCAGCT 180
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QY 181 TCGTGAATTCCTTGAATTCCTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 239
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Db 181 TCGTGAATTCCTTGAATTCCTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 239
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RESULT 2
US-09-092-296-2
Sequence 2, Application US/09092296
Publication No. US20020188114A1
GENERAL INFORMATION:
APPLICANT: BILLING-MEDEL, PATRICIA
APPLICANT: COHEN, MAURICE
APPLICANT: COLPITTS, TRACEY L.
APPLICANT: FRIEDMAN, PAULA N.
APPLICANT: KLASS, MICHAEL R.
APPLICANT: RUSSELL, JOHN C.
APPLICANT: STROUPE, STEPHEN D.
TITLE OF INVENTION: REAGENTS AND METHODS USEFUL
TITLE OF INVENTION: FOR DETECTING DISEASES OF THE LUNG
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
ADDRESSEE: Abbott Laboratories
STREET: 100 Abbott Park Road
CITY: Abbott Park
STATE: IL
COUNTRY: USA
ZIP: 60064-3500
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/092,296
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/048,810
FILING DATE: 05-JUN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Becker, Cheryl L.
REGISTRATION NUMBER: 35,441
REFERENCE/DOCKET NUMBER: 6104, US. 01
TELECOMMUNICATION INFORMATION:

TELEPHONE: 847/935-1729
TELEFAX: 847/938-2623
TELEX:
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 229 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-09-092-296-2

Query Match 95.4%; Score 228; DB 9; Length 229;
Best Local Similarity 99.6%; Pred. No. 2e-67;
Matches 228; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 ACCGGGACTTCAGTGTCTCCATCCAGAGCGCAGTGGCCACTATGGGGTCTGGGCT 64
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Db 1 ACCGGGACTTCAGTGTCTCCATCCAGAGCGCAGTGGCCACTATGGGGTCTGGGCT 60
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QY 65 GCCCTTGTCTCTCTCTTGGCCCTCTTGGCAGCTCACATGGAACAGGCCGGGTATGAC 124
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Db 61 GCCCTTGTCTCTCTCTTGGCCCTCTTGGCAGCTCACATGGAACAGGCCGGGTATGAC 120
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QY 125 TTTCACACTGAAGCTGAAGGAGTCTTTCTGACAAATTCCTCTATGAGTCCAGCTTCT 184
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Db 121 TTTCACACTGAAGCTGAAGGAGTCTTTCTGACAAATTCCTCTATGAGTCCAGCTTCT 180
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QY 185 GGAATTCCTTGAATTCCTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 233
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Db 181 GGAATTCCTTGAATTCCTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 229
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RESULT 3
US-09-992-598-362
Sequence 362, Application US/09992598
Patent No. US20020160384A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Fong, Sherman
APPLICANT: Gerber, Hanspeter
APPLICANT: Giddard, Audrey E.
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Kijavini, Ivar J.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2730PIC20
CURRENT APPLICATION NUMBER: US/09/992,598
CURRENT FILING DATE: 2001-11-14
PRIOR APPLICATION NUMBER: 60/049787
PRIOR FILING DATE: 1997-06-16
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/065186
PRIOR FILING DATE: 1997-11-12
PRIOR APPLICATION NUMBER: 60/065311

[illegible]

[illegible]

QY 1 GGCACCGGACTTCAGTGTCTCTCCATCCAGGAGCGCAGTGGCCACTATGGGCTCG 60
|||||
Db 8 GGCACCGGACTTCAGTGTCTCTCCATCCAGGAGCGCAGTGGCCACTATGGGCTCG 67
|||||
QY 61 GGCTGCCCTTGTCCTCTTGACCCCTCTGGGAGCTCACATGGAACAGGCGCGGTA 120
|||||
Db 68 GGCTGCCCTTGTCCTCTTGACCCCTCTGGGAGCTCACATGGAACAGGCGCGGTA 127
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QY 121 TGACTTTGCAACTGAAGCTGAAGGAGTCTTTTCTGACAAATTCCTCTATGATCCAGCT 180
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Db 128 TGACTTTGCAACTGAAGCTGAAGGAGTCTTTTCTGACAAATTCCTCTATGATCCAGCT 187
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QY 181 TCTTGGAAATGCTTGAATA-NFTTGGCTCTCTCTCCATCTCCCTTCAAGGACACGGTCA 239
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Db 188 TCTTGGAAATGCTTGAATAAGCTCTGCTCTCTCTCCATCTCCCTTCAAGGACACGGTCA 247
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RESULT 6
US-09-989-735-362
; Sequence 362, Application US/09989735
; Publication No. US20020193299A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: E2730PIC61
; CURRENT APPLICATION NUMBER: US/09/989,735
; CURRENT FILING DATE: 2001-11-19
; PRIOR APPLICATION NUMBER: 60/049787
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; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/091982
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/092182
; PRIOR FILING DATE: 1998-07-09

Query Match 95.08; Score 227; DB 9; Length 422;
Best Local Similarity 99.28; Pred. No. 5.3e-67;
Matches 238; Conservative 0; Mismatches 1; Indels 1; Gaps 1;
OY 1 GGCACACGGGACTTCAGTGTCTCTCCATCCAGGAGCGAGTGGCCACTATGSGGTCTG 60
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Db 8 GGCACACGGGACTTCAGTGTCTCTCCATCCAGGAGCGAGTGGCCACTATGSGGTCTG 67
OY 61 GCGTGCCTCTGTCTCTCTTGAACCTCTCTTGGCAGCTCACATGGAACAGGCGCGGTA 120
|||||
Db 68 GCGTGCCTCTGTCTCTCTTGAACCTCTCTTGGCAGCTCACATGGAACAGGCGCGGTA 127
OY 121 TGACTTTGCAACTGAAGCTGAAGAGTCTTTTCTGACAAAATCTCTCTATGAGTCCAGCT 180
|||||
Db 128 TGACTTTGCAACTGAAGCTGAAGAGTCTTTTCTGACAAAATCTCTCTATGAGTCCAGCT 187
OY 181 TCCTGGAATTCCTTGAAAA-NCTGCGCTCCCTCCATCTCCCTTCAGGAGCGCGTCA 239
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Db 188 TCCTGGAATTCCTTGAAAAAGCTCGCTCCCTCCATCTCCCTTCAGGAGCGCGTCA 247

RESULT 7

US-09-990-444-362
; Sequence 362, Application US/09990444
; Publication No. US20020193300A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Faonli, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2730PIC19
; CURRENT APPLICATION NUMBER: US/09/990.444
; CURRENT FILING DATE: 2001-11-14
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; PRIOR FILING DATE: 1998-07-07
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Query Match          95.08;  Score 227;  DB 9;  Length 422;
Best Local Similarity 99.28;  Pred. No. 5,3e-67;
Matches 238;  Conservative 0;  Mismatches 1;  Indels 1;  Gaps 1;

QY 1 GCCACCGGACTTCAGTCTCTCCATCCAGGAGCGCAGTGGCCACTATGGGGTGTG 60
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Db 8 GCCACCGGACTTCAGTCTCTCCATCCAGGAGCGCAGTGGCCACTATGGGGTGTG 67
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QY 61 GCGTGCCTCTGTCCTCTTGGACCTCTTGGCAGCTCACATGGAGCGCGGGTA 120
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Db 68 GCGTGCCTCTGTCCTCTTGGACCTCTTGGCAGCTCACATGGAGCGCGGGTA 127
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QY 121 TCACCTTGCACGTGAGCTGAGAGTCTTTCTGACAAATCTCTGATGAGTCCAGCT 180
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Db 128 TGACTTGCACGTGAGCTGAGAGTCTTTCTGACAAATCTCTGATGAGTCCAGCT 187
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QY 181 TCCCTGGAATGCTTGAATAA-NPCTGCGTCTCTCTCCATCTCCCTTCAGGAGCGCGTCA 239
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Db 188 TCCCTGGAATGCTTGAATAAGCTCTGCGTCTCTCTCCATCTCCCTTCAGGAGCGCGTCA 247
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RESULT 8
US-09-989-730-362
; Sequence 362, Application US/09989730
; Publication No. US20020197674A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Kijavini, Ivar J.
; APPLICANT: Napier, Mary A.
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; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2730PIC69
; CURRENT APPLICATION NUMBER: US/09/989,730
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; PRIOR APPLICATION NUMBER: 60/091360
; PRIOR FILING DATE: 1998-07-01
; PRIOR APPLICATION NUMBER: 60/091478
; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/091544
; PRIOR FILING DATE: 1998-07-01
; PRIOR APPLICATION NUMBER: 60/091519
; PRIOR FILING DATE: 1998-07-02

; PRIOR APPLICATION NUMBER: 60/091626
; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/091633
; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/091978
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/091982
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/092182
; PRIOR FILING DATE: 1998-07-09

Query Match 95.08; Score 227; DB 9; Length 422;
Best Local Similarity 99.28; Pred. No. 5.3e-67;
Matches 238; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

QY 1 GGCCACCGGGACTTCAGTGTCTCTCCATCCAGGAGCGCAGTGGCCACTATGCGGTCTG 60
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Db 8 GGCCACCGGGACTTCAGTGTCTCTCCATCCAGGAGCGCAGTGGCCACTATGCGGTCTG 67
QY 61 GGCTGGCCCTTGTCTCTCTTGTGACCTCTTGGCAGCTCACATGGAGAGCGCGGTA 120
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Db 58 GCGTGGCCCTTGTCTCTCTTGTGACCTCTTGGCAGCTCACATGGAGAGCGCGGTA 127
QY 121 TGACTTTGCAACTGAAGCTGAAGGAGTCTTTTCTGACAAATTCCTCTATGATCCAGCT 180
|||||
Db 128 TGACTTTGCAACTGAAGCTGAAGGAGTCTTTTCTGACAAATTCCTCTATGATCCAGCT 187
QY 181 TCCTGGAATTCCTTGAATAA-NICTGGCTCTCTCTCTCATCTCCCTTCAGGACACCGTCA 239
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Db 188 TCCTGGAATTCCTTGAATAAGCTCTGCTCTCTCTCATCTCCCTTCAGGACACCGTCA 247

RESULT 9
US-09-990-436-362
; Sequence 362, Application US/09990436
; Publication No. US20020198148A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avl J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Rotstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Kijavlin, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2730PIC14
; CURRENT APPLICATION NUMBER: US/09/990,436
; PRIOR APPLICATION NUMBER: 60/049787
; PRIOR FILING DATE: 1997-06-16
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/065186
; PRIOR FILING DATE: 1997-11-12
; PRIOR APPLICATION NUMBER: 60/065311

1	PRIOR APPLICATION NUMBER: 60/089532
2	PRIOR FILING DATE: 1998-06-17
3	PRIOR APPLICATION NUMBER: 60/089538
4	PRIOR FILING DATE: 1998-06-17
5	PRIOR APPLICATION NUMBER: 60/089598
6	PRIOR FILING DATE: 1998-06-17
7	PRIOR APPLICATION NUMBER: 60/089599
8	PRIOR FILING DATE: 1998-06-17
9	PRIOR APPLICATION NUMBER: 60/089600
10	PRIOR FILING DATE: 1998-06-17
11	PRIOR APPLICATION NUMBER: 60/089653
12	PRIOR FILING DATE: 1998-06-17
13	PRIOR APPLICATION NUMBER: 60/089801
14	PRIOR FILING DATE: 1998-06-18
15	PRIOR APPLICATION NUMBER: 60/089907
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21	PRIOR APPLICATION NUMBER: 60/089948
22	PRIOR FILING DATE: 1998-06-19
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31	PRIOR APPLICATION NUMBER: 60/090349
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63	PRIOR APPLICATION NUMBER: 60/090695
64	PRIOR FILING DATE: 1998-06-25
65	PRIOR APPLICATION NUMBER: 60/090696
66	PRIOR FILING DATE: 1998-06-25
67	PRIOR APPLICATION NUMBER: 60/090862
68	PRIOR FILING DATE: 1998-06-26
69	PRIOR APPLICATION NUMBER: 60/090863
70	PRIOR FILING DATE: 1998-06-26
71	PRIOR APPLICATION NUMBER: 60/091360
72	PRIOR FILING DATE: 1998-07-01
73	PRIOR APPLICATION NUMBER: 60/091478

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; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/091978
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/091982
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/092182
; PRIOR FILING DATE: 1998-07-09

Query Match          95.0%; Score 227; DB 9; Length 422;
Best Local Similarity 99.2%; Pred. No. 5.3e-67;
Matches 238; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

QY 1  GGCACCGGACTTCAGTGTCTCTCCATCCAGGAGCGCAGTGGCCACTATGGGFTCTG 60
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Db 8  GGCACCGGACTTCAGTGTCTCTCCATCCAGGAGCGCAGTGGCCACTATGGGFTCTG 67

QY 61 GGTGTCCTTGTCTCTCTTGCACCTCTTGGCAGCTCACATGGAACAGGCGCGGTA 120
      |||||
Db 68 GGTGTCCTTGTCTCTCTTGCACCTCTTGGCAGCTCACATGGAACAGGCGCGGTA 127

QY 121 TGACTTTGCAACTGAAGCTGAAGAGTCTTTTCTGACAAATTCCTCTATGAGTCCAGCT 180
      |||||
Db 128 TGACTTTGCAACTGAAGCTGAAGAGTCTTTTCTGACAAATTCCTCTATGAGTCCAGCT 187

QY 181 TCTGTGAATGCTTGA AAA-NITCGCTCTCTCCATCTCCCTTACGGGACACGGTCA 239
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Db 188 TCTGTGAATGCTTGA AAA-GCTGCTCTCTCTCCATCTCCCTTACGGGACACGGTCA 247

RESULT 10
US-09-991-181-362
; Sequence 362, Application US/09991181
; Publication No. US20020197615A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaud, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2730PIC53
; CURRENT APPLICATION NUMBER: US/09/991,181
; CURRENT FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/049787
; PRIOR FILING DATE: 1997-06-16
; PRIOR APPLICATION NUMBER: 60/062250
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; PRIOR FILING DATE: 1998-06-25
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; PRIOR FILING DATE: 1998-06-26
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; PRIOR FILING DATE: 1998-07-01
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; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/091978
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/091982
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/092182
; PRIOR FILING DATE: 1998-07-09
;
Query Match 95.0%; Score 227; DB 9; Length 422;
Best Local Similarity 99.2%; Pred. No. 5,3e-67;
Matches 238; Conservative 0; Mismatches 1; Indels 1; Gaps 1;
;
QY 1 GGCCACCGGGACTTCAGTGTCTCTCCATCCAGGAGCGAGTGGCCACTATGGGGTCTG 60
Db 8 GGCCACCGGGACTTCAGTGTCTCTCCATCCAGGAGCGAGTGGCCACTATGGGGTCTG 67
;
QY 61 GGCTGCCCTTGTCTCTCTCTTGGACCTCTTGGCAGCTCACATGGAACAGGCGGGTA 120
Db 68 GGCTGCCCTTGTCTCTCTCTTGGACCTCTTGGCAGCTCACATGGAACAGGCGGGTA 127
;
QY 121 TGACTTTGCAACTGAAGCTGAAGGAGTCTTTTTCACAAAATTCCTATGAGTCCAGCT 180
Db 128 TGACTTTGCAACTGAAGCTGAAGGAGTCTTTTTCACAAAATTCCTATGAGTCCAGCT 187
;
QY 181 TCCTGGAATTCCTGAAAA-NCTGTGCTCTCTCTCCATCTCCCTTCAGGAGCAGCGTCA 239
Db 188 TCCTGGAATTCCTGAAAAAGCTCTGCTCTCTCTCCATCTCCCTTCAGGAGCAGCGTCA 247
;
RESULT 11
US-09-993-687-362
; Sequence 362, Application US/09993687
; Publication No. US20020198149A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Goddard, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same

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/ FILE REFERENCE: P2730PIC11
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/ PRIOR FILING DATE: 1997-11-12
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; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/091978
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/091982
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/092182
; PRIOR FILING DATE: 1998-07-09

Query Match          95.0%; Score 227; DB 9; Length 422;
Best Local Similarity 99.2%; Pred. No. 5.3e-67;
Matches 238; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

QY 1  GGCACCGGAGTTCAGTGTCTCTCCATCCAGGAGCGAGTGGCCACTATGGGTCTG 60
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Db 8  GGCACCGGAGTTCAGTGTCTCTCCATCCAGGAGCGAGTGGCCACTATGGGTCTG 67

QY 61 GCGTCCCTTGTCTCTCTCTGACCTCTGCGAGTCCACATGGACAGGCGCGGTA 120
      |||||
Db 68 GCGTCCCTTGTCTCTCTCTGACCTCTGCGAGTCCACATGGACAGGCGCGGTA 127

QY 121 TGACTTGGCACTGAAGCTGAAGGAGTCTTTCTGACAAATCTCTATGAGTCCAGCT 180
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Db 128 TGACTTGGCACTGAAGCTGAAGGAGTCTTTCTGACAAATCTCTATGAGTCCAGCT 187

QY 181 TCCTGGAATGCTTGAATA-NTCCTGCTCTCTCTCCATCTCCCTTCAGGAGCAGCGTCA 239
      |||||
Db 188 TCCTGGAATGCTTGAAGAGCTCTGCGCTCTCTCTCTCCATCTCCCTTCAGGAGCAGCGTCA 247

RESULT 12
US-09-989-734-362
; Sequence 362, Application US/09989734
; Publication No. US20030003531A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Collin K.
```

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; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P27301PC64
; CURRENT APPLICATION NUMBER: US/09/989,734
; CURRENT FILING DATE: 2001-11-19
; PRIOR APPLICATION NUMBER: 60/049787
; PRIOR FILING DATE: 1997-06-16
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/065186
; PRIOR FILING DATE: 1997-11-12
; PRIOR APPLICATION NUMBER: 60/065311
; PRIOR FILING DATE: 1997-11-13
; PRIOR APPLICATION NUMBER: 60/066770
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; PRIOR APPLICATION NUMBER: 60/078910
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; PRIOR APPLICATION NUMBER: 60/083322
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; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/091633
; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/091978
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/091982
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/092182
; PRIOR FILING DATE: 1998-07-09

Query Match 95.0%; Score 227; DB 9; Length 422;
Best Local Similarity 99.2%; Pred. No. 5.3e-67;
Matches 238; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

QY 1 GCCCAGCGGACTTGAGTGTCTCTCGCATCCCGAGAGCGCAGTGGCCACTATGCGGCTG 60
Db 8 GCCCAGCGGACTTGAGTGTCTCTCGCATCCCGAGAGCGCAGTGGCCACTATGCGGCTG 67
QY 61 GCCTGCGCCCTTGCTCTCTCTTGAGCCTCCTTGCGAGCTCACATGGAAGGCGCGGTA 120
Db 68 GCCTGCGCGTGTCTCTCTCTTGACCTCGTTGCGAGCTCACATGGAAGGCGCGGTA 127
QY 121 TGACCTTTGCACTGAGCTGAGGAGTCTTTTCTGACAAATGCTCCTATGAGTCACT 180
Db 128 TGACCTTTGCACTGAGCTGAGGAGTCTTTTCTGACAAATGCTCCTATGAGTCACT 187
QY 181 TCCTGGAATTGCTTGAAAA-NCTGCGCTCCTCCTCCTCCTCAGGACCGCGTCA 239
Db 188 TGCTGGAATTGCTTGAAAAAGGTCTGCTCGTCTCCTCCTCCTCAGGACCGCGTCA 247

RESULT 13
US-09-997-653-362
; Sequence 362, Application US/09997653
; Publication No. US20030008297A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerlitsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James

APPLICANT: Paoni,Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2730PIC38
CURRENT APPLICATION NUMBER: US/09/997,653
CURRENT FILING DATE: 2001-11-15
PRIOR APPLICATION NUMBER: 60/043787
PRIOR FILING DATE: 1997-06-16
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
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PRIOR FILING DATE: 1997-11-12
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; PRIOR FILING DATE: 1998-06-25
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; PRIOR APPLICATION NUMBER: 60/092182
; PRIOR FILING DATE: 1998-07-09
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Query Match          95.0%; Score 227; DB 9; Length 422;
Best Local Similarity 99.2%; Pred. No. 5.3e-67;
Matches 238; Conservative 0; Mismatches 1; Indels 1; Gaps 1;
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QY 1 GGCACCGGAGCTTCAGTGTCTCTCCATCCAGGAGCGAGTGGCCACTATGGGGTCTG 60
Db 8 GGCACCGGAGCTTCAGTGTCTCTCCATCCAGGAGCGAGTGGCCACTATGGGGTCTG 67

QY 61 GGCTGCCCTTGTCTCTCTCTTGACCTCTTGCCAGCTCACATGGAACAGGCGCGGTA 120
Db 68 GGCTGCCCTTGTCTCTCTCTTGACCTCTTGCCAGCTCACATGGAACAGGCGCGGTA 127

QY 121 TGACTTTGCAACTGAAGCTGAAGAGTCTTTCTGACAAATTCCTCTATGAGTCCAGCT 180
Db 128 TGACTTTGCAACTGAAGCTGAAGAGTCTTTCTGACAAATTCCTCTATGAGTCCAGCT 187

QY 181 TCCTGGAATGCTTGAAA-NTCTGCTCTCTCTCCATCTCCCTTCAGGACCGCGTCA 239
Db 188 TCCTGGAATGCTTGAAAAGCTCTGCTCTCTCTCCATCTCCCTTCAGGACCGCGTCA 247
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RESULT 14

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US-10-174-590-241
; Sequence 241, Application US/10174590
; Publication No. US20030008352A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Chen, Jian
; APPLICANT: Desnoyers, Luc
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Smith, Victoria
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
```

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; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3430R1C42
; CURRENT APPLICATION NUMBER: US/10/174,590
; CURRENT FILING DATE: 2002-06-18
; Prior application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 241
; LENGTH: 422
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-174-590-241
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Query Match          95.0%; Score 227; DB 9; Length 422;
Best Local Similarity 99.2%; Pred. No. 5.3e-67;
Matches 238; Conservative 0; Mismatches 1; Indels 1; Gaps 1;
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QY 1 GGCACCGGAGCTTCAGTGTCTCTCCATCCAGGAGCGAGTGGCCACTATGGGGTCTG 60
Db 8 GGCACCGGAGCTTCAGTGTCTCTCCATCCAGGAGCGAGTGGCCACTATGGGGTCTG 67

QY 61 GGCTGCCCTTGTCTCTCTCTTGACCTCTTGCCAGCTCACATGGAACAGGCGCGGTA 120
Db 68 GGCTGCCCTTGTCTCTCTCTTGACCTCTTGCCAGCTCACATGGAACAGGCGCGGTA 127

QY 121 TGACTTTGCAACTGAAGCTGAAGAGTCTTTCTGACAAATTCCTCTATGAGTCCAGCT 180
Db 128 TGACTTTGCAACTGAAGCTGAAGAGTCTTTCTGACAAATTCCTCTATGAGTCCAGCT 187

QY 181 TCCTGGAATGCTTGAAA-NTCTGCTCTCTCTCCATCTCCCTTCAGGACCGCGTCA 239
Db 188 TCCTGGAATGCTTGAAAAGCTCTGCTCTCTCTCCATCTCCCTTCAGGACCGCGTCA 247
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RESULT 15

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US-10-176-758-241
; Sequence 241, Application US/10176758
; Publication No. US20030008353A1
; GENERAL INFORMATION:
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; APPLICANT: Baker, Kevin P.
; APPLICANT: Chen, Jian
; APPLICANT: Desnoyers, Luc
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Smith, Victoria
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
```

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; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3430R1C104
; CURRENT APPLICATION NUMBER: US/10/176,758
; CURRENT FILING DATE: 2002-06-21
; Prior application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 241
; LENGTH: 422
; TYPE: DNA
; ORGANISM: Homo Sapien
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US-10-176-758-241

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Query Match          95.0%; Score 227; DB 9; Length 422;
Best Local Similarity 99.2%; Pred. No. 5.3e-67;
Matches 238; Conservative 0; Mismatches 1; Indels 1; Gaps 1;
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QY 1 GGCACCGGAGCTTCAGTGTCTCTCCATCCAGGAGCGAGTGGCCACTATGGGGTCTG 60
Db 8 GGCACCGGAGCTTCAGTGTCTCTCCATCCAGGAGCGAGTGGCCACTATGGGGTCTG 67

QY 61 GGCTGCCCTTGTCTCTCTCTTGACCTCTTGCCAGCTCACATGGAACAGGCGCGGTA 120
Db 68 GGCTGCCCTTGTCTCTCTCTTGACCTCTTGCCAGCTCACATGGAACAGGCGCGGTA 127
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Db 68 GGCTGCCCTTGTCTCCTCTTGACCCCTCTGGCAGCTCACATGGAACAGGGCGGGTA 127
Qy 121 TGACTTTGCACTGAAGCTGAAGGAGTCTTTCTGACAAATTCCTCTATGAGTCCAGCT 180
Db 128 TGACTTTGCACTGAAGCTGAAGGAGTCTTTCTGACAAATTCCTCTATGAGTCCAGCT 187
Qy 181 TCCTGGAAATGCTTGA AAA - NTCTGCTCTCTCTCCATCTCCCTTCAGGSAACAGCGTCA 239
Db 188 TCCTGGAAATGCTTGA AAAAGCTGTGCTCTCTCTCCATCTCCCTTCAGGSAACAGCGTCA 247

Search completed: May 1, 2003, 05:17:08
Job time : 68.2211 secs

GenCore version 5.1.5
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OM nucleic - nucleic search, using sw model

Run on: May 1, 2003, 03:53:25 ; Search time 43.356 Seconds
(without alignments)
1690.556 Million cell updates/sec

Title: US-09-092-296-1

Perfect score: 239

Sequence: 1 GCCACCGGAGCTTCAGTCT.....CCCTTCAGGACGACGCTCA 239

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 441362 seqs, 153338381 residues

Total number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued_Patents_NA.*

- 1: /cgn2_6ptodata/2/ina/5A_COMB.seq.*
- 2: /cgn2_6ptodata/2/ina/5B_COMB.seq.*
- 3: /cgn2_6ptodata/2/ina/6A_COMB.seq.*
- 4: /cgn2_6ptodata/2/ina/6B_COMB.seq.*
- 5: /cgn2_6ptodata/2/ina/PCTUS_COMB.seq.*
- 6: /cgn2_6ptodata/2/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Length	ID	Description
1	31	13.0	3509	2	US-08-817-436A-1
C 2	30.8	12.9	16063	4	US-09-801-052-3
C 3	30.4	12.7	580	2	US-08-627-610-7
C 4	30.4	12.7	580	3	US-08-581-918A-7
C 5	30.4	12.7	580	4	US-08-346-147B-7
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C 8	30.4	12.7	580	5	PCT-US95-04636-7
C 9	30.4	12.7	1515	4	US-08-928-383B-25
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13	29.4	12.3	1091	4	US-09-219-194-2
C 14	29.2	12.2	3941	4	US-09-408-865-2
C 15	29	12.1	1157	1	US-07-709-949-1
C 16	29	12.1	1316	4	US-09-056-105-24
C 17	29	12.1	2095	1	US-08-405-230-8
C 18	29	12.1	2095	2	US-08-910-990-8
C 19	29	12.1	2259	6	5185254-3
C 20	29	12.1	2564	3	US-08-276-968A-19
C 21	28.8	12.1	1785	3	US-08-729-416C-8
C 22	28.2	11.8	3218	4	US-09-369-364A-6
C 23	27.8	11.6	1396	4	US-09-328-174A-2
C 24	27.8	11.6	2870	4	US-09-221-017B-850
C 25	27.8	11.6	8396	4	US-09-328-174A-1
C 26	27.8	11.6	8409	4	US-09-167-681-37
C 27	27.6	11.5	956	4	US-09-641-638-36

ALIGNMENTS

RESULT 1

US-08-817-436A-1

; Sequence 1, Application US/08817436A

; Patent No. 5882880

; GENERAL INFORMATION:

; APPLICANT: Canaani, Dan

; TITLE OF INVENTION: Human Checkpoint Gene and Gene for

; TITLE OF INVENTION: Antisense RNA thereof

; NUMBER OF SEQUENCES: 3

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Wiman, Cohen, Leitner & Myers

; STREET: 900 17th Street, N.W., Suite 1000

; CITY: Washington

; STATE: D.C.

; COUNTRY: U.S.

; ZIP: 20006

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette 3.5 inch, 1.44Mb storage

; COMPUTER: IBM compatible

; OPERATING SYSTEM: DOS

; SOFTWARE: ASCII

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/817,436A

; FILING DATE: 11-JUN-1997

; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: PCT/US95/12445

; FILING DATE: 11-OCT-1995

; ATTORNEY/AGENT INFORMATION:

; NAME: Cohen, Herbert

; REGISTRATION NUMBER: 25,109

; REFERENCE/DOCKET NUMBER: 0744.066

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 202-463-7700

; TELEFAX: 202-463-6915

; INFORMATION FOR SEQ ID NO: 1:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 3509 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: cDNA to mRNA

; HYPOTHETICAL: NO

; ANTI-SENSE: NO

; ORIGINAL SOURCE:

; ORGANISM: Homo sapiens

; CELL LINE: ESTABLISHED XERODERMA PIGMENTOSUM GM2096-SV3

; IMMEDIATE SOURCE:

; CLONE: RAP-1 cDNA

US-08-817-436A-1

Sequence 37, Appl
Sequence 38, Appl
Sequence 39, Appl
Sequence 628, App
Sequence 4, Appl
Sequence 1, Appl
Sequence 1, Appl
Sequence 40, Appl
Sequence 3, Appl
Sequence 1, Appl
Sequence 12, Appl
Sequence 651, App
Sequence 16, Appl
Sequence 17, Appl
Sequence 9, Appl
Sequence 9, Appl
Sequence 3, Appl
Sequence 2, Appl

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/ GENERAL INFORMATION: Beach, David H.
/
/ APPLICANT: Serrano, Manuel
/ APPLICANT: Depinho, Ronald A.
/
/ TITLE OF INVENTION: Transgenic Animals Having Modified Cell-Cycle
/
/ TITLE OF INVENTION: Regulation
/
/ NUMBER OF SEQUENCES: 13
/
/ CORRESPONDENCE ADDRESS:
/ ADDRESSSEE: LAHIVE & COCKFIELD
/ STREET: 60 State Street
/ CITY: Boston
/ STATE: MA
/ COUNTRY: USA
/
/ ZIP: 02109
/
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS

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; FILING DATE: 14-SEP-1994
; PRIOR APPLICATION DATA: US 08/306,511
; APPLICATION NUMBER: US 08/248,812
; FILING DATE: 25-MAY-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/227,371
; FILING DATE: 14-APR-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/154,915
; FILING DATE: 18-NOV-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/991,997
; FILING DATE: 17-DEC-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Vincent, Matthew P.
; REGISTRATION NUMBER: 36,709
; REFERENCE/DOCKET NUMBER: MIV-071.06
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 832-1299
; TELEFAX: (617) 832-7000
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 580 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 91..480
; US-08-581-918A-7

Query Match 12.7%; Score 30.4; DB 3; Length 580;
Best Local Similarity 57.3%; Pred. No. 0.8;
Matches 55; Conservative 0; Mismatches 41; Indels 0; Gaps 0;

QY 39 GCAGTGGCCACTATGGGCTGTGGGCTGCGCCCTTGTCTCTTGACCTCTCTTGGCAGC 98
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Db 128 GCGTGTGGCCAGGCGCGCTCACTGCTGCGGCCCAACATGCGCCTGTGCCCGTCTGTGGC 69
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY 99 TCACATGGAACAGCGCGGGGTATGACTTTGGCAACTG 134
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Db 68 AGAATGGTCTTCGCGCGCGGTGAGATTGCTACAG 33

RESULT 5
US-08-346-147B-7/c
; Sequence 7, Application US/08346147B
; Patent No. 6211334
; GENERAL INFORMATION:
; APPLICANT: Beach, David H.
; APPLICANT: Demetrick, Douglas J.
; APPLICANT: Serrano, Manuel
; APPLICANT: Hannon, Gregory J.
; TITLE OF INVENTION: Cell-Cycle Regulatory Proteins, and Uses
; TITLE OF INVENTION: Related Thereto
; NUMBER OF SEQUENCES: 47
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley, Hoag & Eliot
; STREET: One Post Office Square
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WordPad
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/346,147B
; FILING DATE: 29-NOV-1994
; CLASSIFICATION: 514

; FILING DATE: 14-SEP-1994
; PRIOR APPLICATION DATA: US 08/248,812
; APPLICATION NUMBER: US 08/227,371
; FILING DATE: 14-APR-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/154,915
; FILING DATE: 18-NOV-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/991,997
; FILING DATE: 17-DEC-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Vincent, Matthew P.
; REGISTRATION NUMBER: 36,709
; REFERENCE/DOCKET NUMBER: MIV-071.06
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 832-1299
; TELEFAX: (617) 832-7000
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 580 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 91..480
; US-08-581-918A-7

Query Match 12.7%; Score 30.4; DB 4; Length 580;
Best Local Similarity 57.3%; Pred. No. 0.8;
Matches 55; Conservative 0; Mismatches 41; Indels 0; Gaps 0;

QY 39 GCAGTGGCCACTATGGGCTGTGGGCTGCGCCCTTGTCTCTTGACCTCTCTTGGCAGC 98
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 128 GCGTGTGGCCAGGCGCGCTCACTGCTGCGGCCCAACATGCGCCTGTGCCCGTCTGTGGC 69
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY 99 TCACATGGAACAGCGCGGGGTATGACTTTGGCAACTG 134
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Db 68 AGAATGGTCTTCGCGCGCGGTGAGATTGCTACAG 33

RESULT 6
US-08-822-936-7/c
; Sequence 7, Application US/08822936
; Patent No. 6242575
; GENERAL INFORMATION:
; APPLICANT: Massegue, Joan
; APPLICANT: Roberts, James M.
; APPLICANT: Koff, Andrew
; APPLICANT: Polyak, Kornelia
; TITLE OF INVENTION: Isolated P27 Protein, Nucleic Acid
; TITLE OF INVENTION: Molecules Encoding Same, Methods of Identifying Agents Acti
; TITLE OF INVENTION: and Uses of Said Agents
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley, Hoag & Eliot, LLP
; STREET: One Post Office Square
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02109-2170
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
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; APPLICATION NUMBER: US/08/822,936
; FILING DATE: 21-FEBRUARY-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Vincent, Matthew P.
; REGISTRATION NUMBER: 36,709
; REFERENCE/DOCKET NUMBER: MIV-079.05
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 832-1000
; TELEFAX: (617) 832-7000
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 580 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 91..480
US-08-822-936-7

Query Match 12.7%; Score 30.4; DB 4; Length 580;
Best Local Similarity 57.3%; Pred. No. 0.8;
Matches 55; Conservative 0; Mismatches 41; Indels 0; Gaps 0;

QY 39 CGACTGGCCACTATGGGGTCTGGGCTGCCCCCTTGTCTCTCTTGACCTCTCTTGCGCAGC 98
Db 128 CGGTGGCCAGCCCGCGGTCTACTGCTGCGGCCCAACATGCCCTTGTCCCCGGTCTGTGGC 69

QY 99 TCACATGGGAACAGCCGCCGGTATGACTTTGCAACTG 134
Db 68 AGAAATGGTCTTCGCGCGCGGTGAGATTGCTACAG 33

RESULT 7
US-08-497-214D-7/C
; Sequence 7, Application US/08497214D
; Patent No. 6331390
; GENERAL INFORMATION:
; APPLICANT: Beach, David H.
; APPLICANT: Demetrick, Douglas J.
; APPLICANT: Serrano, Manuel
; APPLICANT: Hannon, Gregory J.
; TITLE OF INVENTION: Cell-Cycle Regulatory Proteins, and Uses
; TITLE OF INVENTION: Related Thereto
; NUMBER OF SEQUENCES: 47
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley, Hoag & Eliot
; STREET: One Post Office Square
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WordPad
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/497,214D
; FILING DATE: 30-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/346,147
; FILING DATE: 29-NOV-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/305,511
; FILING DATE: 14-SEP-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/248,812
; FILING DATE: 25-MAY-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/227,371

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OM nucleic - nucleic search, using sw model

Run on: May 1, 2003, 03:08:45 ; Search time 1196.9 Seconds
(without alignments)
3233.964 Million cell updates/sec

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Scoring table: IDENTITY_NUC
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Searched: 16154066 seqs, 8097743376 residues

Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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 - 24: em_gss_mus:*
 - 25: em_gss_other:*
 - 26: em_gss_pro:*
 - 27: em_gss_rod:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
c 1	225.4	94.3	449	10 AW293443	AW293443 UI-H-Bi2-
c 2	225.4	94.3	830	13 B1759796	B1759796 603045679
c 3	220	92.1	456	12 BG506690	BG506690 601861290
c 4	219	91.6	422	12 BF002050	BF002050 7498c11.x
c 5	137.6	57.6	865	13 B1820110	B1820110 603037110
c 6	137.2	57.4	895	13 B1820029	B1820029 603037210

c 7	118	49.4	404	9 AI857998	AI857998 wj69b01.x
c 8	95.8	40.1	521	10 BB533837	BB533837 BB533837
c 9	95.8	40.1	522	10 BB664284	BB664284 BB664284
c 10	94	39.3	361	12 BF521842	BF521842 UI-R-C2p-
c 11	74.4	31.1	552	17 AQ718761	AQ718761 HS_551_B
c 12	63.6	26.6	328	9 AI136523	AI136523 UI-R-C2p-
c 13	44.6	18.7	506	17 AZ241329	AZ241329 RPCI-23-7
c 14	44.6	18.7	633	17 AZ079350	AZ079350 RPCI-23-4
c 15	36	15.1	754	12 BG686317	BG686317 602638230
c 16	36	15.1	1020	13 BG686317	BG686317 602638230
c 17	35.6	14.9	509	17 AQ838514	AQ838514 HS_5011_A
c 18	35.6	14.9	1019	13 BM474221	BM474221 AGENCCOURT
c 19	35	14.6	348	14 F06958	F06958 HSC10C101 n
c 20	34.6	14.5	261	10 BB411111	BB411111 BB411111
c 21	34.4	14.4	238	9 AA376266	AA376266 EST88915
c 22	34.4	14.4	264	14 BQ377407	BQ377407 IL5-UM007
c 23	34.4	14.4	412	9 AA769782	AA769782 ah71b05.s
c 24	34.4	14.4	458	9 AI632159	AI632159 LS85el2.x
c 25	34.4	14.4	470	9 AI803529	AI803529 tc42h11.x
c 26	34.4	14.4	516	10 BE613876	BE613876 601504191
c 27	34.4	14.4	543	10 AW851149	AW851149 IL3-CY022
c 28	34.4	14.4	753	13 B1911665	B1911665 603064838
c 29	34.4	14.4	783	10 BE563718	BE563718 601333355
c 30	34.4	14.4	785	13 B1193645	B1193645 602946554
c 31	34.4	14.4	788	12 BG762871	BG762871 602735108
c 32	34.4	14.4	828	12 BG768039	BG768039 602743815
c 33	34.4	14.4	837	13 BM449774	BM449774 AGENCCOURT
c 34	34.4	14.4	871	14 BQ956320	BQ956320 AGENCCOURT
c 35	34.4	14.4	931	12 BF689789	BF689789 602186518
c 36	34.4	14.4	954	14 BQ220846	BQ220846 AGENCCOURT
c 37	34.4	14.4	959	14 BQ940113	BQ940113 AGENCCOURT
c 38	34.4	14.4	999	9 AL551231	AL551231 AL551231
c 39	34.4	14.4	1013	14 BQ953477	BQ953477 AGENCCOURT
c 40	34.4	14.4	1061	14 BQ052186	BQ052186 AGENCCOURT
c 41	34.4	14.4	1129	13 BM464458	BM464458 AGENCCOURT
c 42	34.4	14.4	1138	13 BM564409	BM564409 AGENCCOURT
c 43	34.4	14.4	1232	14 BM911289	BM911289 AGENCCOURT
c 44	34	14.2	271	17 BH244391	BH244391 NYEB57TF
c 45	34	14.2	575	13 B1223412	B1223412 602943001

ALIGNMENTS

RESULT 1	AW293443/c	AW293443	449 bp	mRNA	linear	EST 16-JAN-2000
LOCUS	UI-H-Bi2-ahm-c-08-0-UI.s1	NCI_CGAP_Sub4	Homo sapiens	cdna	clone	
DEFINITION	IMAGE:2727182.3'	mRNA sequence.				
ACCESSION	AW293443					
VERSION	AW293443.1	GI:6700079				
KEYWORDS	EST.					
SOURCE	human.					
ORGANISM	Homo sapiens					
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.					
AUTHORS	1 (bases 1 to 449)					
TITLE	NCI-CGAP http://www.ncbi.nlm.nih.gov/hcicgap.					
JOURNAL	National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index					
COMMENT	Unpublished (1997) Contact: Robert Strausberg, Ph.D. Email: cgapbs-femail.nih.gov					

The sequence contained an oligo-dT track that was present in the oligonucleotide that was used to prime the synthesis of first strand cDNA and therefore this may represent a bonafide poly A tail. cDNA library Preparation: M.B. Soares Lab Clone Distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: www.bio.llnl.gov/bbrp/image/image.html
Seq primer: M13 Forward
POLYA=Yes.

Location/Qualifiers

source

```
1. .449
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:272182"
/clone_lib="NCI_CGAP_Sub4"
/lab_host="DH10B (Life Technologies)"
/note="Vector: pV73D-Pac (Pharmacia) with a modified
polylinker; Site_1: Not I; Site_2: Eco RI; The
NCI_CGAP_Sub4 library is a subtracted library derived from
the NCI_CGAP_Sub2 library which is a subtracted library
derived from the NCI_CGAP_Sub1 library, which is a
subtracted library derived from BI. BI constitutes a
mixture of 21 normalized or subtracted NCI_CGAP
libraries: NCI_CGAP_Co4, NCI_CGAP_Pr22, NCI_CGAP_Pr28,
NCI_CGAP_Co10, NCI_CGAP_Co16, NCI_CGAP_Kid5,
NCI_CGAP_Kid12, NCI_CGAP_Kid3, NCI_CGAP_Kid11,
NCI_CGAP_Lym2, NCI_CGAP_Br2, NCI_CGAP_Co8, NCI_CGAP_CLL1,
NCI_CGAP_Lei2, NCI_CGAP_Brn23, NCI_CGAP_Lu5,
NCI_CGAP_Lu24, NCI_CGAP_Lu19, NCI_CGAP_GC4, NCI_CGAP_GC6,
NCI_CGAP_Brn25. These 21 libraries were pooled and a
single-stranded DNA preparation of the resulting mixture
was used as a tracer in a subtractive hybridization with
a driver whose composition is detailed below:
NCI_CGAP_Kid3 pool 1 : LLAM 3334-3337, 3682-3683,
3798-3803 (IMAGE Clonoids 1322376-1323911,
1456008-1456775, 1500552-1502855) NCI_CGAP_Kid5 pool 1 :
LLAM 3338-3342, 3722-3725, 3776-3778 (IMAGE Clonoids
1323912-1325831, 1471368-1472903, 1492104-1493255)
NCI_CGAP_Lu5 pool 1 : LLAM 3575-3582, 3851-3854 (IMAGE
Clonoids 1414920-1417991, 1520904-1522439) NCI_CGAP_GC4
pool 1 : LLAM 3164-3167, 3716-3720, 3733-3735 (IMAGE
Clonoids 1257096-1258631, 1469064-1470983, 1475592-1476743
) NCI_CGAP_Pr22 pool 1 : LLAM 2457-2459, 2758-2759,
3062-3068 (IMAGE Clonoids 985608-986759, 1101192-1101959,
1217928-1220615) NCI_CGAP_Co10 pool 1 : LLAM 2644-2653,
2871-2872 (IMAGE Clonoids 1057416-1061255, 1144584-1145351)
] Subtraction was performed as previously described
[Bonaldo, Lennon & Soares (1996): Normalization and
Subtraction: Two Approaches To Facilitate Gene Discovery.
Genome Research 6, 791-806.]
TAG_LIB=NCI_CGAP_Co4
TAG_ISSUE=colon
TAG_SEQ=CTTCG"
```

BASE COUNT 104 a 108 c 134 g 103 t

Query Match 94.3%; Score 225.4; DB 10; Length 449;
Best Local Similarity 98.8%; Pred. No. 4.3e-54;
Matches 237; Conservative 0; Mismatches 2; Indels 1; Gaps 1;

QY 1 GGCCACGGGACTTCAGTGTCTCTCCATCCAGAGCGCAGTGGCCACTATGGGGTCTG 60
|||||
Db 437 GGCCACGGGACTTCAGTGTCTCTCCATCCAGAGCGCAGTGGCCACTATGGGGTCTG 378
|||||

QY 61 GGCTGCCCTTGTCTCTCTTGGACCTCTTGGCAGCTCACATGACAGCGCGGGTA 120
|||||

Db 377 GGCTGCCCTTGTCTCTCTTGGACCTCTTGGCAGCTCACATGACAGCGCGGGTA 318
|||||

QY 121 TGACTTTGCAACTGAAGCTGAAGAGTCTTTTCTGACAAATTCCTCTATGAGTCCAGCT 180
|||||

Db 317 TGACTTTGCAACTGAAGCTGAAGAGTCTTTTCTGACAAATTCCTCTATGAGTCCAGCT 258
|||||

QY 181 TCCTGGAATTCCTGAAA-NCTCGCTCCCTCCATCTCCCTTCAGGACCGAGCTCA 239
|||||

Db 257 TCCTGGAATTCCTGAAAAGCTCTGCCTCTCTCCATCTCCCTTCAGGACCGAGCTCA 198
|||||

RESULT 2
BI759796 830 bp mRNA linear EST 25-SEP-2001
LOCUS 603045679f1 NIH_MGC_116 Homo sapiens cDNA clone IMAGE:5186107 5',
DEFINITION mRNA sequence.
ACCESSION BI759796

VERSION
KEYWORDS
SOURCE
ORGANISM

BI759796.1 GI:15751374
EST.
human.

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NIH-MGC http://mgc.nci.nih.gov/.
1 (bases 1 to 830)
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: c9pbbs-r@mail.nih.gov
Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM11464 Row: m Column: 20
High quality sequence stop: 432.
Location/Qualifiers
1. .830
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:5186107"
/clone_lib="NIH_MGC_116"
/lab_host="DH10B"
/note="Organ: pooled colon, kidney, stomach; Vector:
PCMV-SPORT6; Site_1: NotI; Site_2: EcoRV (destroyed); RNA
source anonymous pool of 3 colons, age 26 yo male, 49 yo
female, 71 yo male colon; 46 yo male kidney, and pool of 2
stomachs, 62 yo male and 70 yo female. Library is
oligo-dr primed and directionally cloned (EcoRV site is
destroyed upon cloning). Average insert size 1.4 kb,
insert size range 1-3 kb. Library is normalized and
enriched for full-length clones and was constructed by C.
Gruber (Invitrogen). Research Genetics tracking code
023. Note: this is a NIH_MGC Library."

FEATURES
source

BASE COUNT 175 a 276 c 210 g 168 t
ORIGIN
Query Match 94.3%; Score 225.4; DB 13; Length 830;
Best Local Similarity 98.8%; Pred. No. 5.5e-54;
Matches 237; Conservative 0; Mismatches 2; Indels 1; Gaps 1;

QY 1 GGCCACGGGACTTCAGTGTCTCTCCATCCAGAGCGCAGTGGCCACTATGGGGTCTG 60
|||||
Db 31 GGCCACGGGACTTCAGTGTCTCTCCATCCAGAGCGCAGTGGCCACTATGGGGTCTG 90
|||||

QY 61 GGCTGCCCTTGTCTCTCTTGGACCTCTTGGCAGCTCACATGACAGCGCGGGTA 120
|||||

Db 91 GGCTGCCCTTGTCTCTCTTGGACCTCTTGGCAGCTCACATGACAGCGCGGGTA 150
|||||

QY 121 TGACTTTGCAACTGAAGCTGAAGAGTCTTTTCTGACAAATTCCTCTATGAGTCCAGCT 180
|||||

Db 151 TGACTTTGCAACTGAAGCTGAAGAGTCTTTTCTGACAAATTCCTCTATGAGTCCAGCT 210
|||||

QY 181 TCCTGGAATTCCTGAAA-NCTCGCTCCCTCCATCTCCCTTCAGGACCGAGCTCA 239
|||||

Db 211 TCCTGGAATTCCTGAAAAGCTCTGCCTCTCTCCATCTCCCTTCAGGACCGAGCTCA 270
|||||

RESULT 3
BI7506690
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

BI7506690 456 bp mRNA linear EST 27-MAR-2001
LOCUS 601861290f1 NIH_MGC_77 Homo sapiens cDNA clone IMAGE:4070759 5',
DEFINITION mRNA sequence.
ACCESSION BG506890
VERSION BG506890
KEYWORDS BG506890.1 GI:13468207
EST.
human.
SOURCE Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

NIH-MGC http://mgc.nci.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov

Tissue Procurement: Clontech Laboratories, Inc.
CDNA Library Preparation: Clontech Laboratories, Inc.

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov

Plate: LCM915 row: d column: 24

High quality sequence stop: 401.

FEATURES
source

Location/Qualifiers

1..456

/organism="Homo sapiens"

/db_xref="taxon:9606"

/clone="IMAGE:4070759"

/clone_lib="NIH_MGC_77"

/lab_host="DH10B (T1 phage-resistant)"

/note="Organ: lung; Vector: pBMR-LIB (Clontech); Site:1:

SfiI (ggcgctcgcc); Site_2: SfiI (ggcgctcgcc); 5' and

3' adaptors were used in cloning as follows: 5' adaptor

sequence: 5'-CACGCCATTATGCC-3' and 3' adaptor sequence:

5'-ATTTCAGAGCGGCGGCGGCATG-dt(30)BN-3' (where B = A,

C, or G and N = A, C, G, or T). Average insert size 1.9

kb (range 0.5-4.0 kb). 12/15 colonies contained inserts

by PCR. This library was enriched for full-length clones

and was constructed by Clontech Laboratories (Palo Alto,

CA). Note: this is a NIH-MGC Library."

BASE COUNT 109 a 137 c 106 g 103 t 1 others

Query Match 92.1%; Score 220; DB 12; Length 456;

Best Local Similarity 99.1%; Pred. No. 1.5e-52;

Matches 231; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

QY 8 GGGACTTCAGTCTCTCCATCCAGGAGCGCAGTGGCCACTATGGGTCTGGCTGCC 67

Db 2 GGGACTTCAGTCTCTCCATCCAGGAGCGCAGTGGCCACTATGGGTCTGGCTGCC 61

QY 68 CTTTGTCTCTTGTGACCTCTTTGCGAGCTCAGATGGACAGCGCGGGTATGACTTT 127

Db 62 CTTTGTCTCTTGTGACCTCTTTGCGAGCTCAGATGGACAGCGCGGGTATGACTTT 121

QY 128 GCAACTGAAGCTGAAGGAGTCTTTCTGACAAATTCCTCTATGAGTCCAGCTTCTCTGGA 187

Db 122 GCAACTGAAGCTGAAGGAGTCTTTCTGACAAATTCCTCTATGAGTCCAGCTTCTCTGGA 181

QY 188 ATTGCTTGAANA-NCTGCTCTCTCTCCATCTCCCTTCAGGAGCAGCGTCA 239

Db 182 ATTGCTTGAANAAGCTCTGCTCTCTCTCCATCTCCCTTCAGGAGCAGCGTCA 234

RESULT 4
BF002050/C

LOCUS

DEFINITION

7998cl1.xl NCI_CGAP_Col6 Homo sapiens cdna clone IMAGE:3314516 3',

mrna sequence.

ACCESSION

BF002050

VERSION

BF002050.1

GI:10702325

KEYWORDS

EST.

SOURCE

human.

ORGANISM

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

REFERENCE

1 (bases 1 to 422)

NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

National Cancer Institute, Cancer Genome Anatomy Project (CGAP).

JOURNAL
COMMENT

Tumor Gene Index
Unpublished (1997)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: Ilan Kirsch, M.D., Michael R. Emmert-Buck, M.D., Ph.D.

CDNA Library Preparation: M. Bento Soares, Ph.D.

CDNA Library Arrayed by: Greg Lennon, Ph.D.

DNA Sequencing by: Washington University Genome Sequencing Center

Clone distribution: NCI-CGAP clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL, send email to:

info@image.llnl.gov

Seq primer: -400p from Gibco.

Location/Qualifiers

1..422

/organism="Homo sapiens"

/db_xref="taxon:9606"

/clone="IMAGE:3314516"

/clone_lib="NCI_CGAP_Col6"

/tissue_type="colon tumor, RER+"

/lab_host="DH10B"

/note="Organ: colon; Vector: pT7T3D-Pac (Pharmacia) with a

modified polylinker; Site_1: Not I; Site_2: Eco RI;

Plasmid DNA from the normalized library NCI_CGAP_Col6 was

prepared, and ss circles were made in vitro. Following HAP

purification, this DNA was used as tracer in a subtractive

hybridization reaction. The driver was PCR-amplified cDNAs

from a pool of 5,000 clones made from the same library

(cloneIDs 1057416-1061255, and 1144584-1145351).

Subtraction by Bento Soares and M. Fatima Bonaldo. "

BASE COUNT 102 a 99 c 130 g 88 t 3 others

ORIGIN

Query Match 91.6%; Score 219; DB 12; Length 422;

Best Local Similarity 98.3%; Pred. No. 2.9e-52;

Matches 232; Conservative 0; Mismatches 2; Indels 2; Gaps 1;

QY 6 CCGGGACTTCAGTCTCTCCATCCAGGAGCGCAGTGGCCACTATGGGTCTGGGCTG 65

Db 422 CCGGGANTTTCAGTCTCTCCATCCAGGAGCGCAGTGGCCACTATGGGTCTGGGCTG 363

QY 66 CCCCTTGTCTCTCTTGCACCTCTTGCACCTCAGTGCATGGACAGCGCGGGTATGACT 125

Db 362 CCCCTTGTCTCTCTTGCACCTCTTGCACCTCAGTGCATGGACAGCGCGGGTATGACT 303

QY 126 TTGCAACTGAAGCTGAAGGAGTCTTTTCTGACAAATTCCTCTATGAGTCCAGCTTCTG 185

Db 302 TTGCAACTGAAGCTGAAGGAGTCTTTTCTGACAAATTCCTCTATGAGTCCAGCTTCTG 243

QY 186 GAATGCTTGAANA-NCTGCTCTCTCTCCATCTCCCTTCAGGAGCAGCGTCA 239

Db 242 GAATGCTTGAANAAGNTGCTCTCTCTCCATCTCCCTTCAGGAGCAGCGTCA 187

RESULT 5
BF020110

LOCUS

DEFINITION

603037110F1 NIH_MGC_115 Homo sapiens cdna clone IMAGE:5178170 5',

mrna sequence.

ACCESSION

BF020110

VERSION

BF020110.1

GI:15931660

KEYWORDS

EST.

SOURCE

human.

ORGANISM

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

REFERENCE

1 (bases 1 to 865)

NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: Life Technologies, Inc.

LOCUS BB664284 522 bp mRNA linear EST 26-OCT-2001
 DEFINITION BB664284 RIKEN full-length enriched, 0 day neonate lung Mus
 musculus cDNA clone E030032D13 5', mRNA sequence.
 ACCESSION BB664284
 VERSION BB664284.1 GI:16498038
 KEYWORDS EST.
 SOURCE house mouse.
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 522)
 Arakawa, T., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A.,
 Hiramoto, K., Hori, F., Ishii, Y., Ito, M., Kawai, J., Konno, H., Kouda
 M., Koya, S., Matsuyama, I., Miyazaki, A., Nomura, K., Ono, M.,
 Okazaki, F., Okido, I., Saito, K., Sakai, C., Sakai, K., Sano, H., Sasaki
 D., Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Suzuki, H.,
 Tagami, M., Tagawa, A., Takahashi, F., Takeda, Y., Tanaka, T., Toya, T.,
 Muramatsu, M. and Hayashizaki, Y.
 RIKEN Mouse ESTs (Arakawa, T., et al. 2001)
 UNPUBLISHED (2001)
 Contact: Yoshihide Hayashizaki
 Laboratory for Genome Exploration Research Group, RIKEN Genomic
 Sciences Center (GSC), Yokohama Institute
 The Institute of Physical and Chemical Research (RIKEN)
 1-7-22 Suenro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
 Tel: 81-45-503-9222
 Fax: 81-45-503-9216
 Email: genome-res@gsr.riken.go.jp,
 URL: http://genome.gsc.riken.go.jp/
 Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh
 M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.
 Normalization and subtraction of cap-trapper-selected cDNAs to
 prepare full-length cDNA libraries for rapid discovery of new
 genes. Genome Res. 10 (10), 1617-1630 (2000)
 wagi, K., Fujiwara, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E.,
 Watahiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsumura
 S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and
 Hayashizaki, Y.
 RIKEN integrated sequence analysis (RISA) system--384-format
 sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10
 (11), 1757-1771 (2000)
 Konno, H., Fukunishi, Y., Shibata, K., Itoh, M., Carninci, P., Sugahara
 Y. and Hayashizaki, Y.
 Computer-based methods for the mouse full-length cDNA
 encyclopedia: real-time sequence clustering for construction of a
 nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)
 Kondo, S., Shinagawa, A., Saito, T., Kiyosawa, H., Yamanaka, I., Aizawa
 K., Fukuda, S., Hara, A., Itoh, M., Kawai, J., Shibata, K. and
 Hayashizaki, Y.
 Computational Analysis of Full-length Mouse cDNAs Compared with
 Human Genome Sequences. Mamm. Genome. 12, 673-677 (2001)
 Please visit our web site (http://genome.gsc.riken.go.jp) for
 further details.
 e mouse tissues.
 Location/Qualifiers
 1..522
 /organism="Mus musculus"
 /db_xref="taxon:10090"
 /clone="E030032D13"
 /clone_lib="RIKEN full-length enriched, 0 day neonate
 lung"
 /tissue_type="lung"
 /dev_stage="0 day neonate"
 /lab_host="DH10B"
 /note="Site 1: SalI; Site 2: BamHI; cDNA library was
 prepared and sequenced in Mouse Genome Encyclopedia
 Project of Genome Exploration Research Group in Riken
 Genomic Sciences Center and Genome Science Laboratory in
 RIKEN. Division of Experimental Animal Research in Riken
 contributed to prepare mouse tissues. 1st strand cDNA was
 primed with a primer [5'
 GAGAGAGAGAGCGCGCACTCGAGTTTCTTTTCTTTT 3']. cDNA was
 prepared by using trehalose thermo-activated reverse

transcriptase and subsequently enriched for full-length by
 cap-trapper. Second strand cDNA was prepared with the
 primer adapter of sequence [5'
 GAGAGAGATTTCGATTAAATTAATTAATCCCCCCCCCC 3']. cDNA
 was cleaved with BamHI and XhoI. Vector: a modified
 pluescript KS(+) after bulk excision from Lambda FLIC I."
 BASE COUNT 132 a 151 c 125 g 114 t
 ORIGIN

Query Match 40.1%; Score 95.8; DB 10; Length 522;
 Best Local Similarity 72.6%; Pred. No. 5.8e-17;
 Matches 151; Conservative 0; Mismatches 53; Indels 4; Gaps 2;
 QY 33 AGGAGCGCAGTGGCCACTACTGGGCTCTGGGCTGCCCTCTGCTCTGACCTCTT 92
 Db 144 AGAGCTGGGTAGCCACCACTGGATCTTTGATGGCCTCTTCTCTCTGCGCTCTC 203
 QY 93 GCGAGCTCACATGGRACAGGCGGCTATGACTTTGCACTTGAAGCTGAAGGAGTCTTT 152
 Db 204 AGCAGCTCACAGC--CAGGCGCAAGGTGACTTTGCAGGTAAAGCTGACCGAGACTTTT 260
 QY 153 CTGACAAATTCCTCTATGAGTCCAGCTTCTCTGGAATTGCTTGAAGA-NFCTGCTCTC 211
 Db 261 CAGGACAAAGACCTCCCAAGACTCCAGTGTCTGTGACATGCTCCCAAGATGCTGCTCTC 320
 QY 212 CTCCATCTCCCTTCAGGACGAGGCTCA 239
 Db 321 CTCATCTGCATCAGGACCAATGTCA 348

RESULT 10
 BF521842
 LOCUS BF521842 361 bp mRNA linear EST 11-DEC-2000
 DEFINITION UI-R-C2p-nq-e-02-0-UI-r1 UI-R-C2p Rattus norvegicus cDNA clone
 UI-R-C2p-nq-e-02-0-UI 5', mRNA sequence.
 ACCESSION BF521842
 VERSION BF521842.1 GI:11629809
 KEYWORDS EST.
 SOURCE Norway rat.
 ORGANISM Rattus norvegicus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
 Rattus.

REFERENCE 1 (bases 1 to 361)
 AUTHORS Ronaldo, M.F., Lennon, G. and Soares, M.B.
 TITLE Normalization and subtraction: two approaches to facilitate gene
 discovery
 JOURNAL Genome Res. 6 (9), 791-806 (1996)
 MEDLINE 97044477
 COMMENT Contact: Soares, MB
 Program for Rat Gene Discovery and Mapping
 University of Iowa
 451 Eckstein Medical Research Building Iowa City, IA 52242, USA
 Tel: 319 335 8250
 Fax: 319 335 9565
 Email: msoares@blue.weeg.uiowa.edu

cDNA Library Preparation: M.B. Soares Lab Clone Distribution:
 clones will be available through Research Genetics (www.resgen.com)
 This clone is also available through the I.M.A.G.E. Consortium at
 LLNL (info@image.llnl.gov). IMAGE ID- 1792770
 Seq primer: M13 Forward.
 Location/Qualifiers
 1..361
 /organism="Rattus norvegicus"
 /strain="Sprague-Dawley"
 /db_xref="taxon:10116"
 /clone="UI-R-C2p-nq-e-02-0-UI"
 /clone_lib="UI-R-C2p"
 /dev_stage="adult"
 /lab_host="DH10B (Life Technologies)"
 /note="Vector: pMT3D-Pac (Pharmacia) with a modified
 polylinker; Site 1: Not I; Site 2: Eco RI; The UI-R-C2p
 library is a subtracted library derived from the UI-R-C1

FEATURES
 source

Plate: 438 row: H column: 19

Seq primer: T7

Class: BAC ends

Location/Qualifiers

1. .633
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone_lib="RPCI-23-438H19"
/clone="RPCI-23"
/sex="Female"
/lab_host="DH10B"
/note="Organ: Kidney/Brain; Vector: pBACe3.6; Site: 1;
EcoRI; Site: 2; EcoRI; Female C57BL/6J mouse kidney and/or
brain genomic DNA was isolated and partially digested
with a combination of EcoRI and EcoRI Methyase. Size
selected DNA was cloned into the pBACe3.6 vector at the
EcoRI sites. The ligation products were transformed into
DH10B electrocompetent cells (BRL Life Technologies)."

BASE COUNT 138 a 191 c 161 g 143 t
ORIGIN

Query Match 18.7%; Score 44.6; DB 17; Length 633;
Best Local Similarity 68.1%; Pred. No. 0.029;
Matches 62; Conservative 0; Mismatches 29; Indels 0; Gaps 0;

QY 109 CAGGCGGGTATGCTTGCACACTGAAGCTGAGGAGCTTTTCGACAAATTCCTCCT 168

Db 403 CAGGCGGCAAGGTGACTTTGAGGTAAAGCTACGAGACTTTTCAGGACAGACCTCCC 344

QY 169 ATGAGTCCAGCTCTCTGGAATGCTTGA AAA 199

Db 343 AGAACTCCAGTCTCTGGACATGCTCAAAA 313

RESULT 15

BG686317

LOCUS

DEFINITION 602638230F1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4765975 5',
mRNA sequence.

ACCESSION BG686317

VERSION 1

KEYWORDS EST

SOURCE human.

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 754)

NIH-MGC http://mgi.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-remail.nih.gov

Tissue Procurement: Louis M. Staudt, M.D., Ph.D.

cDNA Library Preparation: Ling Hong/Rubin Laboratory

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov

Plate: LLCM1625 row: 1 column: 08

High quality sequence stop: 750.

Location/Qualifiers

1. .754

FEATURES

source

/organism="Homo sapiens"

/db_xref="taxon:9606"

/clone="IMAGE:4765975"

/clone_lib="NIH_MGC_48"

/tissue_type="primary B-cells from tonsils (cell line)"

/lab_host="DH10B (phage-resistant)"

/note="Organ: B-cells; Vector: pOTB7; Site: 1; XhoI;

Site: 2; EcoRI; cDNA made by oligo-dT priming.

Directionally cloned into EcoRI/XhoI sites using the

following 5' adaptor: GGCACGAG(G). Size-selected >500bp
for average insert size 1.8kb. Library constructed by Ling
Hong in the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH_MGC Library."

BASE COUNT 165 a 206 c 201 g 181 t
ORIGIN

Query Match 15.1%; Score 36; DB 12; Length 754;

Best Local Similarity 64.3%; Pred. No. 8.9;

Matches 54; Conservative 0; Mismatches 30; Indels 0; Gaps 0;

QY 18 TGTCTCTCCATCCAGGAGCGGCGGCTATGGGGTCTGGGCTGCCCTTGTCTCTC 77

Db 249 TGTTCCTCCCTCCGAGGATCCCTTTGGTGAGTATGTTTCAGGATGCACATCACAC 308

QY 78 CTCTTGACCCCTCCTTGGCAGCTCA 101

Db 309 CTCTAGATACCTTCAGGCAACACA 332

Search completed: May 1, 2003, 05:10:01

Job time : 1207.4 secs

GenCore version 5.1.5
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: May 1, 2003, 02:55:40 ; Search time 164.211 Seconds
(without alignments)
3277.661 Million cell updates/sec

Title: US-09-092-296-1

Perfect score: 229

Sequence: 1 GCGCACCGGACTTCAGTGT.....CCCTTCAGGACCAAGCTCA 239

Scoring table: IDENTITY_NUC

.Gapop 10.0 , Gapext 1.0

Searched: 2185239 seqs, 112599159 residues

Total number of hits satisfying chosen parameters: 4370478

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : N_Geneseq_101002.*

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- 2: /SID32/gcgdata/geneseq/geneseq-emb1/NA1981.DAT.*
- 3: /SID32/gcgdata/geneseq/geneseq-emb1/NA1982.DAT.*
- 4: /SID32/gcgdata/geneseq/geneseq-emb1/NA1983.DAT.*
- 5: /SID32/gcgdata/geneseq/geneseq-emb1/NA1984.DAT.*
- 6: /SID32/gcgdata/geneseq/geneseq-emb1/NA1985.DAT.*
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- 22: /SID32/gcgdata/geneseq/geneseq-emb1/NA2001A.DAT.*
- 23: /SID32/gcgdata/geneseq/geneseq-emb1/NA2001B.DAT.*
- 24: /SID32/gcgdata/geneseq/geneseq-emb1/NA2002.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	227	95.0	422	21	AAZ65087
2	227	95.0	422	22	AAZ65087
3	227	95.0	422	22	AAZ65087
4	227	95.0	422	22	AAZ65087
5	227	95.0	422	21	AAZ65087
6	227	95.0	422	21	AAZ65087
7	119	49.8	624	24	ABK81618
8	109.8	45.9	729	23	AAZ65519
9	34.4	14.4	2923	20	AAZ65519

10	34.4	14.4	3417	22	AAK94567	Human full-length
11	34	14.2	27082	21	AAK70447	Human immune/haema
12	33.4	14.0	361	21	AAK30979	Human secreted pro
13	33	13.8	6855	24	ABN83971	Human gene sequenc
14	32	13.4	1128	19	AAV28846	Mouse coxsackievir
15	31.8	13.3	1251	24	ABK09969	Eastern cottonmout
16	31.6	13.2	1243	22	AAH42525	Partial cDNA sequenc
17	31.6	13.2	1498	22	AAH42526	Nucleotide sequenc
18	31.6	13.2	11749	22	AAZ36066	Human musculoskele
19	31.6	13.2	11749	22	AAZ36066	DNA encoding human
20	31.6	13.2	11749	22	AAZ36066	Human reproductive
21	31.6	13.2	11749	22	AAZ36066	Human immune/haema
22	31.6	13.2	11749	22	AAZ36066	Human musculoskele
23	31.6	13.2	30420	22	AAZ36066	DNA encoding human
24	31.6	13.2	30420	22	AAZ36066	Human reproductive
25	31.4	13.1	1206	22	AAH94515	Human foetal cDNA,
26	31.2	13.1	705	22	AAH03213	Human cDNA clone (
27	31.2	13.1	2135	22	AAH13650	Human cDNA sequenc
28	31.2	13.1	2644	23	ABL09867	Drosophila melanog
29	31.2	13.1	6096	23	ABL09866	Human immune/haema
30	31.2	13.1	16596	22	AAK83767	DNA encoding human
31	31.2	13.1	16596	22	AAK83767	RAP-1 radiation pr
32	31	13.0	3510	17	AAZ18696	Human foetal liver
33	30.6	12.8	138	22	ABA70260	Probe #15444 for g
34	30.6	12.8	138	22	ABA36978	Human brain expres
35	30.6	12.8	138	22	AAK18487	Human bone marrow
36	30.6	12.8	138	22	AAK44398	Probe #14784 for g
37	30.6	12.8	138	22	AAZ24851	Human genome-deriv
38	30.6	12.8	138	22	AAZ50394	Human genome-deriv
39	30.6	12.8	138	24	ABZ18633	Toxicologically re
40	30.6	12.8	180	24	ABZ18633	Human digestive sy
41	30.6	12.8	332	22	AAK87952	Human digestive sy
42	30.6	12.8	377	22	AAK89454	Human foetal liver
43	30.6	12.8	471	22	ABA57640	Probe #5527 for ge
44	30.6	12.8	471	22	ABA27061	Human brain expres
45	30.6	12.8	471	22	AAK05694	

ALIGNMENTS

RESULT 1
ID AAZ65087 standard; cDNA; 422 BP.
XX AAZ65087;
AC AAZ65087;

05-APR-2000 (first entry)
Membrane-bound protein PRO1098 encoding cDNA.

Membrane-bound polypeptide; PRO polypeptide; LDL receptor; TIE ligand; pharmaceutical; receptor immunoadhesin; gene mapping; ss.

OS Homo sapiens.

XX WO9963088-A2.

PN WO9963088-A2.

XX 09-DEC-1999.

PD 09-DEC-1999.

XX 02-JUN-1999; 99WO-US12252.

XX 02-JUN-1998; 98US-0087607.

PR 02-JUN-1998; 98US-0087609.

PR 02-JUN-1998; 98US-0087759.

PR 03-JUN-1998; 98US-0087827.

PR 04-JUN-1998; 98US-0088021.

PR 04-JUN-1998; 98US-0088025.

PR 04-JUN-1998; 98US-0088028.

PR 04-JUN-1998; 98US-0088029.

PR 04-JUN-1998; 98US-0088030.

PR 04-JUN-1998; 98US-0088033.

PR 04-JUN-1998; 98US-0088326.

PR 05-JUN-1998; 98US-0088167.
PR 05-JUN-1998; 98US-0088202.
PR 05-JUN-1998; 98US-0088212.
PR 05-JUN-1998; 98US-0088217.
PR 09-JUN-1998; 98US-0088655.
PR 10-JUN-1998; 98US-0088722.
PR 10-JUN-1998; 98US-0088730.
PR 10-JUN-1998; 98US-0088734.
PR 10-JUN-1998; 98US-0088738.
PR 10-JUN-1998; 98US-0088740.
PR 10-JUN-1998; 98US-0088741.
PR 10-JUN-1998; 98US-0088742.
PR 10-JUN-1998; 98US-0088810.
PR 10-JUN-1998; 98US-0088811.
PR 10-JUN-1998; 98US-0088824.
PR 10-JUN-1998; 98US-0088825.
PR 10-JUN-1998; 98US-0088826.
PR 11-JUN-1998; 98US-0088858.
PR 11-JUN-1998; 98US-0088861.
PR 11-JUN-1998; 98US-0088863.
PR 11-JUN-1998; 98US-0088876.
PR 12-JUN-1998; 98US-0089090.
PR 12-JUN-1998; 98US-0089105.
PR 16-JUN-1998; 98US-0089440.
PR 16-JUN-1998; 98US-0089512.
PR 16-JUN-1998; 98US-0089514.
PR 17-JUN-1998; 98US-0089532.
PR 17-JUN-1998; 98US-0089538.
PR 17-JUN-1998; 98US-0089598.
PR 17-JUN-1998; 98US-0089599.
PR 17-JUN-1998; 98US-0089600.
PR 17-JUN-1998; 98US-0089603.
PR 18-JUN-1998; 98US-0089801.
PR 18-JUN-1998; 98US-0089907.
PR 18-JUN-1998; 98US-0089908.
PR 19-JUN-1998; 98US-0089947.
PR 19-JUN-1998; 98US-0089948.
PR 22-JUN-1998; 98US-0089952.
PR 22-JUN-1998; 98US-0090246.
PR 22-JUN-1998; 98US-0090252.
PR 22-JUN-1998; 98US-0090254.
PR 23-JUN-1998; 98US-0090349.
PR 23-JUN-1998; 98US-0090355.
PR 24-JUN-1998; 98US-0090429.
PR 24-JUN-1998; 98US-0090431.
PR 24-JUN-1998; 98US-0090435.
PR 24-JUN-1998; 98US-0090444.
PR 24-JUN-1998; 98US-0090445.
PR 24-JUN-1998; 98US-0090461.
PR 24-JUN-1998; 98US-0090472.
PR 24-JUN-1998; 98US-0090535.
PR 24-JUN-1998; 98US-0090538.
PR 24-JUN-1998; 98US-0090540.
PR 24-JUN-1998; 98US-0090557.
PR 25-JUN-1998; 98US-0090576.
PR 25-JUN-1998; 98US-0090578.
PR 25-JUN-1998; 98US-0090588.
PR 25-JUN-1998; 98US-0090590.
PR 25-JUN-1998; 98US-0090591.
PR 25-JUN-1998; 98US-0090594.
PR 25-JUN-1998; 98US-0090595.
PR 25-JUN-1998; 98US-0090696.
PR 26-JUN-1998; 98US-0090862.
PR 26-JUN-1998; 98US-0090863.
PR 01-JUL-1998; 98US-0091358.
PR 01-JUL-1998; 98US-0091360.
PR 01-JUL-1998; 98US-0091544.
PR 02-JUL-1998; 98US-0091478.
PR 02-JUL-1998; 98US-0091486.
PR 02-JUL-1998; 98US-0091519.
PR 02-JUL-1998; 98US-0091626.
PR 02-JUL-1998; 98US-0091628.
PR 02-JUL-1998; 98US-0091633.

PR 02-JUL-1998; 98US-0091646.
PR 02-JUL-1998; 98US-0091673.
PR 07-JUL-1998; 98US-0091978.
PR 07-JUL-1998; 98US-0091982.
PR 09-JUL-1998; 98US-0092182.
PR 10-JUL-1998; 98US-0092472.
PR 20-JUL-1998; 98US-0093339.
PR 30-JUL-1998; 98US-0094651.
PR 04-AUG-1998; 98US-0095282.
PR 04-AUG-1998; 98US-0095285.
PR 04-AUG-1998; 98US-0095301.
PR 04-AUG-1998; 98US-0095302.
PR 04-AUG-1998; 98US-0095318.
PR 04-AUG-1998; 98US-0095321.
PR 04-AUG-1998; 98US-0095325.
PR 10-AUG-1998; 98US-0095916.
PR 10-AUG-1998; 98US-0095929.
PR 10-AUG-1998; 98US-0096012.
PR 11-AUG-1998; 98US-0096143.
PR 11-AUG-1998; 98US-0096146.
PR 12-AUG-1998; 98US-0096329.
PR 17-AUG-1998; 98US-0096757.
PR 17-AUG-1998; 98US-0096766.
PR 17-AUG-1998; 98US-0096768.
PR 17-AUG-1998; 98US-0096773.
PR 17-AUG-1998; 98US-0096791.
PR 17-AUG-1998; 98US-0096867.
PR 17-AUG-1998; 98US-0096891.
PR 17-AUG-1998; 98US-0096894.
PR 17-AUG-1998; 98US-0096894.
PR 17-AUG-1998; 98US-0096895.
PR 17-AUG-1998; 98US-0096897.
PR 18-AUG-1998; 98US-0096949.
PR 18-AUG-1998; 98US-0096950.
PR 18-AUG-1998; 98US-0096959.
PR 18-AUG-1998; 98US-0096960.
PR 18-AUG-1998; 98US-0097022.
PR 19-AUG-1998; 98US-0097141.
PR 20-AUG-1998; 98US-0097218.
PR 24-AUG-1998; 98US-0097661.
PR 26-AUG-1998; 98US-0097951.
PR 26-AUG-1998; 98US-0097952.
PR 26-AUG-1998; 98US-0097954.
PR 26-AUG-1998; 98US-0097955.
PR 26-AUG-1998; 98US-0097971.
PR 26-AUG-1998; 98US-0097974.
PR 26-AUG-1998; 98US-0097978.
PR 26-AUG-1998; 98US-0097978.
PR 26-AUG-1998; 98US-0097979.
PR 26-AUG-1998; 98US-0097986.
PR 26-AUG-1998; 98US-0098014.
PR 31-AUG-1998; 98US-0098525.
PR 16-SEP-1998; 98US-0100634.
PR 12-JAN-1999; 99US-0115565.

(GETH) GENENTECH INC.

BAKER K, CHEN J, GODDARD A, GURNEY AL, SMITH V, WATANABE CK;
WOOD WL, YUAN J;

WPI; 2000-072883/06.
P-PSDB; AAY66741.

Membrane-bound proteins and related nucleotide sequences -

Claim 2; Fig 257; 822pp; English.

The invention provides membrane-bound PRO polypeptides and polynucleotides encoding them. The PRO sequences of the invention were identified based on extracellular domain homology screening. The PRO sequences have homology with proteins including LDL receptors, TIE ligands and various enzymes. The membrane-bound proteins and receptor molecules are useful as pharmaceutical and diagnostic agents. Receptor immunoadhesins, for instance, can be used as therapeutic agents to block receptor-ligand interactions. The membrane-bound proteins can also be

CC employed for screening of potential peptide or small molecule inhibitors
 CC of the relevant receptor/ligand interaction. The PRO encoding sequences
 CC are useful as hybridization probes, in chromosome and gene mapping and in
 CC the generation of antisense RNA and DNA. PRO nucleic acid sequences
 CC will also be useful for the preparation of PRO polypeptides, especially
 CC by recombinant techniques.
 XX
 SQ Sequence 422 BP; 84 A; 134 C; 104 G; 100 T; 0 other;

Query Match 95.0%; Score 227; DB 21; Length 422;
 Best Local Similarity 99.2%; Pred. No. 2e-62;
 Matches 238; Conservative 0; Mismatches 1; Indels 1; Gaps 1;
 Qy 1 GGCACCGGGACTTCAGTGTCTCTCCATCCAGGAGCGCAGTGGCCACTATGGGTCTG 60
 Db 8 GGCACCGGGACTTCAGTGTCTCTCCATCCAGGAGCGCAGTGGCCACTATGGGTCTG 67
 Qy 61 GGCTGCCCTTGTCTCTCTCTGACCTCTCTGACCTCACATGGACAGGCGCGGTA 120
 Db 68 GGCTGCCCTTGTCTCTCTCTGACCTCTCTGACCTCACATGGACAGGCGCGGTA 127
 Qy 121 TGACTTTGCAACTGAAGTGAAGAGAGTCTTTCTGACAAATTCCTCTATGATGAGTCCAGCT 180
 Db 128 TGACTTTGCAACTGAAGTGAAGAGAGTCTTTCTGACAAATTCCTCTATGATGAGTCCAGCT 187
 Qy 181 TCGTGAATTCGTTGAAA-NFCTGCTCCCTCTCCATCCCTTCAGGAGGACCGGTCA 239
 Db 188 TCGTGAATTCGTTGAAA-NFCTGCTCCCTCTCCATCCCTTCAGGAGGACCGGTCA 247

RESULT 2
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 ID AAS46045 standard; cDNA; 422 BP.
 XX
 AC AAS46045;
 XX
 DT 18-DEC-2001 (first entry)
 XX
 DE Human DNA encoding PRO polypeptide sequence #121.
 XX
 KW PRO polypeptide; mammal; tumour; cancer; human; cattle; horse; sheep; ss;
 KW dog; cat; pig; goat; rabbit; tumour necrosis factor alpha; TNF-alpha;
 KW blood; chondrocyte cell; cell proliferation; cell differentiation; colon;
 KW adrenal; lung; breast; prostate; cervix; liver; genetic disorder;
 KW PCR primer.
 XX
 OS Homo sapiens.
 XX
 PN W0200169848-A2.
 XX
 PD 20-SEP-2001.
 XX
 PF 28-FEB-2001; 2001WQ-US06520.
 XX

01-MAR-2000; 2000WQ-US05601.
 PR 02-MAR-2000; 2000WQ-US05841.
 PR 03-MAR-2000; 2000US-187202P.
 PR 06-MAR-2000; 2000US-186968P.
 PR 14-MAR-2000; 2000US-189320P.
 PR 14-MAR-2000; 2000US-189320P.
 PR 15-MAR-2000; 2000WQ-US06884.
 PR 21-MAR-2000; 2000US-190828P.
 PR 21-MAR-2000; 2000US-191007P.
 PR 21-MAR-2000; 2000US-191048P.
 PR 21-MAR-2000; 2000US-191314P.
 PR 28-MAR-2000; 2000US-192655P.
 PR 29-MAR-2000; 2000US-193032P.
 PR 30-MAR-2000; 2000US-193053P.
 PR 04-APR-2000; 2000WQ-US08439.
 PR 04-APR-2000; 2000US-194449P.
 PR 11-APR-2000; 2000US-195975P.
 PR 11-APR-2000; 2000US-196000P.

PR 11-APR-2000; 2000US-196187P.
 PR 11-APR-2000; 2000US-196690P.
 PR 11-APR-2000; 2000US-196820P.
 PR 18-APR-2000; 2000US-198121P.
 PR 18-APR-2000; 2000US-198585P.
 PR 25-APR-2000; 2000US-199397P.
 PR 25-APR-2000; 2000US-199550P.
 PR 25-APR-2000; 2000US-199654P.
 PR 03-MAY-2000; 2000US-201516P.
 PR 17-MAY-2000; 2000WQ-US13705.
 PR 22-MAY-2000; 2000WQ-US14042.
 PR 30-MAY-2000; 2000WQ-US14941.
 PR 02-JUN-2000; 2000WQ-US15264.
 PR 05-JUN-2000; 2000US-209832P.
 PR 28-JUL-2000; 2000WQ-US20710.
 PR 22-AUG-2000; 2000US-0644848.
 PR 24-AUG-2000; 2000WQ-US23328.
 PR 08-NOV-2000; 2000WQ-US30952.
 PR 01-DEC-2000; 2000WQ-US32678.
 PR 20-DEC-2000; 2000WQ-US34956.
 XX
 PA (GETH) GENENTECH INC.
 XX
 PI Baker KP, Chen J, Desnoyers L, Goddard A, Godowski PJ, Gurney AL;
 PI Pan J, Smith V, Watanabe CK, Wood WI, Zhang Z;
 XX
 WPI: 2001-602746/68.
 DR P-PSDB; AAU29144.
 XX

Novel nucleic acids encoding PRO polypeptides, used to diagnose the
 presence of tumours, such as prostate and breast tumours, in mammals and
 to screen for modulators of the compounds -
 Claim 2; Fig 241; 774pp; English.

Sequences AAS45925-AAS46231 represent DNA molecules encoding and PCR
 primers for PRO polypeptides of the invention. The sequences of the
 invention can be used to detect the presence of a tumour in a mammal by
 comparing the level of expression of a PRO polypeptide in a test sample
 of cells from the animal and a control sample of normal cells, whereby a
 higher level of expression in the test sample indicates the presence of a
 tumour in the mammal. Mammals include dogs, cats, cattle, horses, sheep,
 CC pigs, goats and rabbits but are preferably human. The polypeptides can be
 CC used to stimulate tumour necrosis factor (TNF) alpha release from human
 CC blood, when contacted with it. A specific polypeptide can be used to
 CC stimulate the proliferation or differentiation of chondrocyte cells. The
 CC PRO proteins can be used to determine the presence of tumours and also
 CC susceptibility to tumour development, particularly adrenal, lung, colon,
 CC breast, prostate, rectal, cervical, or liver tumours, in mammalian
 CC subjects. The oligonucleotide probes specific for the PRO nucleic acids
 CC can be used for genetic analysis of individuals with genetic disorders.

SQ Sequence 422 BP; 84 A; 134 C; 104 G; 100 T; 0 other;

Query Match 95.0%; Score 227; DB 22; Length 422;
 Best Local Similarity 99.2%; Pred. No. 2e-62;
 Matches 238; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

Qy 1 GGCACCGGGACTTCAGTGTCTCTCCATCCAGGAGCGCAGTGGCCACTATGGGTCTG 60
 Db 8 GGCACCGGGACTTCAGTGTCTCTCCATCCAGGAGCGCAGTGGCCACTATGGGTCTG 67
 Qy 61 GGCTGCCCTTGTCTCTCTCTGACCTCTCTGACCTCACATGGACAGGCGCGGTA 120
 Db 68 GGCTGCCCTTGTCTCTCTCTGACCTCTCTGACCTCACATGGACAGGCGCGGTA 127
 Qy 121 TGACTTTGCAACTGAAGTGAAGAGTCTTTCTGACAAATTCCTCTATGATGAGTCCAGCT 180
 Db 128 TGACTTTGCAACTGAAGTGAAGAGTCTTTCTGACAAATTCCTCTATGATGAGTCCAGCT 187
 Qy 181 TCGTGAATTCGTTGAAA-NFCTGCTCCCTCTCCATCCCTTCAGGAGGACCGGTCA 239
 Db 188 TCGTGAATTCGTTGAAA-NFCTGCTCCCTCTCCATCCCTTCAGGAGGACCGGTCA 247

RESULT 3
AAAF92090
ID AAF92090 standard; cDNA; 422 BP.
XX
AC AAF92090;
XX
DT 15-MAY-2001 (first entry)
XX
DE Human PRO1098 cDNA.
XX
KW Human; PRO protein; mapping; ss.
XX
OS Homo sapiens.
XX
PN WO200116318-A2.
XX
PD 08-MAR-2001.
XX
PF 24-AUG-2000; 2000WO-US23328.
XX
PR 01-SEP-1999; 99WO-US20111.
XX
PR 15-SEP-1999; 99WO-US21090.
XX
PR 07-DEC-1999; 99US-0169495.
XX
PR 09-DEC-1999; 99US-0170262.
XX
PR 11-JAN-2000; 2000US-0175481.
XX
PR 18-FEB-2000; 2000WO-US04341.
XX
PR 18-FEB-2000; 2000WO-US04342.
XX
PR 22-FEB-2000; 2000WO-US04414.
XX
PR 01-MAR-2000; 2000WO-US05601.
XX
PR 03-MAR-2000; 2000US-0187202.
XX
PR 25-APR-2000; 2000US-0199397.
XX
PR 22-MAY-2000; 2000WO-US14042.
XX
PR 05-JUN-2000; 2000US-0209832.
XX
PA (GETH) GENENTECH INC.
XX
PI Eaton DL, Flivaroff E, Gerritsen ME, Goddard A, Godowski PJ;
PI Grimaldi CJ, Gurney AL, Watanabe CK, Wood WI;
XX
DR WPI; 2001-183260/18.
XX
DR P-PSDB; AAB87558.
XX
XX Eighty four nucleic acids encoding PRO polypeptides, useful in
PT molecular biology, including use as hybridization probes, and in
PT chromosome and gene mapping.
XX
PS Claim 2; Fig 65; 278pp; English.
XX
CC The present sequence is the coding sequence for a human PRO polypeptide
CC (secreted and transmembrane). The PRO protein, and PRO agonists, PRO
CC antagonists or anti-PRO antibodies are useful for preparation of a
CC medicament useful in the treatment of a condition which is responsive to
CC the PRO protein, agonists, antagonists or anti-PRO antibodies. The PRO
CC protein may also be employed as molecular weight markers for protein
CC electrophoresis. The PRO coding sequence has applications in molecular
CC biology, including use as hybridisation probes, and in chromosome and
CC gene mapping.
XX
SQ Sequence 422 BP; 84 A; 134 C; 104 G; 100 T; 0 other;
XX
Query Match 95.0%; Score 227; DB 22; Length 422;
Best Local Similarity 99.2%; Pred. No. 2e-62;
Matches 238; Conservative 0; Mismatches 1; Indels 1; Gaps 1;
Oy 1 GGCCACGGGACTTCAGTGTCTCTCCATCCAGGAGCGCAGTGGCCACTATGGGTCG 60
Db 8 GGCCACGGGACTTCAGTGTCTCTCCATCCAGGAGCGCAGTGGCCACTATGGGTCG 67
Oy 61 GGCCTGCCCTTGTCTCTCTCTGACCTCTCTGACCTCATGACACAGGCGCCGGTA 120
Db 68 GGCCTGCCCTTGTCTCTCTGACCTCTCTGACCTCATGACACAGGCGCCGGTA 127

Oy 121 TGACITTTGCAACTGAAGCTGAAGGAGTCTTTTCTGACAAATTCCTCTATGAGTCCAGCT 180
Db 128 TGACITTTGCAACTGAAGCTGAAGGAGTCTTTTCTGACAAATTCCTCTATGAGTCCAGCT 187
Oy 181 TCCTGGAATTCCTTGAAGAA-NYCTGCGCTCCTCTCCATCTCCCTTCAGGACGAGGTCA 239
Db 188 TCCTGGAATTCCTTGAAGAAAGCTCTGCTCCTCTCTCCATCTCCCTTCAGGACGAGGTCA 247
RESULT 4
AAAF44233
ID AAF44233 standard; cDNA; 422 BP.
XX
AC AAF44233;
XX
DT 02-APR-2001 (first entry)
XX
DE Human PRO1098 (UNQ541) nucleotide sequence SEQ ID NO:362.
XX
KW Human; secreted and transmembrane protein; PRO; cytostatic;
KW cell death; cancer; chromosomal mapping; gene mapping; tissue typing;
KW diagnostic assay; ss.
XX
OS Homo sapiens.
XX
PN WO200073454-A1.
XX
ED 07-DEC-2000.
XX
PF 30-MAR-2000; 2000WO-US08439.
XX
PR 02-JUN-1999; 99WO-US12252.
XX
PR 23-JUN-1999; 99US-0141037.
XX
PR 07-JUL-1999; 99US-0143048.
XX
PR 20-JUL-1999; 99US-0144758.
XX
PR 26-JUL-1999; 99US-0145698.
XX
PR 28-JUL-1999; 99US-0146222.
XX
PR 17-AUG-1999; 99US-0149396.
XX
PR 15-SEP-1999; 99WO-US21090.
XX
PR 08-OCT-1999; 99US-0158663.
XX
PR 30-NOV-1999; 99WO-US28313.
XX
PR 01-DEC-1999; 99WO-US30095.
XX
PR 16-DEC-1999; 99WO-US30911.
XX
PR 20-DEC-1999; 99WO-US00219.
XX
PR 05-JAN-2000; 2000WO-US00376.
XX
PR 06-JAN-2000; 2000WO-US03565.
XX
PR 11-FEB-2000; 2000WO-US04341.
XX
PR 18-FEB-2000; 2000WO-US04414.
XX
PR 24-FEB-2000; 2000WO-US04914.
XX
PR 24-FEB-2000; 2000WO-US05004.
XX
PR 02-MAR-2000; 2000WO-US05841.
XX
PR 15-MAR-2000; 2000WO-US06884.
XX
PR 20-MAR-2000; 2000WO-US07377.
XX
XX (GETH) GENENTECH INC.
XX
XX Ashkenazi AJ, Baker KP, Botstein D, Desnoyers L, Eaton DL;
PI Ferrara N, Fong S, Gerber H, Gerritsen ME, Goddard A, Godowski PJ;
PI Grimaldi CJ, Gurney AL, Kijavini RJ, Napier MA, Pan J, Paoni NF;
PI Roy MA, Stewart TA, Tumas D, Watanabe CK, Williams PM, Wood WI;
PI Zhang Z;
XX
DR WPI; 2001-032160/04.
XX
DR P-PSDB; AAB65264.
XX
XX PRO polynucleotides used to produce polypeptides used to target
PT bioactive molecules such as toxins, radiolabels or antibodies, to
PT specific cells, to cause targeted cell death -
XX
PS Claim 2; Fig 257; 935pp; English.

XX The present invention describes human secreted and transmembrane PRO
CC proteins. The PRO proteins have cytosolic activity. The PRO proteins
CC can be used for targeted delivery of bioactive molecules, such as
CC toxins, radiolabels or antibodies, that cause cell death. PRO nucleotide
CC sequences, and their fragments, can be used as hybridisation probes, in
CC chromosomal and gene mapping, and in the generation of anti-sense RNA
CC and DNA. They may also be used to produce transgenic animals which are
CC used to develop and screen therapeutically useful reagents. The PRO
CC nucleotide and protein sequence can be used for tissue typing and in
CC treating cancer. Anti-PRO antibodies can be used in diagnostic assays.
CC AAF44270 to AAF44470 represent PCR primers and hybridisation probes used
CC in the isolation of human PRO sequences. AAF44087 to AAF44269 and
CC AAB65154 to AAB65300 represent human PRO polynucleotide and protein
CC sequences given in the exemplification of the present invention.
XX
SQ Sequence 422 BP; 84 A; 134 C; 104 G; 100 T; 0 other;
Query Match 95.0%; Score 227; DB 22; Length 422;
Best Local Similarity 99.2%; Pred. No. 2e-62; Mismatches 1; Gaps 1;
Matches 238; Conservative 0; Indels 1; Gaps 1;
QY 1 GCCACCGGAGCTTCAGTGTCTCTCCATCCAGGAGCGCAGTGGCCACTATGGGTCTG 60
DB 8 GCCACCGGAGCTTCAGTGTCTCTCCATCCAGGAGCGCAGTGGCCACTATGGGTCTG 67
QY 61 GGCTGCCCTTGTCTCTCTCTGACCTCTCTGGCAGCTCACATGGAACAGGCGCGGTA 120
DB 68 GGCTGCCCTTGTCTCTCTCTGACCTCTCTGGCAGCTCACATGGAACAGGCGCGGTA 127
QY 121 TGACTTGGCACTGAAGCTGAAGAGTCTTTCTGACAAATCTCTATGAGTCCAGCT 180
DB 128 TGACTTGGCACTGAAGCTGAAGAGTCTTTCTGACAAATCTCTATGAGTCCAGCT 187
QY 181 TCCTGGAATGCTTGAAA-NYCTGGCTCTCTCCATCTCTCCATCTCCCTTCAGGACCGCTCA 239
DB 188 TCCTGGAATGCTTGAAAAGCTCTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 247
RESULT 5
AAZ98124
ID AAZ98124 standard; cDNA; 431 BP.
XX
AC AAZ98124;
XX
DT 11-MAY-2000 (first entry)
XX
DE Human signal peptide containing protein HSP-16 cDNA SEQ ID NO:150.
XX
KW Human; signal peptide-containing protein; HSP; diagnosis; cancer;
KW inflammation; cardiovascular disease; anticancer; anti-inflammatory;
KW antimicrobial; neurotropic; neuroprotective; cardiovascular; hepatotropic;
KW antiasthmatic; gene therapy; cell proliferation; neurological disorder;
KW reproductive disorder; developmental disorder; arteriosclerosis;
KW cirrhosis; psoriasis; acquired immune deficiency syndrome; anaemia;
KW asthma; Crohn's disease; infection; Alzheimer's disease; schizophrenia;
KW Parkinson's disease; Huntington's disease; ovulatory defect;
muscular dystrophy; ss.
XX
OS Homo sapiens.
XX
PN WO200000610-A2.
XX
PD 06-JAN-2000.
XX
PF 25-JUN-1999; 99WO-US14484.
XX
PR 26-JUN-1998; 98US-0090762.
XX
PR 31-JUL-1998; 98US-0094983.
XX
PR 01-OCT-1998; 98US-0102686.
XX
PR 11-DEC-1998; 98US-0112125.
XX
PA (INCY-) INCYTE PHARM INC.

XX
PI Lal P, Tang YT, Gorgone GA, Corley NC, Guegler KJ, Baughn MR;
PI Akersblom IE, Au-Young J, Yue H, Patterson C, Reddy R, Hillman JL;
PI Bandman O;
XX
DR WPI; 2000-160673/14.
DR P-PSDB; AAY87239.
XX
PT New human signal peptide-containing proteins useful in treatment,
PT prevention and diagnosis of e.g. cancer, inflammation and
PT cardiovascular disease
XX
PS Claim 9; Page 261; 327pp; English.
XX
CC AAY98109 to AAY98242 encode AAY87224 to AAY87357 which represent the
CC human signal peptide-containing proteins HSP-1 to HSP-134. HSPs have
CC anticancer, anti-inflammatory, antimicrobial, neurotropic, hepatotropic,
CC neuroprotective, cardiovascular and antiasthmatic activities, and can
CC be used in gene therapy. HSPs can be used to treat or prevent disorders
CC associated with decreased activity or function of HSP. Antagonists of
CC HSP are used to treat or prevent disorders associated with increased
CC activity or function of HSP. Such diseases include cell proliferation
CC (including cancer), inflammation, cardiovascular, neurological,
CC reproductive or developmental disorders, (e.g. arteriosclerosis,
CC cirrhosis, psoriasis, acquired immune deficiency syndrome, anaemia,
CC ischaemic heart disease, microbial or other infections, congestive or
CC diseases, schizophrenia, Alzheimer's, Parkinson's or Huntington's
CC nucleic acids can be used for the recombinant production of HSP, for
CC detecting HSP in standard hybridisation and amplification assays (for
CC diagnosis and monitoring), in gene therapy, as antisense,
CC triplex-forming or ribozyme therapeutics, for detecting related sequences
CC or genetic variations, and for chromosomal mapping. HSP are also used to
CC raise specific antibodies (Ab) and to screen for agonists and
CC antagonists (potential therapeutic agents). Ab are used to diagnose, or
CC monitor, HSP-related diseases (in usual immunoassays), as therapeutic
CC antagonists, in competitive drug screens, and for purification of HSP
CC from natural sources.
XX
SQ Sequence 431 BP; 93 A; 135 C; 101 G; 102 T; 0 other;
Query Match 95.0%; Score 227; DB 21; Length 431;
Best Local Similarity 99.2%; Pred. No. 2.1e-62;
Matches 238; Conservative 0; Mismatches 1; Indels 1; Gaps 1;
QY 1 GCCACCGGAGCTTCAGTGTCTCTCCATCCAGGAGCGCAGTGGCCACTATGGGTCTG 60
DB 1 GGCCACCGGAGCTTCAGTGTCTCTCCATCCAGGAGCGCAGTGGCCACTATGGGTCTG 60
QY 61 GGCTGCCCTTGTCTCTCTCTGACCTCTCTGGCAGCTCACATGGAACAGGCGCGGTA 120
DB 61 GGCTGCCCTTGTCTCTCTCTGACCTCTCTGGCAGCTCACATGGAACAGGCGCGGTA 120
QY 121 TGACTTGGCACTGAAGCTGAAGAGTCTTTCTGACAAATCTCTATGAGTCCAGCT 180
DB 121 TGACTTGGCACTGAAGCTGAAGAGTCTTTCTGACAAATCTCTATGAGTCCAGCT 180
QY 181 TCCTGGAATGCTTGAAA-NYCTGGCTCTCTCCATCTCTCCATCTCCCTTCAGGACCGCTCA 239
DB 181 TCCTGGAATGCTTGAAAAGCTCTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 240
RESULT 6
AAV84366
ID AAV84366 standard; cDNA to mRNA; 439 BP.
XX
AC AAV84366;
XX
DT 30-MAR-1999 (first entry)
XX
DE Human stomach carcinoma cDNA clone HP10408.
XX
KW Transmembrane protein; HP10408; human; stomach cancer; ds.

XX OS Homo sapiens.
XX PN WO200175067-A2.
XX PD 11-OCT-2001.
XX PF 30-MAR-2001; 2001WO-US08631.
XX PR 31-MAR-2000; 2000US-0540217.
XX PR 23-AUG-2000; 2000US-0649167.
XX PA (HYSE-) HYSEQ INC.
XX PI Drmanac RT, Liu C, Tang YT;
XX DR WPI; 2001-639362/73.
XX DR P-PSDB; ABG01332.
XX PT New isolated polynucleotide and encoded polypeptides, useful in
XX PT diagnostics, forensics, gene mapping, identification of mutations
XX PT responsible for genetic disorders or other traits and to assess
XX PT biodiversity -
XX PS Claim 1; SEQ ID No 1323; 103pp; English.
XX CC The invention relates to isolated polynucleotide (I) and
XX CC polypeptide (II) sequences. (I) is useful as hybridisation probes,
XX CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome
XX CC and gene mapping, and in recombinant production of (II). The
XX CC polynucleotides are also used in diagnostics as expressed sequence tags
XX CC for identifying expressed genes. (I) is useful in gene therapy techniques
XX CC to restore normal activity of (II) or to treat disease states involving
XX CC (II). (II) is useful for generating antibodies against it, detecting or
XX CC quantitating a polypeptide in tissue, as molecular weight markers and as
XX CC a food supplement. (III) and its binding partners are useful in medical
XX CC imaging of sites expressing (II). (I) and (II) are useful for treating
XX CC disorders involving aberrant protein expression or biological activity.
XX CC The polypeptide and polynucleotide sequences have applications in
XX CC diagnostics, forensics, gene mapping, identification of mutations
XX CC responsible for genetic disorders or other traits to assess biodiversity
XX CC and to produce other types of data and products dependent on DNA and
XX CC amino acid sequences. AAS64197-AAS94564 represent novel human
XX CC diagnostic coding sequences of the invention.
XX CC Note: The sequence data for this patent did not appear in the printed
XX CC specification, but was obtained in electronic format directly from WIPO
XX CC at ftp.wipo.int/pub/published_pct_sequences.
XX SQ Sequence 729 BP; 187 A; 169 C; 152 G; 146 T; 75 other;
Query Match 45.9%; Score 109.8; DB 23; Length 729;
Best Local Similarity 98.2%; Pred. No. 5.8e-25;
Matches 111; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 34 GCAGCGCAGTGGCCACATGAGCGCTGGCTGCTCTCTGACCCCTCTTG 93
Db 8 GGAGCGCAGAGGCGCATGAGGCTGGCTGCTCTCTGACCCCTCTTG 67
Qy 94 GCAGCTCACATGGAACGAGCGCGGTATGACCTTTCGAACTGAAGCTGAAGGAG 146
Db 68 GCAGCTCACATGGAACGAGCGCGGTATGACCTTTCGAACTGAAGCTGAAGGAG 120
RESULT 9
AAX04326
ID RAX04326 standard; DNA; 2923 BP.
XX AC RAX04326;
XX XX
XX DT 13-APR-1999 (first entry)
XX XX
XX DE Human secreted protein gene 16 clone HSHBQ68.
XX XX
KW Human; secreted protein; fusion protein; gene therapy; protein therapy;
KW diagnosis; tissue; cancer; tumour; neurodegenerative disorder; leukaemia;
KW developmental abnormality; foetal deficiency; blood; allergy; renal; ds;
KW immune system; asthma; lymphocytic disease; brain; hepatic; lymphoma;
KW inflammation; ischaemic shock; Alzheimer's disease; restenosis; AIDS;
KW cognitive disorder; schizophrenia; prostate; obesity; osteoclast; thymus;
KW osteoporosis; arthritis; testis; lung; thyroiditis; thyroid; digestion;
KW endocrine; metabolism; regulation; malabsorption; gastritis; neoplasm.
XX OS Homo sapiens.
XX PN WO9856804-A1.
XX PD 17-DEC-1998.
XX PF 11-JUN-1998; 98WO-US12125.
XX PR 02-OCT-1997; 97US-0061060.
XX PR 13-JUN-1997; 97US-0049547.
XX PR 13-JUN-1997; 97US-0049548.
XX PR 13-JUN-1997; 97US-0049549.
XX PR 13-JUN-1997; 97US-0049550.
XX PR 13-JUN-1997; 97US-0049606.
XX PR 13-JUN-1997; 97US-0049607.
XX PR 13-JUN-1997; 97US-0049608.
XX PR 13-JUN-1997; 97US-0049609.
XX PR 13-JUN-1997; 97US-0049610.
XX PR 13-JUN-1997; 97US-0049611.
XX PR 13-JUN-1997; 97US-0050566.
XX PR 13-JUN-1997; 97US-0050901.
XX PR 13-JUN-1997; 97US-0052989.
XX PR 08-JUL-1997; 97US-0051919.
XX PR 18-AUG-1997; 97US-0055984.
XX PR 12-SEP-1997; 97US-0058665.
XX PR 12-SEP-1997; 97US-0058668.
XX PR 12-SEP-1997; 97US-0058669.
XX PR 12-SEP-1997; 97US-0058750.
XX PR 12-SEP-1997; 97US-0058971.
XX PR 12-SEP-1997; 97US-0058972.
XX PR 12-SEP-1997; 97US-0058975.
XX PR 02-OCT-1997; 97US-0060834.
XX PR 02-OCT-1997; 97US-0060841.
XX PR 02-OCT-1997; 97US-0060844.
XX PR 02-OCT-1997; 97US-0060865.
XX PR 02-OCT-1997; 97US-0061059.
XX PA (HUMA-) HUMAN GENOME SCI INC.
XX PI Brewer LA, Ebner R, Ferrie AM, Feng P, Greene JM, Lafleur DW;
PI Moore PA, Ni J, Olsen HS, Rosen CA, Ruben SM, Shi Y, Young P;
PI Yu GL;
XX WPI; 1999-080881/07.
XX P-PSDB; AAW78141.
XX DR New isolated human genes and the secreted polypeptides they encode -
XX PT useful for diagnosis and treatment of e.g. cancers, neurological
XX PT disorders, immune diseases, inflammation or blood disorders
XX PS Claim 1; Page 180-182; 380pp; English.
XX CC This sequence represents a nucleic acid molecule which encodes a
XX CC secreted human protein. The gene number, and the clone it is derived
XX CC from, are detailed in the descriptor line. The gene can be used to
XX CC generate fusion proteins by linking to the gene to a human immunoglobulin
XX CC Fc portion (e.g. AAX04302) for increasing the stability of the fused
XX CC protein as compared to the human protein only.
XX CC The invention relates to 86 novel genes and their fragments (nucleic
XX CC acid sequences: AAX04311-X04410; amino acid sequences AAW78126-W78225)
XX CC which are useful for preventing, treating or ameliorating medical
XX CC conditions e.g. by protein or gene therapy. Also, pathological
XX CC conditions can be diagnosed by determining the amount of the new
XX CC polypeptides in a sample or by determining the presence of mutations in

the new polynucleotides. Specific uses are described for each of the 86 polynucleotides, based on which tissues they are most highly expressed in (see AAX04311 for described uses).


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PR 05-SEP-2000; 2000US-0229513.
PR 06-SEP-2000; 2000US-0230437.
PR 06-SEP-2000; 2000US-0230438.
PR 08-SEP-2000; 2000US-0231242.
PR 08-SEP-2000; 2000US-0231243.
PR 08-SEP-2000; 2000US-0231244.
PR 08-SEP-2000; 2000US-0231413.
PR 08-SEP-2000; 2000US-0231414.
PR 08-SEP-2000; 2000US-0232080.
PR 08-SEP-2000; 2000US-0232081.
PR 12-SEP-2000; 2000US-0231968.
PR 14-SEP-2000; 2000US-0232397.
PR 14-SEP-2000; 2000US-0232398.
PR 14-SEP-2000; 2000US-0232399.
PR 14-SEP-2000; 2000US-0232400.
PR 14-SEP-2000; 2000US-0232401.
PR 14-SEP-2000; 2000US-0233063.
PR 14-SEP-2000; 2000US-0233064.
PR 14-SEP-2000; 2000US-0233065.
PR 21-SEP-2000; 2000US-0234223.
PR 21-SEP-2000; 2000US-0234274.
PR 25-SEP-2000; 2000US-0234997.
PR 25-SEP-2000; 2000US-0234998.
PR 26-SEP-2000; 2000US-0235484.
PR 27-SEP-2000; 2000US-0235834.
PR 27-SEP-2000; 2000US-0235836.
PR 29-SEP-2000; 2000US-0236327.
PR 29-SEP-2000; 2000US-0236367.
PR 29-SEP-2000; 2000US-0236368.
PR 29-SEP-2000; 2000US-0236369.
PR 29-SEP-2000; 2000US-0236370.
PR 02-OCT-2000; 2000US-0236802.
PR 02-OCT-2000; 2000US-0237037.
PR 02-OCT-2000; 2000US-0237038.
PR 02-OCT-2000; 2000US-0237039.
PR 02-OCT-2000; 2000US-0237040.
PR 13-OCT-2000; 2000US-0239935.
PR 13-OCT-2000; 2000US-0239937.
PR 20-OCT-2000; 2000US-0240960.
PR 20-OCT-2000; 2000US-0241221.
PR 20-OCT-2000; 2000US-0241785.
PR 20-OCT-2000; 2000US-0241786.
PR 20-OCT-2000; 2000US-0241787.
PR 20-OCT-2000; 2000US-0241808.
PR 20-OCT-2000; 2000US-0241809.
PR 01-NOV-2000; 2000US-0244617.
PR 08-NOV-2000; 2000US-0246474.
PR 08-NOV-2000; 2000US-0246475.
PR 08-NOV-2000; 2000US-0246476.
PR 08-NOV-2000; 2000US-0246477.
PR 08-NOV-2000; 2000US-0246478.
PR 08-NOV-2000; 2000US-0246523.
PR 08-NOV-2000; 2000US-0246524.
PR 08-NOV-2000; 2000US-0246525.
PR 08-NOV-2000; 2000US-0246526.
PR 08-NOV-2000; 2000US-0246527.
PR 08-NOV-2000; 2000US-0246528.
PR 08-NOV-2000; 2000US-0246532.
PR 08-NOV-2000; 2000US-0246609.
PR 08-NOV-2000; 2000US-0246610.
PR 08-NOV-2000; 2000US-0246611.
PR 08-NOV-2000; 2000US-0246613.
PR 17-NOV-2000; 2000US-0249207.
PR 17-NOV-2000; 2000US-0249208.
PR 17-NOV-2000; 2000US-0249209.
PR 17-NOV-2000; 2000US-0249210.
PR 17-NOV-2000; 2000US-0249211.
PR 17-NOV-2000; 2000US-0249212.
PR 17-NOV-2000; 2000US-0249213.
PR 17-NOV-2000; 2000US-0249214.
PR 17-NOV-2000; 2000US-0249215.
PR 17-NOV-2000; 2000US-0249216.
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PR 17-NOV-2000; 2000US-0249217.
PR 17-NOV-2000; 2000US-0249218.
PR 17-NOV-2000; 2000US-0249244.
PR 17-NOV-2000; 2000US-0249245.
PR 17-NOV-2000; 2000US-0249264.
PR 17-NOV-2000; 2000US-0249265.
PR 17-NOV-2000; 2000US-0249297.
PR 17-NOV-2000; 2000US-0249299.
PR 17-NOV-2000; 2000US-0249300.
PR 01-DEC-2000; 2000US-0250160.
PR 01-DEC-2000; 2000US-0250391.
PR 05-DEC-2000; 2000US-0251030.
PR 05-DEC-2000; 2000US-0251988.
PR 05-DEC-2000; 2000US-0256719.
PR 06-DEC-2000; 2000US-0251479.
PR 08-DEC-2000; 2000US-0251856.
PR 08-DEC-2000; 2000US-0251868.
PR 08-DEC-2000; 2000US-0251869.
PR 08-DEC-2000; 2000US-0251989.
PR 08-DEC-2000; 2000US-0251990.
PR 11-DEC-2000; 2000US-0254097.
PR 05-JAN-2001; 2001US-0259678.
XX (HUMA-) HUMAN GENOME SCI INC.
XX Rosen CA, Barash SC, Ruben SM;
PI WPT; 2001-483426/52.
XX
XX Nucleic acids encoding human immune/hematopoietic antigen polypeptides,
PT useful for preventing, diagnosing and/or treating cancers and
PT metastasis.
XX
XX PS Disclosure; SEQ ID NO 25259; 3071bp + Sequence Listing; English.
XX
XX AAK54951 to AAK64702 encode the human Immune/hematopoietic antigen (I)
CC amino acid sequences given in AAM82170 to AAM91921. (I) have cytostatic
CC activity, and can be used in gene therapy and vaccine production. (I)
CC proteins and polynucleotides may be used in the prevention, diagnosis and
CC treatment of diseases associated with inappropriate (I) expression. For
CC example, they may be used to treat disorders associated with decreased
CC expression by rectifying mutations or deletions in a patient's genome
CC that affect the activity of (I) by expressing inactive proteins or to
CC supplement the patients own production of (I). Additionally, (I)
CC polynucleotides may be used to produce the secreted (I); by inserting the
CC the nucleic acids into a host cell and culturing the cell to express the
CC protein. (I) proteins and polynucleotides may be used to prevent,
CC diagnose and treat immune/hematopoietic-related diseases, especially
CC cancers and cancer metastases of hematopoietic-derived cells. AAK64703
CC to AAK87694 represent human immune/hematopoietic antigen genomic
CC sequences from the present invention. AAK54942 to AAK54950 and AAM82169
CC represent sequences used in the exemplification of the present invention.
XX
SQ Sequence 27082 BP; 5963 A; 7786 C; 7711 G; 5622 T; 0 other;
Query Match 14.2%; Score 34; DB 22; Length 27082;
Best Local Similarity 54.9%; Pred. No. 3.3;
Matches 67; Conservative 0; Mismatches 55; Indels 0; Gaps 0;
QY 19 GTCTCTCCATCCGAGGAGCGAGTGGCCACTATGGGCTCTGGGCTGCCCTTGTCCTCC 78
DB 13016 GGCTACTCTCTAGGAGTAAGCCCCCGGTCCTCATCTCCCTGCCAGTGTCCCTGACCCCA 13075
QY 79 TCTTGACCTCTCTTGCGAGCTACATGGACAGCGCGGTATGACTTTGCAACTGAAGC 138
DB 13076 TCTACTCTCTCTGGGAGCTTCTCAGCCACAGGCTGGGCTGGACTTCACTCACTGAGC 13135
QY 139 TG 140
DB 13136 TG 13137
RESULT 12
```

```
AAAC30979
ID  AAC30979 standard; cDNA; 361 BP.
XX
AC  AAC30979;
XX
DT  06-OCT-2000 (first entry)
XX
DE  Human secreted protein 5' EST, SEQ ID NO: 35054.
XX
KW  Human; 5' EST; expressed sequence tag; secreted protein; cDNA isolation;
KW  gene therapy; chromosome mapping; ss.
XX
OS  Homo sapiens.
XX
PN  EP1033401-A2.
XX
PD  06-SEP-2000.
XX
PF  21-FEB-2000; 2000EP-0200610.
XX
PR  26-FEB-1999; 99US-0122487.
XX
PA  (GEST ) GENSET.
XX
PI  Dumas Milne Edwards J, Duclert A, Giordano J;
XX  WPI; 2000-500381/45.
XX
PT  New nucleic acid that is a 5' expressed sequence tag (5' EST) for
PT  obtaining cDNAs and genomic DNAs that correspond to 5'ESTs and for
PT  diagnostic, forensic, gene therapy and chromosome mapping procedures -
XX  Claim 1: SEQ ID 35054; 71pp + CD-ROM; English.
XX
CC  The present sequence is one of a large number of 5' ESTs derived from
CC  mRNAs encoding secreted proteins. No ORF has yet been conclusively
CC  identified within the present sequence. The 5' ESTs were prepared from
CC  total human RNAs or poly(A)+ RNAs derived from 30 different tissues. EST
CC  sequences usually correspond mainly to the 3' untranslated region (UTR)
CC  of the mRNA because they are often obtained from oligo-dT primed cDNA
CC  libraries. Such ESTs are not well suited for isolating cDNA sequences
CC  derived from the 5' ends of mRNAs and even in those cases where longer
CC  cDNA sequences have been obtained, the full 5' UTR is rarely included.
CC  5' ESTs are derived from mRNAs with intact 5' ends and can therefore be
CC  used to obtain full length cDNAs and genomic DNAs. 5' ESTs are also used
CC  in diagnostic, forensic, gene therapy and chromosome mapping procedures.
CC  They are used to obtain upstream regulatory sequences and to design
CC  expression and secretion vectors.
XX
SQ  Sequence 361 BP; 69 A; 100 C; 85 G; 105 T; 2 other;

Query Match      14.0%; Score 33.4; DB 21; Length 361;
Best Local Similarity 50.0%; Pred. No. 1;
Matches 82; Conservative 0; Mismatches 82; Indels 0; Gaps 0;

QY  52  TGGGGTGTGGGCTGGCCCTTGTCTCTCTTGACCCCTCTTGGCAGCTCACATGGAACAG 111
    |||||  |  |||||  |  |||||  |  |||||  |  |||||  |  |||||  |
Db  170  TGGGATCACTAAGAGATTCTTCTGCTGGGAACCTACGCTGGCCTGGGAATCAAGAA 229
    |||||  |  |||||  |  |||||  |  |||||  |  |||||  |  |||||  |
QY  112  GGCCGGTATGACTTTGCAACTGAAGTCTTTTCTGACAAATTCCTCCTATG 171
    |||||  |  |||||  |  |||||  |  |||||  |  |||||  |  |||||  |
Db  230  GACCGAGTCTTCTCTGTCGCCCGGCTGGAGTGGAGTGTGATCTGGCTCACACGCA 289
    |||||  |  |||||  |  |||||  |  |||||  |  |||||  |  |||||  |
QY  172  AGTCCAGCTTCTTGGAAATGTGTTGAAATTCGCTCTCTCTCC 215
    |||||  |  |||||  |  |||||  |  |||||  |  |||||  |  |||||  |
Db  290  ACCTCCACCTCCCGGTTTCAGATGATTCCTCTGCTCAGCCTCC 333
    |||||  |  |||||  |  |||||  |  |||||  |  |||||  |  |||||  |

RESULT 13
ABN83971/c
ID  ABN83971 standard; DNA; 6855 BP.
XX
AC  ABN83971;
```

```
XX
DT  06-SEP-2002 (first entry)
XX
DE  Human gene sequence #18.
XX
KW  Human; brain; tonsil; hippocampus; foetal brain; diagnosis; gene; ds.
XX
OS  Homo sapiens.
XX
FH  Key Location/Qualifiers
FT  CDS 4465..4695
FT     /*tag= a
XX
PN  WC200252005-A1.
XX
PD  04-JUL-2002.
XX
PF  20-DEC-2001; 2001WO-JP11217.
XX
PR  22-DEC-2000; 2000JP-0389742.
XX
PA  (KAZU-) KAZUSA DNA RES INST FOUND.
PA  (CELE-) CELESTAR LEXICO-SCI LTD.
XX
PI  Ohara O, Nagase T, Nakajima D;
XX  WPI; 2002-500762/53.
XX  P-PSDB; ABB97951.
XX
PT  Genes and their expression products cloned from human cDNA libraries
PT  for treatment and diagnosis of diseases associated with their
PT  expression -
XX
PS  Claim 1(a); Page 136-140; 238pp; Japanese.
XX
CC  The invention relates to DNA encoding polypeptides directly cloned from
CC  cDNA libraries originating in adult whole brain, human tonsil, human
CC  adult hippocampus and human foetal whole brain. Polypeptides and
CC  polynucleotides of the invention may be used in the investigation of
CC  differential expression of the DNA sequences in normal subjects and
CC  disease patients. They may also be used in the production of antibodies,
CC  oligonucleotide probes and DNA chips for diagnosis and identification
CC  of drugs for treatment of diseases with which the DNA sequences are
CC  associated. The sequences given in records ABN83954-ABN83984 represent
CC  human gene sequences of the invention.
XX
SQ  Sequence 6855 BP; 1752 A; 1535 C; 1489 G; 2079 T; 0 other;

Query Match      13.8%; Score 33; DB 24; Length 6855;
Best Local Similarity 55.3%; Pred. No. 4.1;
Matches 63; Conservative 0; Mismatches 51; Indels 0; Gaps 0;

QY  91  TTGGCAGCTCACATGGAACAGGCGGGTATGACTTCCAACTGAAGCTGAAGGAGTCTT 150
    |||||  |  |||||  |  |||||  |  |||||  |  |||||  |  |||||  |
Db  2684  TTCCCACTCCATCCGCCAGGTTTGTATAGACTTTTCAAAAGCAAGGTAGGTGTAAC 2625
    |||||  |  |||||  |  |||||  |  |||||  |  |||||  |  |||||  |
QY  151  TTCTGCAAAATTCCTCTATAGTCCAGCTTCTCTGGAATTCCTTGAANAATCTG 204
    |||||  |  |||||  |  |||||  |  |||||  |  |||||  |  |||||  |
Db  2624  TGTAGAAGAGTTCAATGTTATAAGTACCGCAACTTGTATTCTCTGAAGTCTGTG 2571
    |||||  |  |||||  |  |||||  |  |||||  |  |||||  |  |||||  |

RESULT 14
AAV28846
ID  AAV28846 standard; DNA; 1128 BP.
XX
AC  AAV28846;
XX
DT  03-AUG-1998 (first entry)
XX
DE  Mouse coxsackievirus and adenovirus receptor encoding DNA.
XX
KW  Mouse; coxsackievirus; adenovirus; receptor; CAR; cardiac infection;
KW  myocarditis; pericarditis; dilated cardiomyopathy; meningoencephalitis;
```


comprising amino acid residues 22val (V)-145V, 19Ser-145V, 17Tyr-145V or 1Met-145V of a sequence comprising 145 amino acids fully defined in the specification. The invention is useful for decreasing blood pressure, causing vascular permeability, binding heparin and inducing proliferation or mitogenesis in cells. Other uses of the invention include regulating organ development and regeneration and in pathological processes where therapeutic treatments or diagnostics are required, including cancer, vasculogenesis and angiogenesis, rheumatoid arthritis, diabetic retinopathy, ischaemic limb disease, vascular disease, myocardial infarction, atherosclerosis, haemangioma formation and treating inflammatory disorders including psoriasis. Antibodies of the invention are useful for modulating cardiovascular function and blood pressure, stimulating tissue development or repair, cellular differentiation or proliferation, treatment of full thickness skin wounds including ulcers and skin grafting, to promote vessel repair, and to stimulate haematopoiesis. Antibodies are also useful as anti-venom therapy for snake bite victims, and to diminish pro-fibrotic responses. The present nucleic acid sequence encodes the eastern cottonmouth snake zsnk1 protein of the invention.

Sequence 1251 BP; 298 A; 334 C; 325 G; 294 T; 0 other;

Query Match 13.3%; Score 31.8; DB 24; Length 1251;
 Best Local Similarity 56.1%; Pred. No. 5.2;
 Matches 60; Conservative 0; Mismatches 47; Indels 0; Gaps 0;
 QY 12 CTTTCAGTGTCTCCTCCATCCAGGAGGCGAGTGGCCACTATGGGCTCTGGGCTGCCCTT 71
 Db 165 CTTCTGAGCAGCTGTGAAGCCAGGAGGAGATAGGCCATGGCTGTACCTGTGGCAGTT 224
 QY 72 GTCTCTCTCTTGACCTCTCTTGGCAGCTCAGTGGAGAGGCGCGG 118
 Db 225 GCCATCTCTCTTGTGCATCCAGGCGTGGCCATCAGGAGCAGTGC AAG 271

Search completed: May 1, 2003, 03:07:47
 Job time : 176.211 secs

GenCore version 5.1.5
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OM nucleic - nucleic search, using sw model

Run on: May 1, 2003, 02:59:25 ; Search time 781.492 Seconds
(without alignments)
8900.373 Million cell updates/sec

Title: US-09-092-296-1
Perfect score: 239
Sequence: 1 GCCACCGGAGCTTCAGTGT.....CCCTTCAGGAGCACGCGTCA 239

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2054640 seqs, 14551402878 residues
Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

- 1: gb.ba.*
- 2: gb.htg.*
- 3: gb.in.*
- 4: gb.om.*
- 5: gb.ov.*
- 6: gb.pat.*
- 7: gb.ph.*
- 8: gb.pl.*
- 9: gb.pr.*
- 10: gb.ro.*
- 11: gb.sts.*
- 12: gb.sy.*
- 13: gb.un.*
- 14: gb.vi.*
- 15: en.ba.*
- 16: en.fun.*
- 17: en.hum.*
- 18: en.in.*
- 19: en.mu.*
- 20: en.om.*
- 21: en.or.*
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- 23: en.pat.*
- 24: en.ph.*
- 25: en.pl.*
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- 27: en.sts.*
- 28: en.un.*
- 29: en.vi.*
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- 31: en.htg_inv.*
- 32: en.htg_other.*
- 33: en.htg_mus.*
- 34: en.htg_pln.*
- 35: en.htg_rod.*
- 36: en.htg_man.*
- 37: en.htg_vit.*
- 38: en.sy.*
- 39: en.htgo_hum.*
- 40: en.htgo_mus.*
- 41: en.htgo_other.*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	227	95.0	422	6	AX092334	Sequence
2	227	95.0	422	6	AX376174	Sequence
3	227	95.0	422	6	AX403475	Sequence
4	225.4	94.3	484	9	AY102070	Homo sapi
5	119	49.8	624	6	AX472955	Sequence
6	113.4	47.4	47323	9	AC005937	Homo sapi
7	113.4	47.4	84474	9	AL662854	Human DNA
8	113.4	47.4	104154	2	AL773541	Homo sapi
9	113.4	47.4	156272	9	AL669830	Human DNA
10	113.4	47.4	178688	2	AL713893	Homo sapi
11	113.4	47.4	192650	9	AB023048	Homo sapi
12	113.4	47.4	200000	9	AP000511	Homo sapi
13	68	28.5	349980	6	AX344553	Sequence
14	68	28.5	349980	6	AX344554	Sequence
15	61.2	25.6	349980	6	AX344571	Sequence
16	44.6	18.7	175345	2	AC022301	Mus muscu
17	43.8	18.3	132977	2	RN510D20	Rattus no
18	43.8	18.3	337832	2	AC099175	Rattus no
19	38.2	16.0	130742	2	AP005653	Oryza sat
20	37.8	15.8	185154	2	AC127110	Rattus no
21	36	15.1	158406	2	AC105514	Rattus no
22	35.8	15.0	196840	9	AC104435	Homo sapi
23	35.8	15.0	203773	9	AC097369	Homo sapi
24	35.4	14.8	176994	2	AC118783	Rattus no
25	35.4	14.8	243644	2	AC097608	Rattus no
26	35	14.6	141272	9	AP001976	Homo sapi
27	35	14.6	154937	2	AP002382	Homo sapi
28	35	14.6	202995	2	AC019134	Homo sapi
29	34.8	14.6	188082	2	AC121784	Mus muscu
30	34.8	14.6	188406	2	AC079560	Mus muscu
31	34.8	14.6	197344	2	AC102613	Mus muscu
32	34.8	14.6	203155	2	AC079473	Mus muscu
33	34.8	14.6	292172	2	AC125207	Mus muscu
34	34.6	14.5	77691	9	AC120118	Homo sapi
35	34.6	14.5	100521	9	AC119397	Homo sapi
36	34.6	14.5	173126	9	AC008878	Homo sapi
37	34.4	14.4	2032	9	AK025566	Homo sapi
38	34.4	14.4	77322	9	HS0144C9	Human DNA
39	34.4	14.4	146399	9	AC025835	Homo sapi
40	34.4	14.4	172033	9	AL136131	Human DNA
41	34.4	14.4	177560	2	AC016695	Homo sapi
42	34.4	14.4	189623	2	AC018640	Homo sapi
43	34.4	14.4	193332	2	AL355349	Homo sapi
44	34.4	14.4	219428	9	AC078846	Homo sapi
45	34.4	14.4	333841	2	AL161641	Homo sapi

ALIGNMENTS

RESULT 1	AX092334	422 bp	DNA	linear	PAT 21-MAR-2001
LOCUS	AX092334	Sequence 65 from Patent WO0116318.			
DEFINITION	AX092334				
ACCESSION	AX092334.1	GI:13444481			
VERSION					
KEYWORDS	human.				
SOURCE	human sapiens				
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.				
REFERENCE	1 (bases 1 to 422)				
AUTHORS	Eaton,D.L., Filvaroff,E., Gerritsen,M.E., Goddard,A., Godowski,P.J., Grimaldi,C.J., Gurney,A.L., Watanabe,C.K. and Wood,W.I.				

TITLE Secreted and transmembrane polypeptides and nucleic acids encoding the same

JOURNAL Patent: WO 0116318-A 65 08-MAR-2001; Genentech, Inc. (US)

FEATURES Location/Qualifiers

1..422

/organism="Homo sapiens"

/db_xref="taxon:9606"

84 a 134 c 104 g 100 t

BASE COUNT

ORIGIN

Query Match 95.0%; Score 227; DB 6; Length 422;

Best Local Similarity 99.2%; Pred. No. 4.1e-61;

Matches 238; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

QY 1 GGCCACCGGACTTCAGTGTCTTCATCCAGGAGCGCAGTGGCCACATATGGGTCTG 60

|||||

Db 8 GGCCACCGGACTTCAGTGTCTTCATCCAGGAGCGCAGTGGCCACATATGGGTCTG 67

|||||

QY 61 GGCTGCCCTTGCTCCTCTTGACCTTCCTGGAGCTCACATGGAACAGGCCGGGTA 120

|||||

Db 68 GGCTGCCCTTGCTCCTCTTGACCTTCCTGGAGCTCACATGGAACAGGCCGGGTA 127

|||||

QY 121 TGACTTTGCAACTGAAGCTGAAGGAGTCTTTCTGACAAATTCCTCTATGATCCAGCT 180

|||||

Db 128 TGACTTTGCAACTGAAGCTGAAGGAGTCTTTCTGACAAATTCCTCTATGATCCAGCT 187

|||||

QY 181 TCCTGGAATTCCTTGAAAA-NFTCTGCTCCTCTCCATCCCTTCAGGAGCCAGCTCA 239

|||||

Db 188 TCCTGGAATTCCTTGAAAA-NFTCTGCTCCTCTCCATCCCTTCAGGAGCCAGCTCA 247

|||||

RESULT 2

AX376174

LOCUS AX376174 422 bp DNA linear PAT 01-MAR-2002

DEFINITION Sequence 241 from Patent WO0168848.

ACCESSION AX376174

VERSION AX376174.1 GI:19170479

KEYWORDS

SOURCE human.

ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.

AUTHORS Baker,K.P., Chen,J., Desnoyers,L., Goddard,A., Godowski,P.J., Gurney,A.L., Pan,J., Smith,V., Watanabe,C.K., Wood,W.I. and Zhang,Z.

TITLE Secreted and transmembrane polypeptides and nucleic acids encoding the same

JOURNAL Patent: WO 0168848-A 241 20-SEP-2001; Genentech, Inc. (US)

FEATURES Location/Qualifiers

1..422

/organism="Homo sapiens"

/db_xref="taxon:9606"

84 a 134 c 104 g 100 t

BASE COUNT

ORIGIN

Query Match 95.0%; Score 227; DB 6; Length 422;

Best Local Similarity 99.2%; Pred. No. 4.1e-61;

Matches 238; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

QY 1 GGCCACCGGACTTCAGTGTCTTCATCCAGGAGCGCAGTGGCCACATATGGGTCTG 60

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Db 8 GGCCACCGGACTTCAGTGTCTTCATCCAGGAGCGCAGTGGCCACATATGGGTCTG 67

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QY 61 GGCTGCCCTTGCTCCTCTTGACCTTCCTGGAGCTCACATGGAACAGGCCGGGTA 120

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Db 68 GGCTGCCCTTGCTCCTCTTGACCTTCCTGGAGCTCACATGGAACAGGCCGGGTA 127

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QY 121 TGACTTTGCAACTGAAGCTGAAGGAGTCTTTCTGACAAATTCCTCTATGATCCAGCT 180

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|||||

Db 188 TCCTGGAATTCCTTGAAAA-NFTCTGCTCCTCTCCATCCCTTCAGGAGCCAGCTCA 247

|||||

RESULT 3

AX403475

LOCUS AX403475 422 bp DNA linear PAT 14-JUN-2002

DEFINITION Sequence 362 from Patent WO0073454.

ACCESSION AX403475

VERSION AX403475.1 GI:21436973

KEYWORDS

SOURCE human.

ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.

AUTHORS Ashkenazi,A.J., Baker,K.P., Botstein,D., Desnoyers,L., Eaton,D., Ferrara,N., Gerber,H., Gerritsen,M., Goddard,A., Godowski,P., Grimaldi,C.J., Gurney,A.L., Kijavini,I., Napier,M.A., Pan,J., Paoletti,N.F., Roy,W., Stewart,T.A., Tumas,D., Watanabe,C.K., Williams,P., Wood,W.I. and Zhang,Z.

TITLE Secreted and transmembrane polypeptides and nucleic acids encoding the same

JOURNAL Patent: WO 0073454-A 362 07-DEC-2000; Genentech Inc. (US)

FEATURES Location/Qualifiers

1..422

/organism="Homo sapiens"

/db_xref="taxon:9606"

84 a 134 c 104 g 100 t

BASE COUNT

ORIGIN

Query Match 95.0%; Score 227; DB 6; Length 422;

Best Local Similarity 99.2%; Pred. No. 4.1e-61;

Matches 238; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

QY 1 GGCCACCGGACTTCAGTGTCTTCATCCAGGAGCGCAGTGGCCACATATGGGTCTG 60

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Db 8 GGCCACCGGACTTCAGTGTCTTCATCCAGGAGCGCAGTGGCCACATATGGGTCTG 67

|||||

QY 61 GGCTGCCCTTGCTCCTCTTGACCTTCCTGGAGCTCACATGGAACAGGCCGGGTA 120

|||||

Db 68 GGCTGCCCTTGCTCCTCTTGACCTTCCTGGAGCTCACATGGAACAGGCCGGGTA 127

|||||

QY 121 TGACTTTGCAACTGAAGCTGAAGGAGTCTTTCTGACAAATTCCTCTATGATCCAGCT 180

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Db 128 TGACTTTGCAACTGAAGCTGAAGGAGTCTTTCTGACAAATTCCTCTATGATCCAGCT 187

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QY 181 TCCTGGAATTCCTTGAAAA-NFTCTGCTCCTCTCCATCCCTTCAGGAGCCAGCTCA 239

|||||

Db 188 TCCTGGAATTCCTTGAAAA-NFTCTGCTCCTCTCCATCCCTTCAGGAGCCAGCTCA 247

|||||

RESULT 4

AX102070

LOCUS AX102070 484 bp mRNA linear PRI 18-JUN-2002

DEFINITION Homo sapiens surfactant associated protein G mRNA, partial sequence.

ACCESSION AX102070

VERSION AX102070.1 GI:21464498

KEYWORDS

SOURCE human.

ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.

AUTHORS Walker,M.G. and Spiro,P.

TITLE Genes co-expressed with pulmonary surfactants

JOURNAL Unpublished

REFERENCE 2 (bases 1 to 484)

Walker,M.G. and Spiro,P.

TITLE Direct Submission
JOURNAL Submitted (07-MAY-2002) Incyte Genomics, 1475 Flamingo Way,
Sunnyvale, CA 94087-3405, USA
FEATURES
source Location/Qualifiers
1..484
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="236582"
gene <1..>484
/gene="surfactant associated protein G"
/note="SFTPG"
BASE COUNT 124 a 149 c 110 g 101 t
ORIGIN
Query Match 94.3% Score 225.4; DB 9; Length 484;
Best Local Similarity 98.8%; Pred. No. 1.3e-60;
Matches 237; Conservative 0; Mismatches 2; Indels 1; Gaps 1;
QY 1 GCCACCGGACTTCAGTGTCTCTCCATCCAGGAGCGAGTGGCCACTATGGGTCTG 60
Db 5 GCCACCGGACTTCAGTGTCTCTCCATCCAGGAGCGAGTGGCCACTATGGGTCTG 64
QY 61 GCGTGGCCCTTGTCTCTCTCTTACCTCTCTTGGCAGCTCACATGGAACAGGCGCGGTA 120
Db 65 GCGTGGCCCTTGTCTCTCTTACCTCTCTTGGCAGCTCACATGGAACAGGCGCGGTA 124
QY 121 TGACTTTGCACTGAAGTGAAGAGTCTTTCTGACAAATTCCTCTATGAGTCCAGCT 180
Db 125 TGACTTTGCACTGAAGTGAAGAGTCTTTCTGACAAATTCCTCTATGAGTCCAGCT 184
QY 181 TCCTGGAATGCTTGAAA-NMTCGTGCTCTCTCCATCTCCATCTCCCTTCAGGACACGCTCA 239
Db 185 TCCTGGAATGCTTGAAAAGCTGTGCTCTCTCTCCATCTCCCTTCAGGACACGCTCA 244
RESULT 5
LOCUS AX472955 624 bp DNA linear PAT 09-AUG-2002
DEFINITION Sequence 4 from Patent WO0218576.
ACCESSION AX472955
VERSION AX472955.1 GI:22207742
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Chen,S.Y., Macina,R.A., Sun,Y. and Recipon,H.
TITLE Compositions and methods relating to lung specific genes
JOURNAL Patent: WO 0218576-A 4 07-MAR-2002;
Diadexus, Inc. (US)
FEATURES
source Location/Qualifiers
1..624
/organism="Homo sapiens"
/db_xref="taxon:9606"
BASE COUNT 129 a 175 c 182 g 138 t
ORIGIN
Query Match 49.8% Score 119; DB 6; Length 624;
Best Local Similarity 98.5%; Pred. No. 8.9e-27;
Matches 130; Conservative 0; Mismatches 1; Indels 1; Gaps 1;
QY 109 CAGGGCGGGTATGACTTTGCACTGAAGCTGAAGGAGTCTTTTCTGACAAATTCCTCCT 168
Db 314 CAGGGCGGGTATGACTTTGCACTGAAGCTGAAGGAGTCTTTTCTGACAAATTCCTCCT 373
QY 169 ATGAGTCCAGCTTCCTGCAATGCTGAAA-NMTCGTGCTCTCTCCATCTCCCTTCAG 227
Db 374 ATGAGTCCAGCTTCCTGCAATGCTGAAAAGCTCTGCTCTCTCTCCATCTCCCTTCAG 433
QY 228 GGACCAGCGTCA 239
Db 434 GGACCAGCGTCA 445

RESULT 6
LOCUS AC005937 47323 bp DNA linear PRI 05-NOV-1998
DEFINITION Homo sapiens clone UWGC:370M23.002 from 6p21, complete sequence.
AC005937
VERSION AC005937.1 GI:3845393
KEYWORDS
SOURCE Homo sapiens.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 47323)
AUTHORS Janer,M., Guillaudeau,T., Vu,Q., Kutayavin,T., Harter,H. and
Geraghty,D.E.
TITLE Large scale sequence analysis of the human MHC class I region
JOURNAL Unpublished (1998)
REMARK Fred Hutchinson Cancer Research Center
The Clinical Research Division
1100 Fairview Ave. N., P.O. Box 19024
Seattle, WA 98109-1024
2 (bases 1 to 47323)
AUTHORS Geraghty,D.E. and Olson,M.V.
TITLE Direct Submission
JOURNAL Submitted (05-NOV-1998) Human Genome Center, University of
Washington, Box 352145, Seattle, WA 98195, USA
REMARK University of Washington Human Genome Center
Box 352145 Seattle, WA 98195
Contact: Daniel E. Geraghty (geraghty@fhcrc.org)
Overlapping Sequences:
5': UWGC:370M23.013 (Genbank Accession: AC005530)
3': UWGC:y67c112 (Genbank Accession: AC004211)

Sequence Quality Assessment:
This entry has been annotated with sequence quality
estimates computed by the Phrap assembly program.
All manually edited bases have been reduced to quality zero.
Quality levels above 40 are expected to have less than
1 error in 10,000 bp.
Base-by-base quality values are not generally visible from the
Genbank flat file format but are available as part
of this entry's ASN.1 file.
Double stranded (DS) coverage: 75.5%
DS or two chemistry coverage: 98.9%
Single stranded regions: 3

Sequence Validation:
This sequence has been validated by Multiple Complete Digest
Mapping. Comparison of the experimentally derived map digest
fragments with sequence-predicted fragments is given below.
Small fragments below a variable cutoff (approximately 400-600bp)
are not mapped and hence do not appear in the table. There are no
significant remaining discrepancies between the experimental and
predicted values. Uniquely ordered fragment groups are separated
by dashed lines.
BgIII HindIII NsiI
Map Seq Map Seq Map Seq
1069.11 1050.00 889.55 866.00 30541.40 30653.00
2020.67 20855.00 1050.18 1015.00 3279.08 3231.00
2171.50 2147.00 7268.78 7196.00
2560.20 2531.00 10085.80 9992.00
4335.42 4269.00 11212.78 11131.00
2698.62 2628.00
1927.50 1887.00

BASE COUNT 19363 a 22004 c 21777 g 21330 t
 ORIGIN

Query Match 47.4%; Score 113.4; DB 9; Length 84474;
 Best Local Similarity 95.1%; Pred. No. 8e-25;
 Matches 117; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 GGCACCGGACTTCAGTGTCTCTCCATCCAGGAGCGGACGATGGGCTCTG 60
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 Db 56564 GGCACCGGACTTCAGTGTCTCTCCATCCAGGAGCGGACGATGGGCTCTG 60
 |||||

QY 61 GGCTGCCCTTGTCTCTCTGACCCCTCTTGGACGCTCACATGGACAGGCGGGTA 120
 |||||
 Db 56504 GGCTGCCCTTGTCTCTCTGACCCCTCTTGGACGCTCACATGGACAGGCTGAGGCT 56445
 |||||

QY 121 TGA 123
 ||
 Db 56444 AGA 56442

RESULT 8
 AL773541
 LOCUS Human DNA sequence from clone Xxbac-11J22, *** SEQUENCING IN
 DEFINITION complete sequence.
 ACCESSION AL773541
 VERSION AL773541.4 GI:22204637
 KEYWORDS HTG; HTGS_PHASE2; HTGS_ACTIVEFIN; HTGS_DRAFT; HTGS_FULLTOP.
 SOURCE human.

ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 104154)
 AUTHORS Almeida, J.
 TITLE Direct Submission
 JOURNAL Submitted (31-JUL-2002) Wellcome Trust Sanger Institute, Hinxton,
 Cambridgeshire, CB10 1SA, UK. E-mail enquiries:
 humquers@sanger.ac.uk
 COMMENT On Aug 11, 2002 this sequence version replaced gi:21621737.
 ----- Genome Center
 Center: Wellcome Trust Sanger Institute
 Center code: SC
 Web site: http://www.sanger.ac.uk
 Contact: humquers@sanger.ac.uk
 ----- Project Information
 Center project name: bQb1J22
 ----- Summary Statistics
 Assembly program: XGAP4; version 4.5
 Chemistry: Dye-terminator; 100% of reads
 Consensus quality: 104135 bases at least Q40
 Consensus quality: 104142 bases at least Q30
 Consensus quality: 104145 bases at least Q20
 Insert size: 104154; sum-of-contigs
 Insert size: 110727; 1.1% error; agarose-
 Quality coverage: 19.52x in Q20 bases; sum-of-contigs Quality
 coverage: 18.64x in Q20 bases; agarose-

* NOTE: This is a 'working draft' sequence.
 * This sequence will be replaced
 * by the finished sequence as soon as it is available and
 * the accession number will be preserved.

FEATURES
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 /db_xref="taxon:9606"
 /chromosome="6"
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 /clone.lib="DNA-arts-BAC.1-QBL.1"
 misc_feature 1..104154
 /note="assembly_fragment:00090"
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 ORIGIN

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 Best Local Similarity 95.1%; Pred. No. 8.2e-25;
 Matches 117; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 GGCCACCGGACTTCAGTGTCTCTCCATCCAGGAGCGGACGATGGGCTCTG 60
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 Db 67498 GGCCACCGGACTTCAGTGTCTCTCCATCCAGGAGCGGACGATGGGCTCTG 67557
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QY 61 GGCTGCCCTTGTCTCTCTGACCCCTCTTGGACGCTCACATGGACAGGCGGGTA 120
 |||||
 Db 67558 GGCTGCCCTTGTCTCTCTGACCCCTCTTGGACGCTCACATGGACAGGCTGAGGCT 67617
 |||||

QY 121 TGA 123
 ||
 Db 67618 AGA 67620

RESULT 9
 AL669830/c
 LOCUS Human DNA sequence from clone Xxbac-118E17 on chromosome 6,
 DEFINITION complete sequence.
 ACCESSION AL669830
 VERSION AL669830.9 GI:20135762
 KEYWORDS HTG.
 SOURCE human.

ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1
 AUTHORS Johnson, C.
 TITLE Direct Submission
 JOURNAL Submitted (23-APR-2002) Wellcome Trust Sanger Institute, Hinxton,
 Cambridgeshire, CB10 1SA, UK. E-mail enquiries:
 humquers@sanger.ac.uk
 COMMENT On Apr 10, 2002 this sequence version replaced gi:20067510.
 During sequence assembly data is compared from overlapping clones.
 Where differences are found these are annotated as variations
 together with a note of the overlapping clone name. Note that the
 variation annotation may not be found in the sequence submission
 corresponding to the overlapping clone, as we submit sequences with
 only a small overlap as described above.

This sequence was finished as follows unless otherwise noted: all
 regions were either double-stranded or sequenced with an alternate
 chemistry or covered by high quality data (i.e., phred quality >= 30);
 an attempt was made to resolve all sequencing problems, such
 as compressions and repeats; all regions were covered by at least
 one plasmid subclone or more than one M13 subclone; and the
 assembly was confirmed by restriction digest. The following
 abbreviations are used to associate primary accession numbers given
 in the feature table with their source databases: Em: EMBL; Sw: SWISSPROT; Tr: TREMBL; Wp: WORMPEP; Information on the WORMPEP
 database can be found at
 http://www.sanger.ac.uk/Projects/C_elegans/wormpep
 Xxbac-118E17 is
 from a CHORI-501 human bac - PGF cell line library VECTOR:
 PTARBAC2.1

This sequence was generated from part of bacterial clone contigs
 constructed by the MHC Haplotype Consortium and collaborators.
 Further information can be found at
 http://www.sanger.ac.uk/HGP/Chr6/MHC.

FEATURES
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 /db_xref="taxon:9606"
 /chromosome="6"
 /clone="XXbac-118E17"
 /clone.lib="CHORI-501"
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 ORIGIN

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 Best Local Similarity 95.1%; Pred. No. 8.5e-25;
 Matches 117; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

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QY 1 GGCACCGGAGTCTAGTCTCTCCATCCAGGAGCGCAGTGGCCACTATGGGGTCTG 60
Db 25906 GGCACCGGAGTCTAGTCTCTCCATCCAGGAGCGCAGTGGCCACTATGGGGTCTG 25847

QY 61 GCGTCCCTTGTCTCCCTCTGACCTCTCTGGCAGCTCACATGGAACAGGCCGGCTA 120
Db 25846 GCGTCCCTTGTCTCCCTCTGACCTCTCTGGCAGCTCACATGGAACAGGTGAGGGCT 25787

QY 121 TGA 123
Db 25786 AGA 25784

RESULT 10
LOCUS AL713893 178688 bp DNA linear HTG 28-MAR-2002
DEFINITION Homo sapiens chromosome 6 clone XXbac-307M4, *** SEQUENCING IN
PROGRESS ***, 6 unordered pieces.
ACCESSION AL713893
VERSION AL713893.5 GI:19847952
KEYWORDS HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_FULLTOP.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1
Sims.S.
Direct Submission
Submitted (26-MAR-2002) Wellcome Trust Sanger Institute, Hinxton,
Cambridgeshire, CB10 1SA, UK. E-mail enquiries:
humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
On Mar 29, 2002 this sequence version replaced gi:19772907.
----- Genome Center
Center: Wellcome Trust Sanger Institute
Center code: SC
Web site: http://www.sanger.ac.uk
Contact: humquery@sanger.ac.uk
----- Project Information
Center project name: bpg307M4
----- Summary Statistics
Assembly program: XGAP4; version 4.5
Chemistry: Dye-terminator Big Dye; 100% of reads
Consensus quality: 177277 bases at least Q40
Consensus quality: 177708 bases at least Q30
Consensus quality: 177956 bases at least Q20
Insert size: 178188; sum-of-contigs
Insert size: 192613; 0.9% error; agarose-fp
Quality coverage: 8.57x in Q20 bases; sum-of-contigs Quality
coverage: 8.00x in Q20 bases; agarose-fp
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* NOTE: This is a 'working draft' sequence. It currently
* consists of 6 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
1 37410: contig of 37410 bp in length
37411 37510: gap of 100 bp
37511 82372: contig of 44862 bp in length
82373 82472: gap of 100 bp
82473 142457: contig of 59985 bp in length
142458 142557: gap of 100 bp
142558 152855: contig of 10302 bp in length
152860 152959: gap of 100 bp
152960 172054: contig of 19095 bp in length
172055 172154: gap of 100 bp
172155 178688: contig of 6534 bp in length.
Location/Qualifiers
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/organism="Homo sapiens"

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/chromosome="6"
/clone="XXbac-307M4"
/clone.lib="CHORI-501"

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    fragment_chain:1"
    82473..142457
    /note="assembly_fragment:03231"
    fragment_chain:1"
    142558..152859
    /note="assembly_fragment:03008"
    fragment_chain:1"
    152960..172054
    /note="assembly_fragment:04309"
    fragment_chain:1"
    172155..178688
    /note="assembly_fragment:03507"
    fragment_chain:1"
    clone_end:17
    vector_side:right"
BASE COUNT 46316 a 40707 c 42166 g 48998 t 501 others
ORIGIN

Query Match 47.4%; Score 113.4; DB 2; Length 178688;
Best Local Similarity 95.1%; Pred No. 8.6e-25;
Matches 117; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 GGCACCGGAGTCTAGTCTCTCCATCCAGGAGCGCAGTGGCCACTATGGGGTCTG 60
Db 173447 GGCACCGGAGTCTAGTCTCTCCATCCAGGAGCGCAGTGGGGTCTG 173506

QY 61 GCGTCCCTTGTCTCTCTTGACCTCTCTGGCAGCTCACATGGAACAGGCCGGSTA 120
Db 173507 GCGTCCCTTGTCTCTCTTGACCTCTCTGGCAGCTCACATGGAACAGGTGAGGGCT 173566

QY 121 TGA 123
Db 173567 AGA 173569

RESULT 11
LOCUS AB023048 192650 bp DNA linear PRI 20-NOV-1999
DEFINITION Homo sapiens genomic DNA, chromosome 6p21.3, HLA class I region,
clone:53L9, complete sequence.
ACCESSION AB023048
VERSION AB023048.1 GI:5672603
KEYWORDS HTG.
SOURCE Homo sapiens cell_line:978SK DNA, clone:53L9.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (sites)
Shiina,T., Tamiya,G., Oka,A., Takishima,N., Yamagata,T.,
Kikkawa,E., Iwata,K., Tomizawa,M., Okuaki,N., Kuwano,Y.,
Watanabe,K., Fukuzumi,Y., Itakura,S., Sugawara,C., Ono,A.,
Yamazaki,M., Tashiro,H., Ando,A., Ikemura,T., Soeda,E., Kimura,M.,
Bahram,S. and Inoko,H.
Molecular dynamics of MHC genesis unraveled by sequence analysis of
the 1,796,938-bp HLA class I region
Proc. Natl. Acad. Sci. U.S.A. 96 (23), 13282-13287 (1999)
20027539
2 (bases 1 to 192650)
Shiina,T. and Takishima,N.
Direct Submission
Submitted (29-JAN-1999) Takashi Shiina, Tokai University School of
Medicine, Department of Molecular Life Science 2; Bohseidai,
Isehara, Kanagawa 259-1193, Japan
(E-mail:tshiina@is.icc.u-tokai.ac.jp, Tel:81-463-93-1121,

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FEATURES
  source
    Fax:81-463-94-8884)
    Location/Qualifiers
      1..192650
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        /db_xref="taxon:9606"
        /chromosome="6"
        /map="6p21.3"
        /clone="5319"
        /cell_line="978SK"
BASE COUNT 49862 a 44743 c 45833 g 52212 t
ORIGIN
Query Match 47.4%; Score 113.4; DB 9; Length 192650;
Best Local Similarity 95.1%; Pred. No. 8.6e-25;
Matches 117; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
QY 1 GGCACCGGACTTCAGTGTCTCTCCATCCAGGAGCGAGTGGCCACTATGGGGTCTG 50
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Db 177631 GGCACCGGACTTCAGTGTCTCTCCATCCAGGAGCGAGTGGCCACTATGGGGTCTG 177690
QY 61 GGCTGCCCTTGTCTCTTGTGACCTCTCTTGCGAGCTCAGTGAACAGGCGCGGTA 120
|||||
Db 177691 GGCTGCCCTTGTCTCTTGTGACCTCTCTTGCGAGCTCAGTGAACAGTGGGGCT 177750
QY 121 TGA 123
||
Db 177751 AGA 177753

RESULT 12
APO00511
LOCUS APO00511 200000 bp DNA linear PRI 22-AUG-2001
DEFINITION Homo sapiens genomic DNA, chromosome 6p21.3, HLA Class I region,
section 10/20
ACCESSION APO00511 BA0000025
VERSION APO00511.1 GI:5926698
KEYWORDS
SOURCE
  ORGANISM
    Homo sapiens DNA.
    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
    Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
  1
    Shilna.S., Tamiya.G., Oka.A. and Inoko.H.
  Homo sapiens 2,229,817bp genomic DNA of 6p21.3 HLA class I region
  Published Only in Database (1999)
  2 (bases 1 to 200000)
  Hirakawa,M., Yamaguchi,H., Imai,K. and Shimada,J.
  Submitted (21-SEP-1999) Mika Hirakawa, Japan Science and Technology
  Corporation (JST), Advanced Databases Department; 5-3, Yonbancho,
  Chiyoda-ku, Tokyo 102-0081, Japan (E-mail:mika@tokyo.jst.go.jp,
  URL:http://www-alis.tokyo.jst.go.jp/, Tel:81-3-5214-8491,
  Fax:81-3-5214-8470)
  This sequence is conducted by Tokai University as a JST sequencing
  Team.
  Principal Investigator: Hidetoshi Inoko Ph.D
  Phone:+81-463-93-1121, Fax:+81-463-94-8884,
  The sequence is submitted by Human Genome Sequencing in ALIS
  project of JST
  Japan Science and Technology Corporation (JST)
  5-3, Yonbancho, Chiyoda-ku, Tokyo, 102-0081 Japan
  For further information about this sequences, please visit our
  sequence archive Web site (http://www-alis.tokyo.jst.go.jp/HGS/top.
  html) or send email to webmaster@www-alis.tokyo.jst.go.jp.
  Location/Qualifiers
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      /chromosome="6"
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        /note="SHGC-12985;The location is between each flanking
FEATURES
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    130596..130664,130826..130937,131154..131242,
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    HFVGVSPSAVSDIAQLISQALGKMSSTFEPGPGCITSAGFQFLLDITPAQLWFMLO
    LYQTAQSRGMDLVEILSFQLSFSTLGDYI SVEGNSDLSLLNQLHRLFGVLVFKRK
    KSRVYPTLAI NLSGVSAGGTVHPGFI VVETNRYLAYT ESELQALIALSEM
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14493. .144711,144949. .145076,145225. .145469,
146576. .146886,147419. .147584,148667. .148818,
148927. .149022,149548. .149794,149902. .150089,
150614. .150712,150972. .151119,152662. .152890,
153082. .153184,153278. .153362)
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141936. .142934
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/number=17
142030. .142159
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/note="SHGC-16870;the location is between each flanking
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/db_xref="GDB:741215"
complement(142085. .142322)
/note="RH18132;The location is between each flanking site
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complement(142479. .142740)
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/note="SHGC-10808;The location is between each flanking
site of PCR primers."
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145225. .145469,146576. .146686,147419. .147584,
148667. .148818,148927. .149022,149548. .149794,
149902. .150089,150614. .150712,150972. .151119,
152662. .152890,153082. .153184,153278. .153362))
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145225. .145469,146576. .146686,147419. .147584,
148667. .148818,148927. .149022,149548. .149794,
149902. .150089,150614. .150712,150972. .151119,
152662. .152890,153082. .153184,153278. .153362))
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ALRVFPRADRYMSVCLVELYGLWRDGLSYAPYQQTWLYSEAYLINDSTDGH
TVGGLQGLGLQADGVGLDDERKSELRWGDIYGVGNHSFSSGIVEMEFEDR
LAPGQVYNNHHTLGARLPGVECFRRGPPAMAEPEPRNGLNGLPDPRARV
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144493. .144711
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144949. .145076
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145225. .145469
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Best Local Similarity 95.1%; Pred. No. 8.6e-25;
Matches 117; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

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Db 109958 GGGCACCGGGACTTCAGTGTCTCTCCATCCAGGAGGCGAGTGGCCACTATATGGGTCGTG 110017

QY 61 GGCTGGCCCTTGCTCTCTCTGACCTCTGCGAGCTCAGTCAGACGAGCGCGGTA 120
Db 110018 GGCTGGCCCTTGCTCTCTCTGACCTCTGCGAGCTCAGTCAGACGAGCGCGGTA 110017

QY 121 TGA 123
Db 110078 AGA 110080

RESULT 13
AX344553/c
LOCUS AX344553 349980 bp DNA linear PAT 01-FEB-2002
DEFINITION Sequence 4 from Patent WO0200932.
ACCESSION AX344553
VERSION AX344553.1 GI:18492439
KEYWORDS synthetic construct.
SOURCE synthetic construct.
ORGANISM synthetic construct.
artificial sequences.
REFERENCE 1
AUTHORS Olek,A., Piepenbrock,C. and Berlin,K.
TITLE Diagnosis of known genetic parameters within the mhc
JOURNAL Patent: WO 0200932-A 4 03-JAN-2002;
Epigenomics AG (DE)
FEATURES
Source
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Location/Qualifiers
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/db_xref="taxon:32630"
/note="chemically treated genomic DNA (Homo sapiens)-Original length of seq 1: 3.673778 <223>-split as follows.-seq 01 0.000.001 TO 0.349.980-seq 02 0.300.001 649.980-seq 03 600.001 949.980-seq 04 900.001 1.249.980-seq 05 1.200.001 1.549.980-seq 06 1.500.001 1.849.980-seq 07 1.800.001 2.149.980-seq 08 2.100.001 2.449.980-seq 09 2.400.001 2.749.980-seq 10 2.700.001 3.049.980-seq 11 3.000.001 3.349.980-seq 12 3.300.001 3.649.980-seq 13 3.600.001 3.673.778 <223>-Original length of seq 2: 3.673778 <223>-split as follows.-seq 14 0.000.001 TO 0.349.980-seq 15 0.300.001 649.980-seq 16 600.001 949.980-seq 17 900.001 1.249.980-seq 18 1.200.001 1.549.980-seq 19 1.500.001 1.849.980-seq 20 1.800.001 2.149.980-seq 21 2.100.001 2.449.980-seq 22 2.400.001 2.749.980-seq 23 2.700.001 3.049.980-seq 24 3.000.001 3.349.980-seq 25 3.300.001 3.649.980-seq 26 3.600.001 3.673.778"
BASE COUNT 86882 a 5859 c 85073 g 172166 t
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RESULT 14
AX344554/c
LOCUS AX344554 349980 bp DNA linear PAT 01-FEB-2002
DEFINITION Sequence 5 from Patent WO0200932.
ACCESSION AX344554
VERSION AX344554.1 GI:18492440
KEYWORDS
SOURCE synthetic construct.
ORGANISM synthetic construct.
artificial sequences.
REFERENCE
1
AUTHORS Olek, A., Piepenbrock, C. and Berlin, K.
TITLE Diagnosis of known genetic parameters within the mhc
JOURNAL Patent: WO 0200932-A 5 03-JAN-2002;
Epigenomics AG (DE)
FEATURES
Location/Qualifiers
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/organism="synthetic construct"
/db_xref="taxon:32630"
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BASE COUNT 92349 a 5068 c 82248 g 170315 t
ORIGIN

Query Match 28.5%; Score 68; DB 6; Length 349980;
Best Local Similarity 76.9%; Pred. No. 2.4e-10;
Matches 83; Conservative 0; Mismatches 25; Indels 0; Gaps 0;

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RESULT 15
AX344571
LOCUS AX344571 349980 bp DNA linear PAT 01-FEB-2002
DEFINITION Sequence 22 from Patent WO0200932.
ACCESSION AX344571
VERSION AX344571.1 GI:18492457
KEYWORDS
SOURCE synthetic construct.
ORGANISM synthetic construct.
artificial sequences.
REFERENCE
1
AUTHORS Olek, A., Piepenbrock, C. and Berlin, K.
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TITLE Diagnosis of known genetic parameters within the mhc
JOURNAL Patent: WO 0200932-A 22 03-JAN-2002;
Epigenomics AG (DE)
FEATURES
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BASE COUNT 91992 a 5703 c 86514 g 165771 t
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OY 110 AGGGCCGGTATGACCTTTCACACTGAAGGAGTCTTTCTGACAAATTCCTCCTA 169
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Db 54267 AGGGTCGGTATGATTTTCTTAATTGAAGTTGAAGGAGTTTTTTTGTATAATTTTTTTA 54326
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